



**Decision support tool for aquaculture-based
fisheries enhancement**

Manual

BETA RELEASE FOR USER TESTING

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The **EnhanceFish** software:

Medley, P.A.H & Lorenzen, K. (2006) **EnhanceFish**: A decision support tool for aquaculture-based fisheries enhancement. Software package. London: Imperial College.

For the scientific basis of the **EnhanceFish** model, please refer to:

Lorenzen, K. (2005) Population dynamics and potential of fisheries stock enhancement: practical theory for assessment and policy analysis. *Philosophical Transactions of the Royal Society B*. 360: 171-189.

The **EnhanceFish** decision tool and all related documents are available from www.aquaticresources.org/enhancefish.

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Summary

- (1) **EnhanceFish** is a decision support tool for the analysis of aquaculture-based fisheries enhancements. **EnhanceFish** can be used to assess quantitatively the impacts of fisheries enhancement on yield, abundance and structure of the natural stock, and economic performance indicators of the fishery. **EnhanceFish** thus allows to evaluate enhancement approaches relative to other measures such as effort control.
- (2) At the heart of **EnhanceFish** is a mathematical population model that predicts fisheries catch and other biological and production attributes for different management controls such as stocking density and fishing effort.
- (3) The **EnhanceFish** model is a dynamic pool fisheries model designed specifically to allow the modelling of enhancements. It has been extended over conventional dynamic pool models by (a) making mortality size-dependent throughout the lifecycle, (b) incorporating regulation in the recruited stock through density-dependent growth, (c) unpacking the stock-recruitment relationship to describe survival of hatchery fish released at any pre-recruit stage, and (d) separating the population into components of wild type, stocked hatchery type, and naturally produced hatchery type fish.
- (4) Input data required for **EnhanceFish** analyses may be obtained from stock assessments, release experiments, and comparative studies. Comparative data make it possible to define likely ranges for key parameters even where fishery-specific data are very limited. **EnhanceFish** may thus be used in all stages of an enhancement programme, from initial appraisals to the optimization of operational enhancements.
- (5) The **EnhanceFish** tool may be used in conjunction with the **EnhanceFish** guide, a framework for the integrated assessment and development of enhancement systems.

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1. Introduction

1.1 Purpose and structure of this document

EnhanceFish is a computerized decision support tool for the analysis of aquaculture-based fisheries enhancements. The purpose of this document (the **EnhanceFish** manual) is to guide aquatic resource management professionals in the use of the **EnhanceFish** decision tool.

The manual consists of five main parts. The introduction (Chapter 1) provides general background on **EnhanceFish** and its use. The scientific background to **EnhanceFish** is described briefly in Chapter 2. A more in-depth review may be found in Lorenzen (2005), and we strongly recommend that you read this paper in addition to the manual. Chapter 3 is a step-by-step guide and reference to running **EnhanceFish**. Chapter 4 sets out how to define, conduct and interpret **EnhanceFish** analyses in different management situations. It also provides guidance on setting up models in data-poor situations, and includes several worked examples. **EnhanceFish** is supplied with a spreadsheet-based tool for analysing release experiments, which is described in Chapter 5.

1.2 Aquaculture-based fisheries enhancement

Aquaculture-based fisheries enhancement is the use of cultured fish or invertebrates to enhance fisheries. Aquaculture-based fisheries are a diverse family of approaches that differ in their objectives, technologies, management practices, and outcomes. However, three main types of aquaculture-based enhancements may be distinguished according to technical criteria:

- **Culture-based fisheries** where catches of the target species are based entirely on stocking, with no or very little natural recruitment
- **Stock enhancement**, where catches of the target species are based on a combination of stocked and naturally recruited fish
- **Restocking or stock rebuilding**, where stocking is carried out as a temporary measure aimed at rebuilding a depleted stock

All of these approaches may be used in the pursuit of a variety of objectives such as producing food, increasing the income of fishers, or restoring a population.

Aquaculture-based enhancements are widespread in inland and increasingly, coastal fisheries. Whilst there are good examples of enhancements that are technically effective, economically beneficial and environmentally sound, many enhancements perform poorly in some or all these respects. Problems that may be associated with enhancements include:

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- Lack of ecological-technical effectiveness: enhancement has no effect on stock abundance and fisheries yield;
- Detrimental ecological and genetic impacts on wild fish stocks arising from stocking and harvesting of cultured fish;
- Poor economic performance: low or negative economic returns or contributions to resource user livelihoods;
- Distributional problems and conflicts: benefits from enhancement may not be shared equitably by different resource users, and this may lead to conflicts;
- Low institutional sustainability: difficulties in developing and maintaining rules and regulations required to make the enhancement “work”, and compliance with them.

Such problems can often be alleviated by better management of the enhancement system or its components (e.g. seed production technique, harvesting regime etc.). In other cases the natural or social environment, or technical constraints may make it impossible to develop beneficial enhancements. The purpose of the ***EnhanceFish*** toolkit is to promote better management of aquaculture-based fisheries enhancements.

Readers unfamiliar with aquaculture-based enhancements and related management issues are strongly recommended to read some of the recent reviews on the topic, such as Cowx (1994), Blankenship & Leber (1995), Munro & Bell (1997), Travis et al. (1998), Welcomme & Bartley (1998), Waples (1999), Leber (2001), Lorenzen et al. (2001), Bell et al. (2005), Lorenzen (2005), and the ***EnhanceFish*** Guide.

1.3 The EnhanceFish tool

1.3.1 What is Enhancefish?

EnhanceFish is a decision support toolkit for the analysis of aquaculture-based fisheries enhancements. The purpose of ***EnhanceFish*** is to aid better management of aquaculture-based fisheries enhancements by supporting quantitative evaluation of management options, and facilitating broad-based analysis of enhancement systems. ***EnhanceFish*** may be used in assessing whether enhancement is beneficial at all in a particular situation and if so, how the enhancement should be managed in order to achieve its objectives.

The ***EnhanceFish*** toolkit consists of three parts

- (1) The ***EnhanceFish*** decision tool: a software package for quantitative assessment of enhanced fisheries
- (2) The ***EnhanceFish*** manual: a technical manual that explains the scientific principles behind the ***EnhanceFish*** package and its use in assessment

- (3) The **EnhanceFish** guide: practical guidance on how to use **EnhanceFish** in the planning and management of enhancements, particularly in developing countries

The **EnhanceFish** tool is designed to help you analyse quantitatively many of the key management issues in fisheries enhancement such as:

- Effects of different enhancement measures on fisheries yield
- Impacts of enhancement on natural populations of the target species
- Economic performance of enhancement
- Tradeoffs and synergies between stocking and fishing regulations

At the heart of **EnhanceFish** is a mathematical population model that predicts fisheries catch and other biological and production attributes for different management controls such as stocking density and fishing effort. **EnhanceFish** also calculates basic economic performance indicators such as fishing income, resource rent or the net present value of enhancement approaches.

1.3.2 What kind of enhancements can **EnhanceFish** be used for

EnhanceFish can be used for the analysis of any enhancement of organisms that have the life history and ecological traits assumed in the model (see Section 2.1). This includes most of the commonly exploited marine and freshwater organisms such as fish, crustaceans and molluscs. Much of the research on which **EnhanceFish** is based has been conducted on teleost fish ('finfish') populations. However, the dynamics of many crustacean and mollusc populations are subject to similar ecological processes so that **EnhanceFish** may be used for analysing many invertebrates. Indeed, the same basic assessment methods are commonly used for fish, crustacean and mollusc populations. An important group of enhancements to which **EnhanceFish** is not readily applicable are those involving semelparous species (species that breed only once), such as salmon. Before applying **EnhanceFish** to a particular fishery, you should review how well the basic biological assumptions of **EnhanceFish** are met.

1.3.3 Using the **EnhanceFish** tool in management

The **EnhanceFish** tool helps you to analyse quantitatively the relationship between inputs and outputs of the enhanced fishery, and its economic performance. It does not model how these inputs are determined (e.g. how different management rules influence the level of fishing effort), or how outputs contribute to wider objectives (e.g. whether increased fish catches will alleviate poverty in a fishing community). It is crucially important to understand these issues, and to engage constructively with management stakeholders in order to

achieve real improvements in the management of enhancements. The **EnhanceFish** guide sets out a broad framework for the analysis and development of enhancement systems, which may be used in conjunction with the **EnhanceFish** tool.

The broader process assists fishers and other stakeholders to enter a cycle of learning, management planning, implementation and evaluation. It consists of six stages that take the user from engaging stakeholders (Stage 1), understanding the enhancement system (Stage 2) through undertaking the **EnhanceFish** analysis (Stage 3), initiating management action and monitoring (Stage 4), to evaluation (Stage 5) and re-starting the cycle with an improved understanding of the enhancement system. Use of the **EnhanceFish** tool comes in Stage 3 of the wider process.

1.4 What are the prerequisites for using EnhanceFish?

1.4.1 System Requirements

The **EnhanceFish** Software should run on any computer with a Windows 2000 or later operating system. However, the software can use significant CPU (central processing unit), memory and hard disk resources. Some applications of **EnhanceFish** involve Monte Carlo simulations which require repeating calculations many times and storing results. Machines with CPU clock speeds less than 500MHz may be very slow and this will make these applications difficult to use.

Note that you may need Administrator-level access rights on the computer you are using in order for the Software to run properly. If you have limited User access rights, seek greater access permissions from your system administrator.

1.4.2 Skills

The Software, when used together with this Manual, is designed to be suitable for users without *specialist* knowledge of fisheries stock assessment. However, basic knowledge of fisheries assessment is required for you to understand and manipulate the Software, use its more advanced functionalities, and interpret the outputs correctly.

The following skills are recommended for using the **EnhanceFish** software:

- Computer literate;
- Understanding of fisheries enhancement systems and issues (see 1.2)
- Understanding of the basics of fisheries stock assessment

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For an introduction to fisheries assessment consult Hilborn & Walters (1992) or Haddon (2001).

1.4.3 Preparation

When using ***EnhanceFish*** in a management context, we recommend that you consult the using ***EnhanceFish Guide*** and go through Stages 1 – 2 of the suggested management process:

1. Engage stakeholders
2. Understanding the enhancement system

However you may want to familiarise yourself with the ***EnhanceFish Tool*** before initiating the wider process, and conduct some analyses based on existing knowledge and data.

1.5 Continued development of EnhanceFish

The development of ***EnhanceFish*** is an ongoing initiative. We will periodically incorporate new features into the software and publish revised versions of the software and the associated documentation. Please visit the of ***EnhanceFish*** homepage www.aquaticresources.org/enhancefish for the latest news and updates.

We are always interested to hear from ***EnhanceFish*** users – please let us know how you are getting on with using the tool and toolkit, and report problems or bugs by email to: enhancefish@aquaticresources.org.

2 Scientific background

This section provides a brief overview of the scientific basis of the **EnhanceFish** tool. It is important for you to understand this material in order to set up models and interpret the results correctly. An extended and more fully referenced discussion of the scientific basis of **EnhanceFish** is given in Lorenzen (2005), and we strongly recommend that you read this paper in conjunction with the manual.

2.1 The EnhanceFish population model

Analysing quantitatively key management questions in fisheries enhancement such as the influence of stocking size and density on yield, impacts of stocking on wild populations of the target species, or economic performance requires a population dynamics model of the enhanced stock. **EnhanceFish** uses a dynamic pool fisheries model, extended to incorporate key processes in the dynamics of fisheries enhancements.

2.1.1 The population

EnhanceFish assumes that the modelled wild population is a self-recruiting unit without immigration or emigration, and without any ecological or genetic sub-structure. It also assumes that management actions of stocking and fishing apply to the whole population. These assumptions are the same as used in most other fisheries assessment models.

2.1.2 The extended dynamic pool model

The commonly used form of the dynamic pool model first formulated by Beverton & Holt (1957) divides the life history of exploited fish into a pre-recruit, and a recruited phase. Biological (mortality and growth) processes in the pre-recruit phase are not considered explicitly. Instead, only the outcome of these processes is described in the form of a stock-recruitment relationship (a statistical relationship between spawning stock abundance and the number of recruits generated by the spawning stock). In conventional dynamic pool models, all density-dependence in the life cycle is assumed to occur in the pre-recruit phase and thus described by the stock-recruitment relationship. In the recruited phase, the biological processes of mortality, growth and reproduction are considered explicitly. However, no density-dependence is assumed to occur and natural mortality is assumed to be constant and independent of size.

Four extensions are required to the conventional dynamic pool models in order to allow analysis of fisheries enhancements (Lorenzen 2005):

- (a) The size dependence of natural mortality must be described explicitly. Size dependence in natural mortality is a key determinant of optimal stocking size.
- (b) Density-dependent processes in the recruited stock must be considered. Density-dependence in the recruited stock plays an important role in population regulation. Stocking of large hatchery fish may partially circumvent density-dependence in pre-recruit stages, so that density-dependence in the recruited stock becomes the critical regulatory process in enhancements.
- (c) The stock-recruitment relationship must be “unpacked” so that survival in the pre-recruit phase is described explicitly. This is essential for the analysis of enhancements because hatchery fish are usually stocked at a pre-recruit size.
- (d) Population components of wild fish, stocked hatchery fish and naturally produced offspring of hatchery fish must be differentiated. This is important because the components may differ in life history traits, and impacts on the wild stock component are often a key management issue.

2.1.3 Population dynamics processes throughout the life cycle

For the reasons outlined above, the **EnhanceFish** model is based on a fairly detailed representation of key size and density-dependent population processes. The representation is derived from research results which show that:

- Natural mortality is size-dependent throughout the life cycle of fish. Approximately, natural mortality is inversely proportional to body length (Lorenzen 1996b, 2000).
- Density-dependence tends to be compensatory in nature, i.e. survival, growth or reproductive output decline with increasing density and thereby limit abundance or biomass to a level known as the carrying capacity. Depensatory density-dependence may occur at very low abundance, but does not appear to be common (Liermann & Hilborn 1999; Rose et al. 2001).
- Vital rates of early life stages (eggs and larvae) tend to be highly variable, but density-independent (Myers & Cadigan 1993a; Leggett & DeBlois 1994).
- Mortality in early juveniles is usually density-dependent, but the strength of density dependence declines in older juveniles (Myers & Cadigan 1993b).
- Growth in larger juvenile and adult fish tends to be density-dependent (Post et al. 1999; Lorenzen & Enberg 2002).

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- Maturation tends to occur at a relatively constant length even where growth is highly density-dependent (Rochet 1998; Beverton 2002).

An overview of these processes in different stages of the life cycle is given in Table 1. The life cycle is divided into four stages (eggs/larvae, pre-recruit juveniles, recruited juveniles, and adults). Between these stages there are three major transitions (larval-juvenile transition, recruitment and maturation). During each transition, some population processes change while others may remain the same.

Table 1. Overview of the population processes represented in *EnhanceFish* at different life stages

Different life stages					
Life stage or transition	Growth	Natural mortality		Reproduction	Management
Eggs & Larvae	Constant rate of larval production per unit biomass of mature fish (Spawning Stock)				
Larval-juvenile transition (settlement)					
Pre-recruit juveniles	Linear in length, density-independent	Size-dependent	Density-dependent		Stocking
Recruitment					
Recruited juveniles	Von Bertalanffy, density-dependent	Size-dependent	Density-independent		Fishing
Maturation					
Adults	Von Bertalanffy, density-dependent	Size-dependent	Density-independent	Spawning	Fishing

Processes in the egg and larval stage (Table 1) are not represented explicitly. Rather, larval production is assumed to occur at a constant rate per unit of spawning stock biomass. Implicitly this means that growth and mortality are constant and independent of density in this stage. In pre-recruit juveniles, growth is assumed to be linear while mortality is both size and density-dependent. Abundance at this stage is thus regulated through density-dependent mortality. Recruited juveniles and adults are subject to the same processes of body growth and mortality, but only the adults are mature and thus contribute to spawning. The biomass and reproductive output of recruited juveniles and adults is regulated by density-dependent growth. In *EnhanceFish*, stocking can only be carried out in the pre-recruit juvenile phase, while fishing affects only recruited juveniles and adults. The life cycle transitions thus have important implications for natural population processes, as well as the management actions fish can be subjected to.

2.1.4 Unpacking recruitment

EnhanceFish 'unpacks' the stock-recruitment relationship in order to predict survival of stocked fish up to the size at recruitment. In doing so, **EnhanceFish** uses information from the stock-recruitment relationship, together with a growth model for pre-recruits and the general size-dependent mortality model also applied to the recruited stock. The approach to unpacking is described in more detail in Lorenzen (2005) and Appendix A1 of this manual. In a nutshell, it involves the following two steps:

- **EnhanceFish** uses a linear growth and size-dependent mortality model to predict the level of mortality from the size at larval-juvenile transition to the size at stocking, and from the size at stocking to the size at recruitment. This step is carried out for a particular, user-defined reference spawning stock biomass (SSB). By quantifying mortality from larval-juvenile transition to recruitment, the model also defines the corresponding rate of larval production per unit spawning stock biomass.
- **EnhanceFish** then calculates density-dependent parameters for the two pre-recruit mortality rates. This is done in such a way that the overall density-dependence implicit in the stock-recruitment relationship is preserved, and allocated to the pre- and post-stocking phases in proportion the corresponding length intervals.

2.1.5 Ecological and genetic differentiation between wild and hatchery fish

Hatchery fish tend to differ from wild fish, to a varying extent, in terms of their ecological performance and genetic makeup. Ecological performance (fitness) differences between wild and hatchery fish arise from developmental plasticity, and natural or artificial selection in the hatchery environment. The extent of differentiation is influenced by broodstock establishment and management, and the husbandry of early life stages and juveniles which influences development and the natural selection regime (Olla *et al.* 1998; Utter 1998). The relative importance of developmental and genetic factors may vary. Differences due to developmental plasticity diminish over the lifetime of a cohort as a result of increasing adaptation of individuals and the action of natural selection, and are not passed on to offspring produced in the wild (bar possible maternal effects). Differences induced by selection in the hatchery are passed on to the following generation, but will diminish over successive generations due to natural selection in the wild.

Which ecological traits are most likely to differ between wild and hatchery fish, and by how much? In general, natural mortality rates of released hatchery fish are higher than those of wild conspecifics of similar size, often by a substantial

margin (Lorenzen 2000, Fleming & Petersson 2001). Reproductive success of hatchery fish in the wild also tends to be substantially below that of their wild conspecifics, at least in salmonids (Fleming & Petersson 2001). By contrast, no strong or consistent differences have been reported for growth (Svasand *et al.* 2000; Fleming & Petersson 2001). **EnhanceFish** allows users to specify different mortality and reproductive success parameters between wild and stocked/hatchery types.

2.1.6 How **EnhanceFish** represents the enhanced population

A simple and straightforward way of accounting for ecological differences between wild and hatchery fish in population dynamics modelling is to disaggregate the population into components with different life history parameters (Figure 1). The three components considered are wild (wild phenotype, naturally recruited), hatchery (hatchery phenotype, naturally recruited) and stocked (hatchery phenotype, stocked). Normally the hatchery component will be less well adapted than the wild component, and this will be reflected in poorer values of performance traits. Natural selection will act to move the average performance of the combined population towards that of the wild component, and this process may be modelled as transition of offspring from the hatchery component into the wild component at a rate equal to the heritability h^2 . This simple model of phenotypic evolution in the enhanced fishery can be used to assess the implications of a wide range of possible ecological differences and assumptions about their genetic and/or developmental basis.

It should be noted here that the distinction between the stocked component on the one hand and the self-recruiting wild and hatchery components on the other is dichotomous and directly observable in the field (for example if marked fish are stocked). The sharp distinction between the two self-recruiting components (wild and hatchery), however, is made for mathematical convenience. In most cases, interbreeding will produce offspring of various degrees of mixed hatchery/wild, as well as pure hatchery or wild genotype. Hence it will not normally be possible to observe the dichotomous split in real populations unless there is virtually no interbreeding of the two components. Whilst **EnhanceFish** does not explicitly model the mixed genotype components, the dichotomous split does not misrepresent the dynamics of fitness as long as individuals of mixed genotype show an intermediate level of fitness. This is often, but not always the case (outbreeding depression may give rise to individuals of lower fitness than either parental stock).

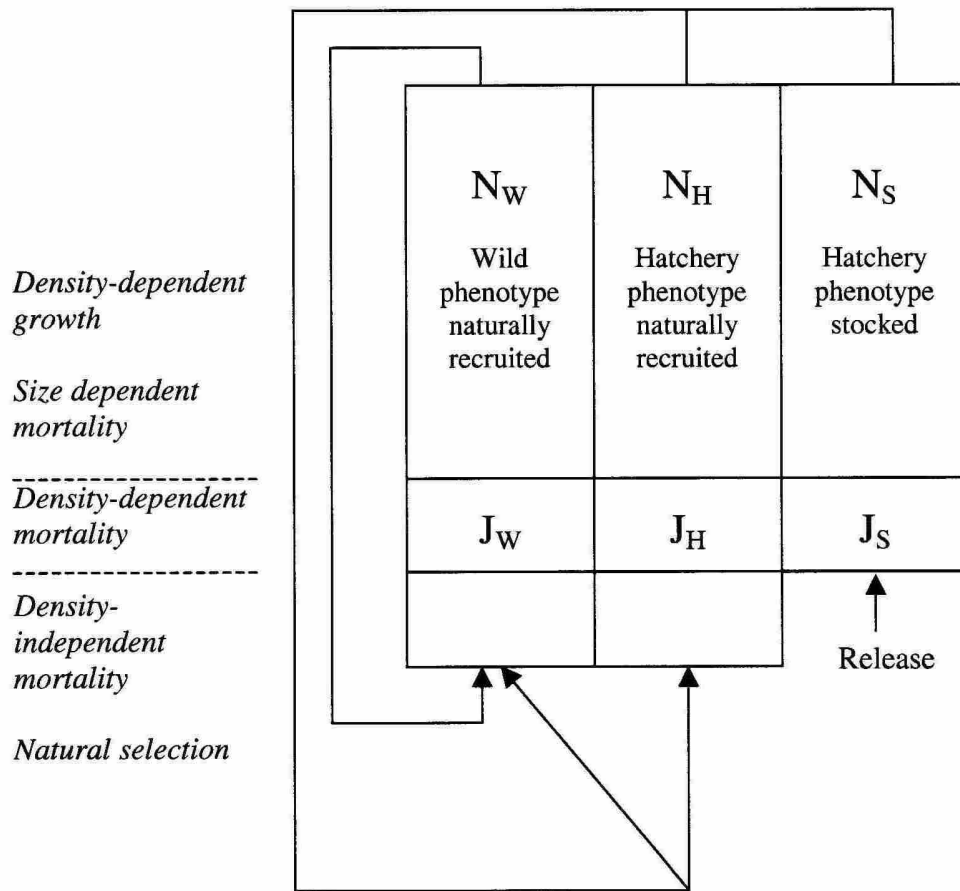


Figure 1. Representation of the enhanced population in **EnhanceFish**.

2.2 The economic model

Management decision making almost inevitably involves making tradeoffs between inputs and outcomes measured and valued in different ways, such as fishing effort and release numbers or yield and abundance. Valuing inputs and outcomes in monetary terms and combining them in economic performance indicators allows tradeoffs to be considered directly. **EnhanceFish** uses a simple economic model to predict two indicators of economic performance: the overall resource rent generated at equilibrium, and the net present value of changes in management such as the introduction of enhancement.

Resource rent is the difference between the revenue generated from a fishery, and the total costs of inputs. In enhanced fisheries, these inputs comprise fishing effort and stocking. Fishing effort is generated through the use of both capital (e.g. boats and gear) and labour, and costs of fishing effort are the total costs incurred in using these inputs. Stocking costs arise from hatchery production, transport and release of hatchery fish. See Arnason (2001) for a wide ranging review on the economics of fisheries enhancements, and Lorenzen (2005) for more information on the bio-economic model underlying **EnhanceFish**.

2.3 Uncertainty analysis by Monte Carlo simulation

EnhanceFish allows users to quantify the uncertainty of predictions using an approach called Monte Carlo simulation. In Monte Carlo simulation, statistical sampling distributions are defined by the user for one or more input parameters (such as the mortality rate of stocked fish). **EnhanceFish** then runs the analysis many times, each time scoring the parameter values at random from the distribution. Of course, predictions will differ in every run due to the variation in the input parameter(s). **EnhanceFish** stores all these predictions and then calculates the statistical distribution of the output variables (such as stock abundance or yield). This allows users to assess how uncertainty in input parameters translates into uncertainty in outcomes. Monte Carlo simulation is a very useful tool for uncertainty analysis and risk assessment.

3 Running *EnhanceFish*

This Section describes the basic functionality of **EnhanceFish** and guides you through some example analyses. We recommend that you follow this section on the computer.

3.1 *Installing and opening the software*

3.1.1 Installation

The Software is distributed as a single 'EnhanceFishSetup.exe' file. You should run this executable file and follow the instructions in the InstallShield Wizard. The software will give you an opportunity to change the locations of files. See the Readme.rtf file for more information.

3.1.2 Opening the software

To open the **EnhanceFish** Software, install it (see above), then double-click on the **EnhanceFish** icon or select **EnhanceFish** from 'All Programs' under the 'Start' menu.

3.2 *The main page*

3.2.1 Overview

The **EnhanceFish** Software is split into five steps, which guide you through the process of model setup and analysis. These five steps are laid out on the main page of the software (Figure 2), and in summary are as follows:

- (1) Entry of basic information
- (2) Set up of biological parameters
- (3) Set up of controls
- (4) Economic parameters
- (5) Analysis

Each Step has a page associated with it in the Software. In the case of Step 1, this is the Main Page. For Step 2, this is the Parameter page etc.

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You should go through each step in turn to ensure that your analysis will run correctly, but you have the opportunity to revisit all of the steps at any time to alter information and settings.

Press F1 or select Help from the menu to get help at any time. Hints are displayed when you move the mouse cursor over a button, edit box or input table. They give an explanation of the item.

The main page contains 'File' and 'Help' functions in the drop-down menu, while the page is split into two vertical areas:

- the main area on the left-hand area shows the steps involved and buttons to take you to those steps;
- the Check List on the right-hand side shows the different components available which charts your progress through the software.

The screenshot shows the EnhanceFish software interface. At the top, there's a menu bar with 'File' and 'Help'. Below it, a text box labeled 'Assessment and File Name' contains the word 'Sole'. The main area is divided into two vertical sections. The left section contains five steps, each with a progress bar and a right-pointing arrow: 'Step 1: Basic Information' (active), 'Step 2: Set up parameters', 'Step 3: Controls', 'Step 4: Economics', and 'Step 5: Analysis'. The right section is titled 'CHECK LIST' and contains three groups of checkboxes: 'Parameter Components Available' (with 'All parameters covered' and 'Mortality PDF' checked), 'Control Components Available' (with 'Controls set', 'Effort', 'Length 50% Selectivity', 'Stocking Density', and 'Stocking Size' checked), and 'Economic Components Available' (with 'Economic model set' checked). The bottom status bar shows the file path 'C:\Documents and Settings\klo\My Documents\EnhanceFish\Sole.efa'.

Parameter	Current Value	Description
Mw	3	Wild natural mortality at unit length
Ms	3	Stock natural mortality at unit length
Linf	46	Asymptotic mean length with biomass=0
K	0.3	Instantaneous growth rate
g	4.6E-5	Density-dependent growth factor
Wa	1E-8	Alpha length-weight

Figure 2. *EnhanceFish* main page.

3.2.2 The File functions



The file functions in the top left hand corner of the screen let you save and load files with parameter values and analysis scenarios.

To save input data and analyses to a file, press 'Save' in the file menu at any time. The first time you do this, a file will be created with the name entered in the 'Assessment and File Name' field. This file will be updated every time you press 'Save' again without changing the content of the 'Assessment and File Name' field. Note that the file is NOT automatically updated when you change parameters or run new analyses. If you want to save your work for future sessions, press 'Save' before closing the session.

You can open a saved file at any time by pressing 'Open' on the file menu and selecting from the available files shown in a new window.

The installation of **EnhanceFish** comes with several data files containing the case studies used in this manual. We recommend that you now load file 'Sole.efa' which will be used for illustrative purposes for the remainder of this section.

3.2.3 The main area

The white arrows  will take you to the respective pages of the software, for building Probability Models, inputting Preferences, Controls and carrying out Analysis. The back arrow () in the top left hand corner of each of these pages will take you back to the main page.

The first text field is the 'Assessment and File Name' field. The name you enter here will become the file name when you first press 'Save' in the file menu.

3.2.4 The Check List

The check list illustrates whether you have inputted the required information for the analysis, and also shows what different components are available, which depends on the data that has been inputted.

For example, to undertake an analysis, the following check boxes, that appear on the first line of each part of the Check List, must be ticked:

- All parameters covered (addressed in Step 3)
- Controls set (addressed in Step 5)

3.3 Basic information (Step 1)

Basic information is entered on the main page itself (See Figure 2). This basic information includes:

- Name of the fishery
- Area of the fishery
- Target species
- Catch unit
- Effort unit
- Length unit
- Time unit

Also in this step, you must define the gear types used in the fishery. **EnhanceFish** allows you to specify multiple gear types. You can add, rename and delete the selected gear in the list using the buttons (Add, Ren and Del). All gear names must be unique. As each gear type requires parameters, you should keep the numbers of gears as small as possible. Finely dividing gears into different types when you cannot provide information is not useful. Assume gears have the same catchability unless you can demonstrate otherwise. In very mixed-gear fisheries it may be more practical to lump gear types into just one 'mixed' group.

3.4 Setting up parameters (Step 2)

Setting up parameters is perhaps the single most important step in the analysis, as it defines the model upon which all results will be based. An overview of the parameters needed to run **EnhanceFish** analyses is given in Table 2. For the moment, do not worry about how to get all the detailed information required for analysing 'your' fishery! We will deal with this problem in Section 4. In the present section, our focus is on understanding what the parameters mean and how to set them up.

From the main page, click on the arrow associated with Step 2 to open the parameter setup page (Figure 3). Parameters are entered in several sub-pages corresponding to the sub-models for growth, mortality, etc. The page has links to the sub-pages in the upper left-hand field, and a summary of parameter values entered in the right hand field.

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Table 2. Model parameters and their values in the North Sea sole example.

Parameter	Definition	Value in the North Sea sole example
Life cycle L_0 L_r a_r	Length at larval/juvenile transition (settlement) Length at recruitment Age at recruitment	2 cm 14 cm 1 year
Growth $L_{\infty L}$ K g α β	Asymptotic length at $B \rightarrow 0$ Growth rate Competition coefficient Coefficient of length-weight relationship Exponent of length-weight relationship	46 cm 0.3 year^{-1} $4.6 \times 10^{-5} \text{ cm t}^{-1}$ 1.0×10^{-8} 3
Natural mortality $M_{1,W}$ $M_{1,S}$	Mortality of wild phenotype at $L=1 \text{ cm}$ Mortality of hatchery phenotype at $L=1 \text{ cm}$	3.0 year^{-1} 3.0 year^{-1}
Reproduction L_m p r	Length at maturity Steepness of maturity curve Relative reproductive performance of stocked fish	26 cm -1 1
Recruitment a^* b^* v f a_1 b_1 a_2 b_2	Initial slope of stock-recruitment relationship Asymptotic recruitment level Linear growth rate of juveniles Juvenile production per unit spawner biomass Survival over stage 1 juvenile period at $J \rightarrow 0$ Density dependence in stage 1 Survival over stage 2 juvenile period at $J \rightarrow 0$ Density dependence in stage 2	22500 t^{-1} 104938271 12 cm year^{-1} (calculated) (calculated, variable) (calculated, variable) (calculated, variable) (calculated, variable)
Fishing F_{∞} L_c q	Fishing effort asymptote Gear selection length Steepness of selectivity curve	0.6 year^{-1} 26 cm -1
Evolution h^2	Heritability of life history traits	0.2
Economics Y_1 Y_2 κ_2 κ_2 κ_2 κ_2 π δ	Unit cost of hatchery fish Unit cost of fishing mortality Control cost Control cost Control cost Control cost Ex-vessel price of fish Discount rate	(empirical model) $2.6 \times 10^8 \text{ US\$}$ 0 US\$ 0 US\$ 0 US\$ 0 US\$ $1000 \text{ US\$ t}^{-1}$ $10 \% \text{ year}^{-1}$

You can use the 'Model Assistant' to guide you through the setup, or move through the setup sub-pages independently. The purpose of the Model Assistant is to ensure that you enter parameters in the sequence they are needed, because some setup-pages use results from previous pages.

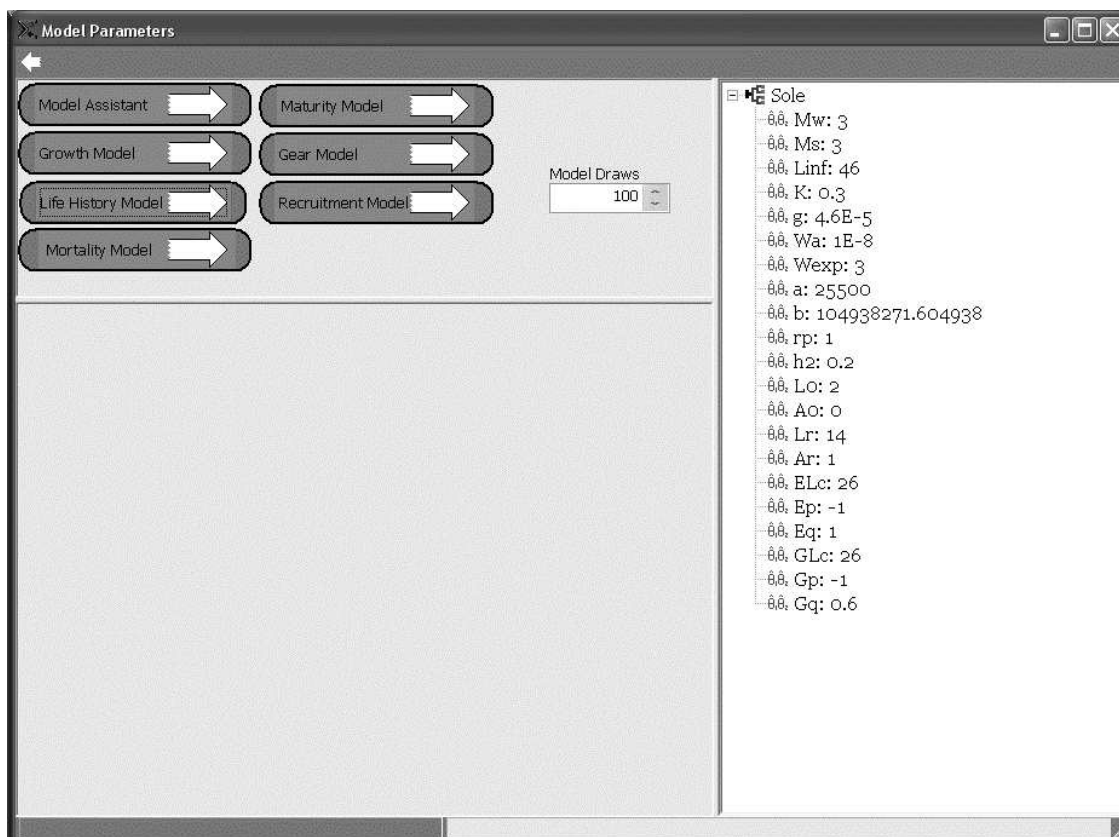


Figure 3. Parameter setup page.

We recommend that while familiarising yourself with the software, you either load the 'Sole.efa' file using the file menu and move through the parameter setup sub-pages in the order of the text below, or use the model assistant to enter the values given in Table 2.

Most setup pages include graphs to illustrate the sub-model you have set up by entering parameter values. If you are unfamiliar with the sub-models being used and the interpretation of the parameters, try changing parameter values to see how that influences the relevant sub-model.

All setup sub-pages do, in the first instance, require you to enter fixed values for the parameters. Each page also has a link 'Define PDF' which may be used to set up sampling distributions for Monte Carlo simulation (PDF = probability density function). This advanced feature is described in Section 3.4.7. We recommend that you do not use this feature until you have familiarized yourself with the basic functionality of the Software.

3.4.1 Life history

This form is used to define the cornerstones of the life cycle (refer to Table 1 for explanation), and some fundamental biological process parameters:

- L_0 : length at larval-juvenile transition
- L_r : length at recruitment
- A_0 : age at larval-juvenile transition
- A_r : age at recruitment
- h^2 : heritability
- rp : relative reproductive success of stocked/hatchery type fish

The 'Define PDF' button leads you to a new page where you can set up sampling distributions for Monte Carlo simulation.

Life History

Length at settlement (L_0) Length at recruitment (L_r)

Age at settlement (A_0) Age at recruitment (A_r)

Length and age at settlement and recruitment: "Settlement" or larval-juvenile transition is the point in the fish's life history when metamorphosis from larvae to juvenile occurs. "Recruitment" is the point from which fish may be harvested in the fishery and are no longer subject to density-dependent juvenile mortality. See the EnhanceFish manual Table 1 for further details.

Heritability (h^2) Reproduction hatchery : wild (rp)

Define PDF

Figure 4. Life history setup page

These cornerstones need to be chosen carefully because they define the population processes acting at different sizes, and determine the size ranges over which the fish can be stocked and harvested. Remember:

- Mortality is directly density-dependent only in juveniles between L_0 and L_r . When unpacking the stock-recruitment relationship (SRR), **EnhanceFish** will allocate the full degree of density-dependence in the SRR to the size range between L_0 and L_r .
- Fish larger than L_r will not be subject to direct density-dependent mortality.
- In **EnhanceFish**, only fish of lengths between L_0 and L_r can be stocked, and only fish larger than L_r can be harvested.

Heritability h^2 is the rate at which the quantitative trait values of stocked/hatchery fish change towards those of wild fish, as a result of natural selection. In **EnhanceFish**, the target fish population is divided into distinct components of wild and stocked/hatchery phenotype, and h^2 is the transition rate from the stocked/hatchery to the wild phenotype (see Section 2.1.6).

- When h^2 is set to a realistic value (about 0.01-0.2 for fitness traits), this mimics the process of adaptation by natural selection.

- When $h^2 = 1$, then all offspring of stocked fish are of the wild phenotype. This corresponds to the assumption that performance differences between stocked and wild fish are exclusively due to phenotypic plasticity.
- When $h^2 = 0$, then there is no adaptation to the natural environment in stocked/hatchery fish even over a long time horizon.

The reproductive performance of stocked/hatchery relative to wild fish can be set at values between 0 and 1, where 0 means that stocked/hatchery fish do not reproduce at all (e.g. when sterile fish are released), and 1 means they reproduce as effectively as wild fish.

3.4.2 Growth

Growth in recruited fish is described by a density-dependent von Bertalanffy growth function (VBGF), where asymptotic length L_∞ is a linear function of population biomass (Lorenzen 1996a, Lorenzen & Enberg 2002). The full set of parameters that need to be entered is:

- $L_{\infty L}$: asymptotic length at very low biomass
- K: growth rate
- a: coefficient of the length-weight relationship
- b: exponent of the length-weight relationship
- g: density-dependent growth factor

Together, these parameters describe growth in length and weight.

Growth parameters are entered in cells at the top of the growth page (Figure 5). The length and weight growth curves are illustrated in the lower field. The graph shows both the maximum growth curves (at very low population biomass) and the growth curves at the biomass entered in the biomass cell. You can use the slide rule to the right of the biomass cell to change the biomass and see how this affects the growth curves. The 'Define PDF' button leads you to a new page where you can set up sampling distributions for Monte Carlo simulation.

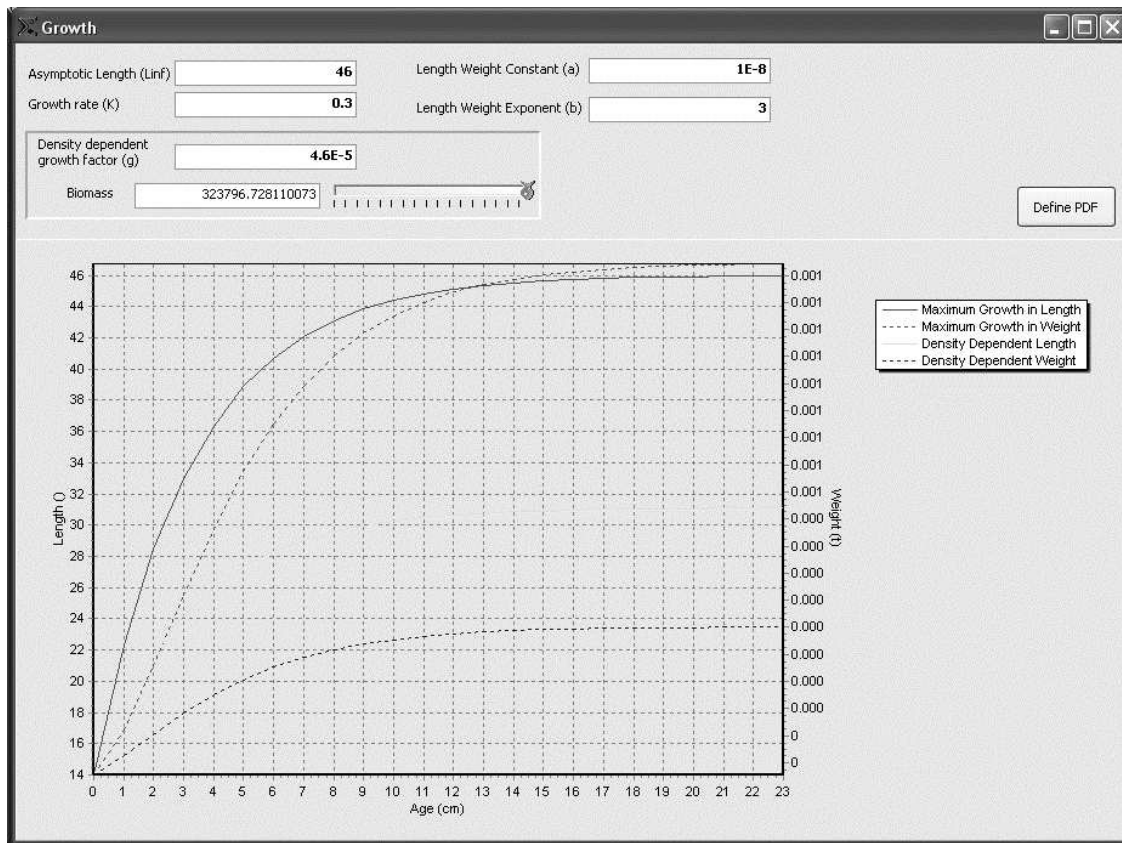


Figure 5. Growth parameter setup page

3.4.3 Mortality

Natural mortality throughout the juvenile and adult stages is described by a length-dependent mortality model. The model assumes that mortality is inversely proportional to length, i.e. the slope of the mortality-length relationship is fixed (Lorenzen 2000). Hence the model has only one parameter, the natural mortality rate at unit length M_1 , which may however differ between wild and hatchery types:

- $M_{1,W}$: Mortality rate at unit length for wild type fish
- $M_{1,S}$: Mortality rate at unit length for stocked/hatchery type fish

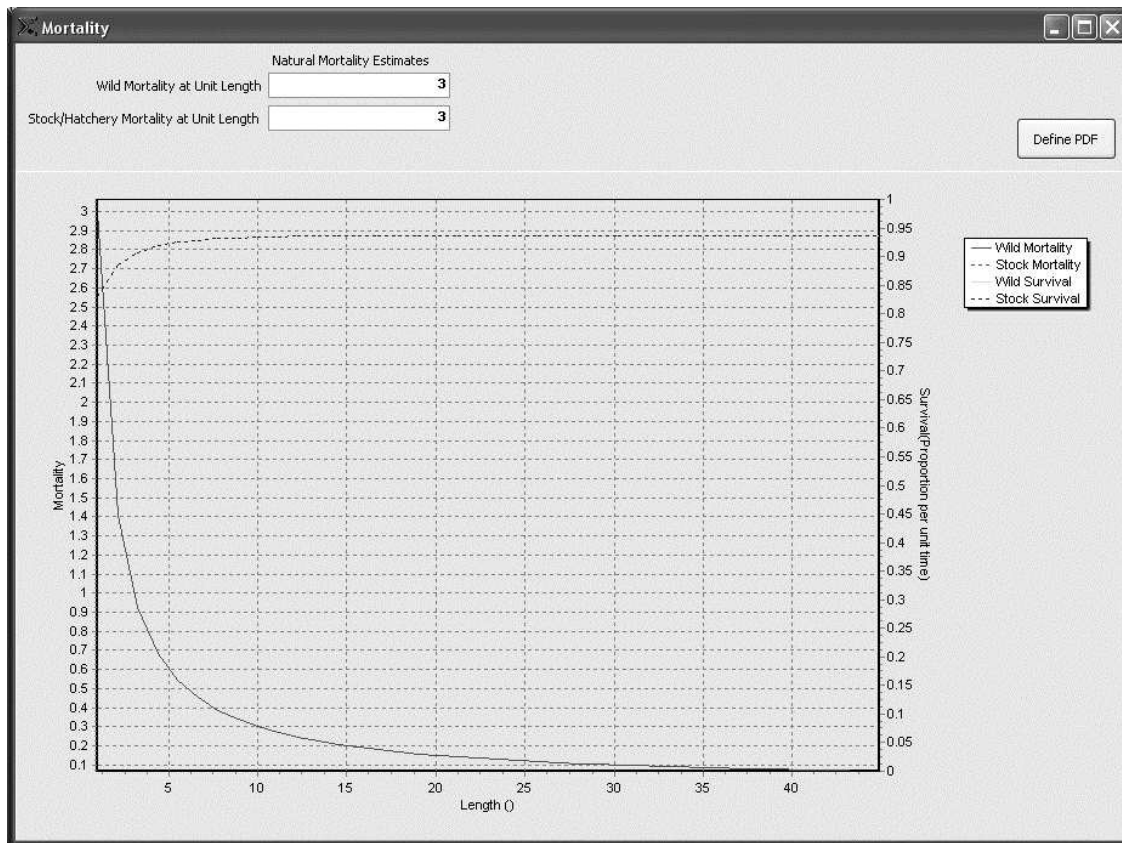


Figure 6. Mortality setup page.

The graph at the bottom of the mortality page (Figure 6) shows the instantaneous mortality rate and proportional survival as a function of length for the wild and stocked/hatchery components. The 'Define PDF' button leads you to a new page where you can set up sampling distributions for Monte Carlo simulation.

3.4.4 Maturity

The proportion of mature fish at length is described by a length-based logistic model with three parameters (Figure 7):

- Maximum proportion mature (default 1)
- L_m : Length at 50% maturity
- p : Steepness of maturity curve

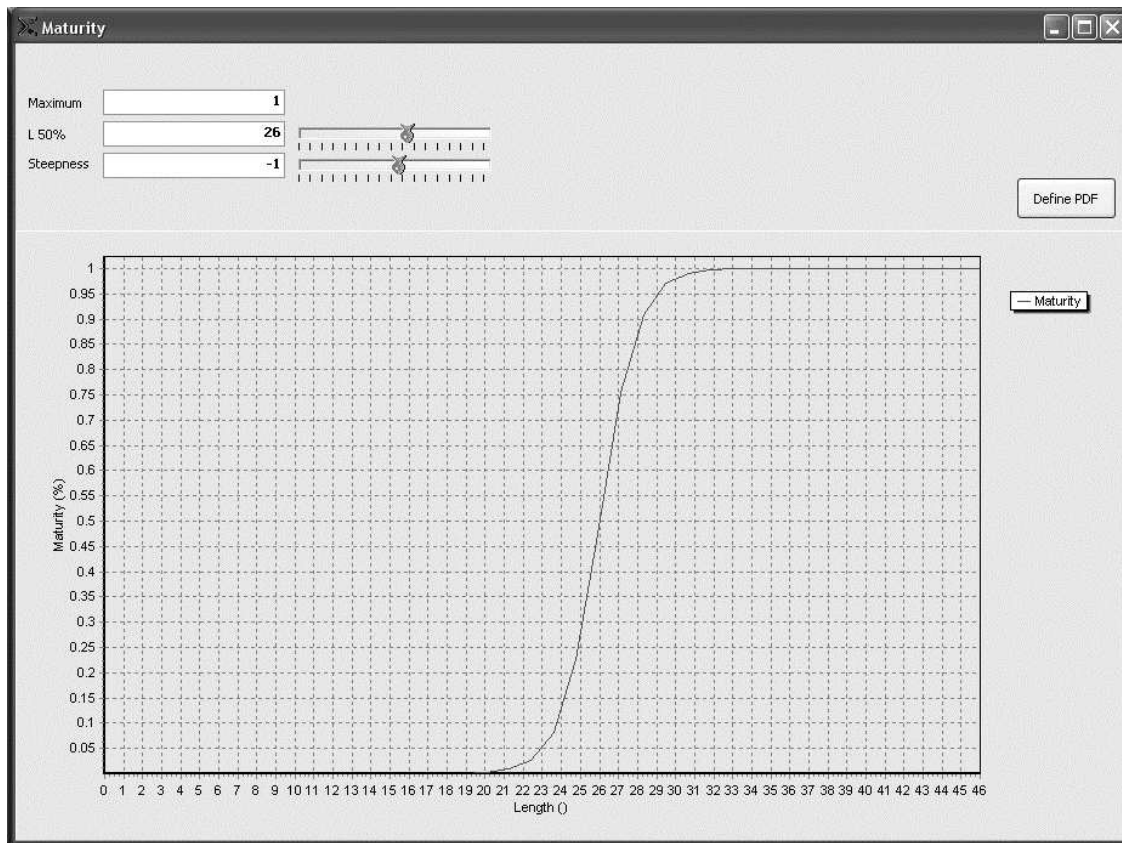


Figure 7. Maturity setup page

The 'Define PDF' button leads you to a new page where you can set up sampling distributions for Monte Carlo simulation.

3.4.5 Fishing gear

The fishing gear page is used to set up the fishing mortality pattern for each gear type (Figure 8). Various functional forms of the relationship between fishing mortality and length may be used:

- Constant
- Logistic
- Domed logistic

For most applications, including mixed-gear fisheries the logistic model is likely to be most appropriate. The domed logistic model may be used for example for gill net fisheries, while the constant model may be used where all sizes are exploited to the same extent (this may be the case in some tropical inland fisheries).

The logistic model has three parameters:

- F_{∞} : Fishing effort asymptote
- L_c : Gear selection length
- q : Steepness of selectivity curve

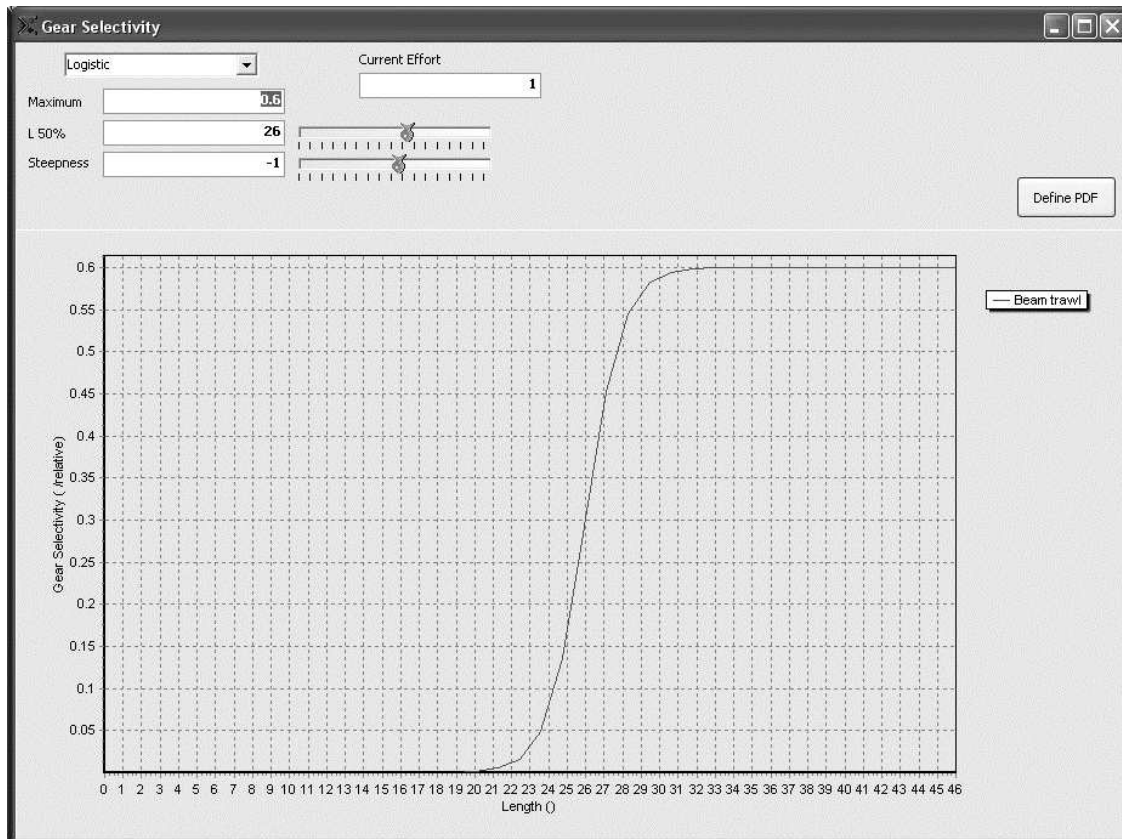


Figure 8. Gear setup page

You must also set the fishing effort associated with the fishing mortality pattern in the 'current effort' box. Set current fishing effort to 1 if you want to express effort in relative terms.

The 'Define PDF' button leads you to a new page where you can set up sampling distributions for Monte Carlo simulation.

3.4.6 Recruitment

The recruitment page is used to set up the stock-recruitment relationship (SRR), and then 'unpack' it (see Section 2.1). The recruitment page (Figure 9) is comparatively complex, but only a few of the parameter values shown actually need to be entered by the user.

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A SRR must be defined in order to run *EnhanceFish*, even if you are modelling a culture-based fishery where natural recruitment is negligible. When modelling a culture-based fishery, simply define an SRR with a level of maximum average recruitment (b^*) that is very low relative to the numbers stocked.

Setting up the stock-recruitment relationship

If the stock-recruitment relationship for the population is known (i.e. has been estimated directly in a stock assessment), simply enter the parameters:

- a^* : Initial slope of the stock-recruitment relationship
- b^* : Asymptotic level of recruitment

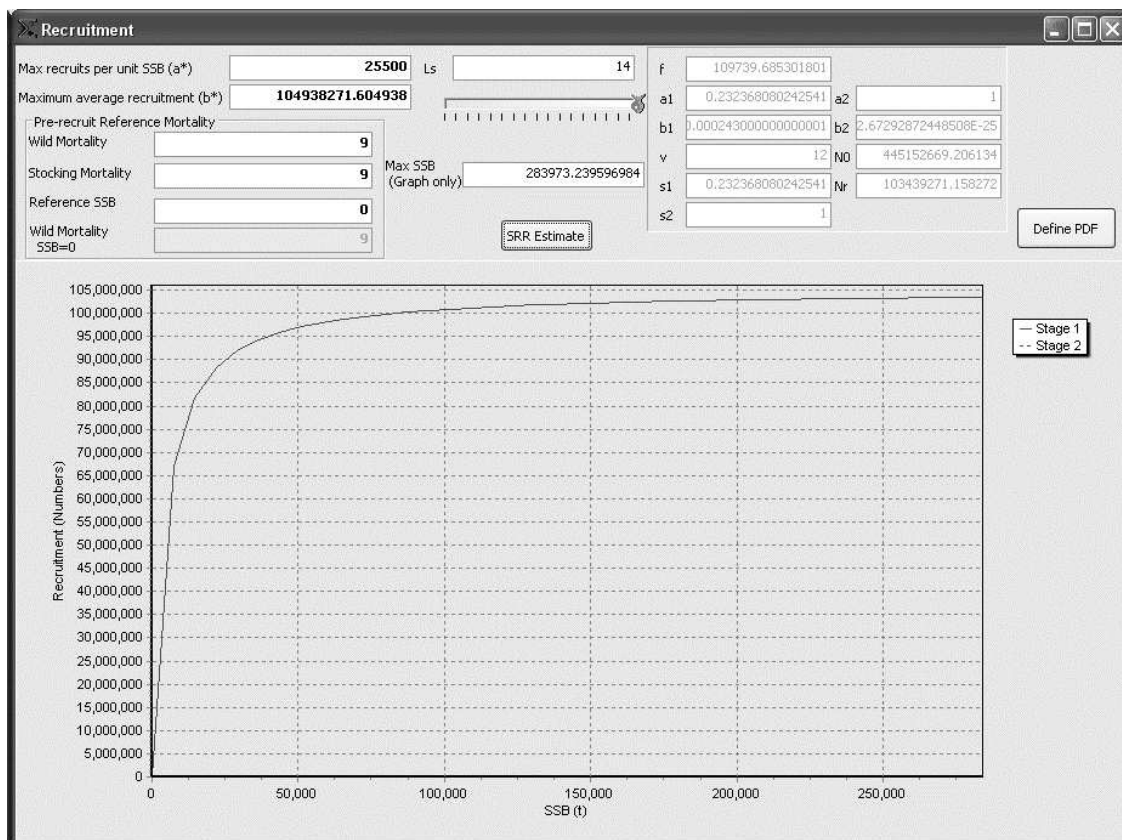


Figure 9. Recruitment setup page.

SRR Estimate

If the stock-recruitment relationship is *not* known, **EnhanceFish** offers the option of *constructing* a relationship based on the life history parameters already entered, and estimates of yield and standardized slope at the origin of the SRR. Pressing the 'SRR Estimate' button brings up a new field in the top right hand corner of the page (Figure 10). You need to enter

- The current catch (the catch corresponding to the current effort entered in the gear setup page)
- An estimate of Myers' standardized slope \tilde{a} . This is typically between 1 and 7 (see Section 4 and Myers 2001).

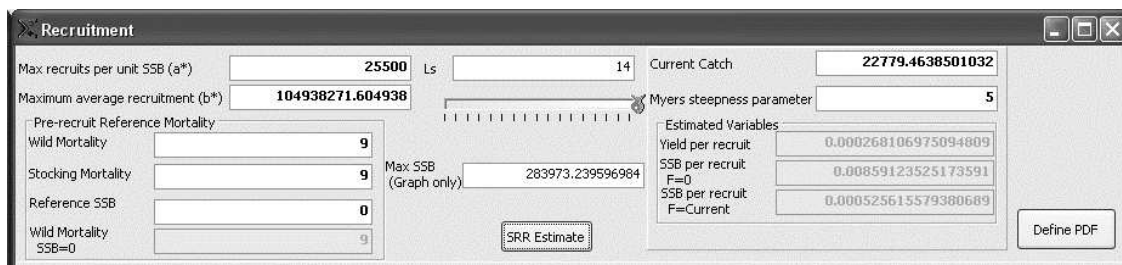


Figure 10. Obtaining an estimate of a stock-recruitment relationship where no specific data exist.

The 'SRR Estimate' field is dynamically linked to the a^* and b^* fields, so that changes in the current catch and \tilde{a} parameters immediately translate into changes in the estimated stock recruitment relationship (a^* and b^*).

Note that the 'SRR Estimate' function serves merely to provide a 'guesstimate' of the SRR to allow you to set up a model and conduct exploratory analyses in very data-poor situations. You should generate SRRs for a range of plausible values of \tilde{a} , and/or run corresponding Monte Carlo simulations to gauge the uncertainty in predictions resulting from the SRR guesstimate.

Unpacking the stock-recruitment relationship

In order to unpack the SRR, **EnhanceFish** uses a size-dependent mortality model for the pre-recruit stage. The model is structurally the same as that used in the recruited stock (i.e. mortality is described by an inverse function of length), but you can specify different natural mortality rates at unit length M_1 for the pre-recruit phase. The parameters to be entered for unpacking are found in the 'pre-recruit reference mortality' field of the recruitment page (Figure 9):

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- $M_{1,W}$: Pre-recruit mortality rate at unit length for wild type fish
- $M_{1,S}$: Pre-recruit mortality rate at unit length for stocked/hatchery type fish
- Reference SSB for which the above mortality rates hold in the pre-recruit stage (where mortality is density-dependent and thus changes with SSB)

Using this information, ***EnhanceFish*** unpacks the stock recruitment relationship into two stages with their own parameters:

- (1) Pre-recruit stage 1 from spawning to the length at stocking
 - f : larval production per unit spawner biomass
 - a_1 : stage 1 survival at SSB=0
 - b_1 : stage 1 density-dependent parameter
- (2) Pre-recruit stage 2 between the length at stocking and the length at recruitment
 - a_2 : stage 2 survival at SSB=0
 - b_2 : stage 2 density-dependent parameter

The parameters of the unpacked stock-recruitment relationship are shown in the top right hand field when the 'SRR Estimate' field is switched off. The unpacking result is shown graphically as the first and second stage stock recruitment relationship for a given length at stocking L_s . L_s may be entered in the corresponding cell or set using the slide rule underneath the cell.

3.5 Controls (Step 3)

The controls are variables that can be influenced directly by management. There are four controls in ***EnhanceFish***, two relating to fishing and two relating to stocking:

- Fishing effort
- Length at 50% gear selectivity
- Stocking density
- Stocking size

Fishing effort is the physical effort expended at fishing (measured for example as the number of fisher-days, the number of boats etc.). Fishing effort is usually assumed to be proportional to fishing mortality. Note that the current level of fishing effort has been set on the gear page (see Section 3.4.5).

Stocking density is the number of fish stocked into the population per unit time. Stocking size is the length of fish at release. Stocking size must be between L_0 (length at larval-juvenile transition) and L_r (length at recruitment).

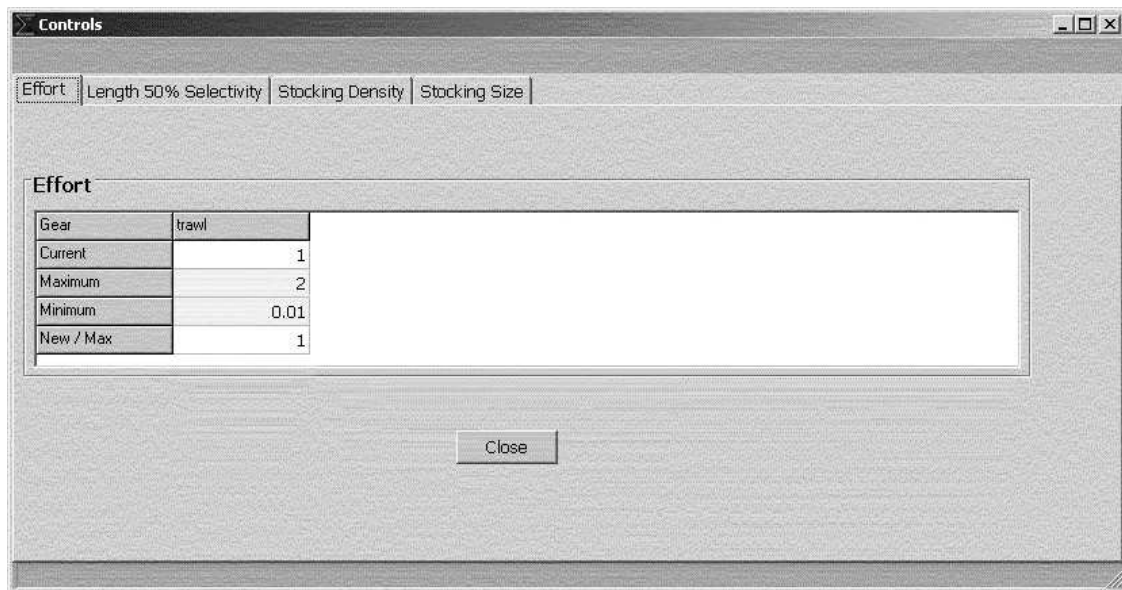


Figure 11. Control setup page

The control setup page has separate sheets for each control (Figure 11). Use the tab at the top of the page to move between controls.

For each control, the controls page shows

- the current value
- the minimum value to be used in simulations
- the maximum value to be used in simulations
- the new value to be used as default

In the analysis (Step 5), **EnhanceFish** varies one or two controls between the minimum and maximum values set up here, while the other controls are kept constant at the new (default) value also set up here. You must set up controls prior to running the analyses, but you can return to this page from the analysis page to modify your settings.

3.6 Economics (Step 4)

In the economics page (Figure 12), you set up the price, cost and discount rate parameters used to calculate the economic utility of different management options. The economic parameters are

- The price of the catch per unit biomass
- The cost of fishing at the default (current) effort level
- Control costs
- Stocking costs per released fish.
- The discount rate to be used when calculating net present value (NPV)

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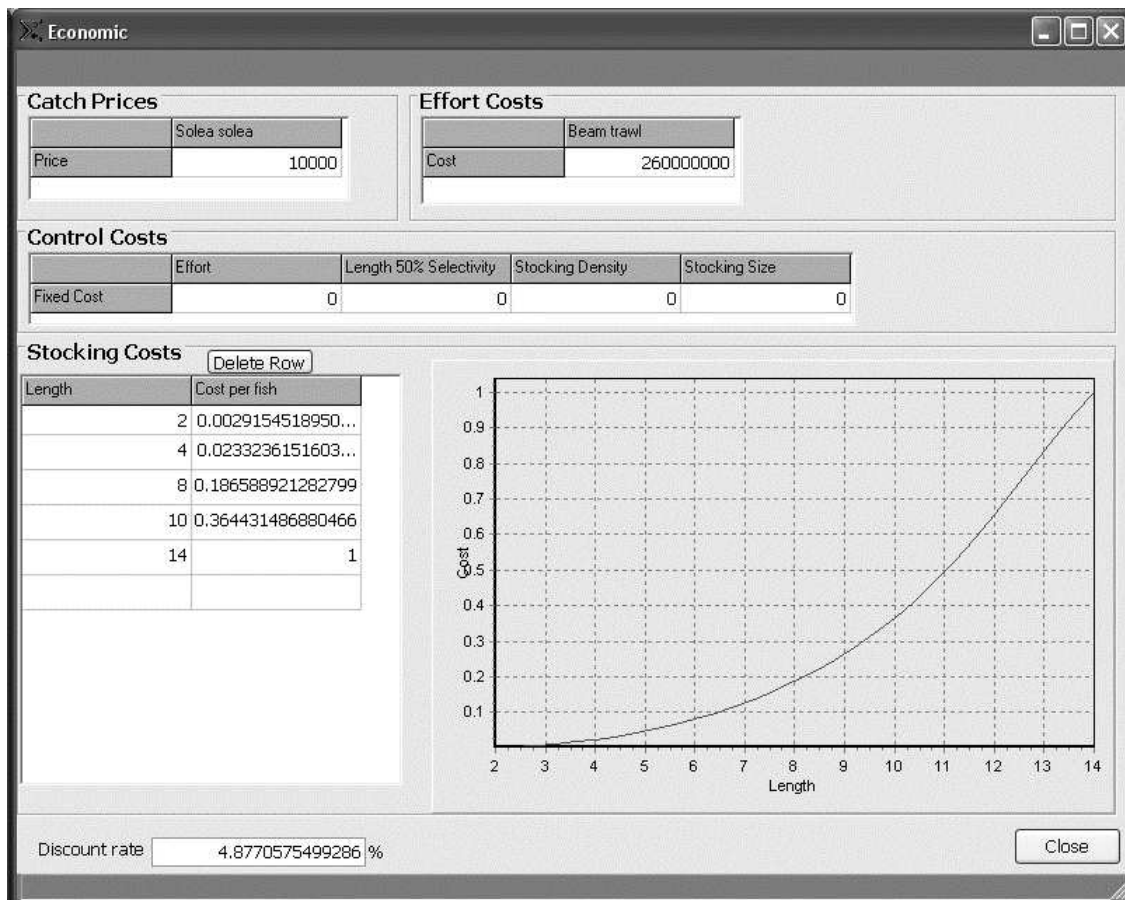


Figure 12. Economics setup page

The cost of fishing at the current effort level is the total cost of fishing associated with the fishing mortality pattern set up in the gear page (Section 3.4.5). This cost should include fixed and variable costs associated with all inputs to fishing such as depreciation of boats, purchase of gear, fuel, and labour.

Control costs are costs associated with maintaining controls at particular levels. This may include the cost fisheries monitoring and surveillance, or research.

Stocking costs are usually dependent on the size of fish to be released. **EnhanceFish** constructs a size-dependent cost function from input data on costs at different sizes provided by the user.

3.7 Analyses (Step 5)

You can proceed to run analyses once you have:

- input basic data (Step 1);
- set up the parameters (Step 2);
- set up controls (Step 3);
- set up economic parameters (Step 4).

3.7.1 The analysis page

The Analysis page (Figure 13) is split into three main areas:

- Analysis Panel (right hand side);
- Graph area (left hand side);
- Lower bar containing the Scenarios box.

The Analysis Panel on the right hand side of the Analysis page allows you to set the controls and scenarios you are going to run. Here you can also set what control type to implement, and the variables for the simulation.

The Graph area is where the results of the analyses are displayed in graphical form. You can select which graph is displayed from the drop-down list to the right of the graph, and rotate and zoom in or out on the graphs.

The lower bar contains the Scenarios box, which displays the previous scenarios you have run, and allows you to re-load the results. To save a new scenario, click on 'new'. You can change the default name of the scenario ('Scenario Number X') in the field next to the 'Run Analysis' box. To save scenarios for future sessions, you need to press 'Save' in the file menu before closing your session.

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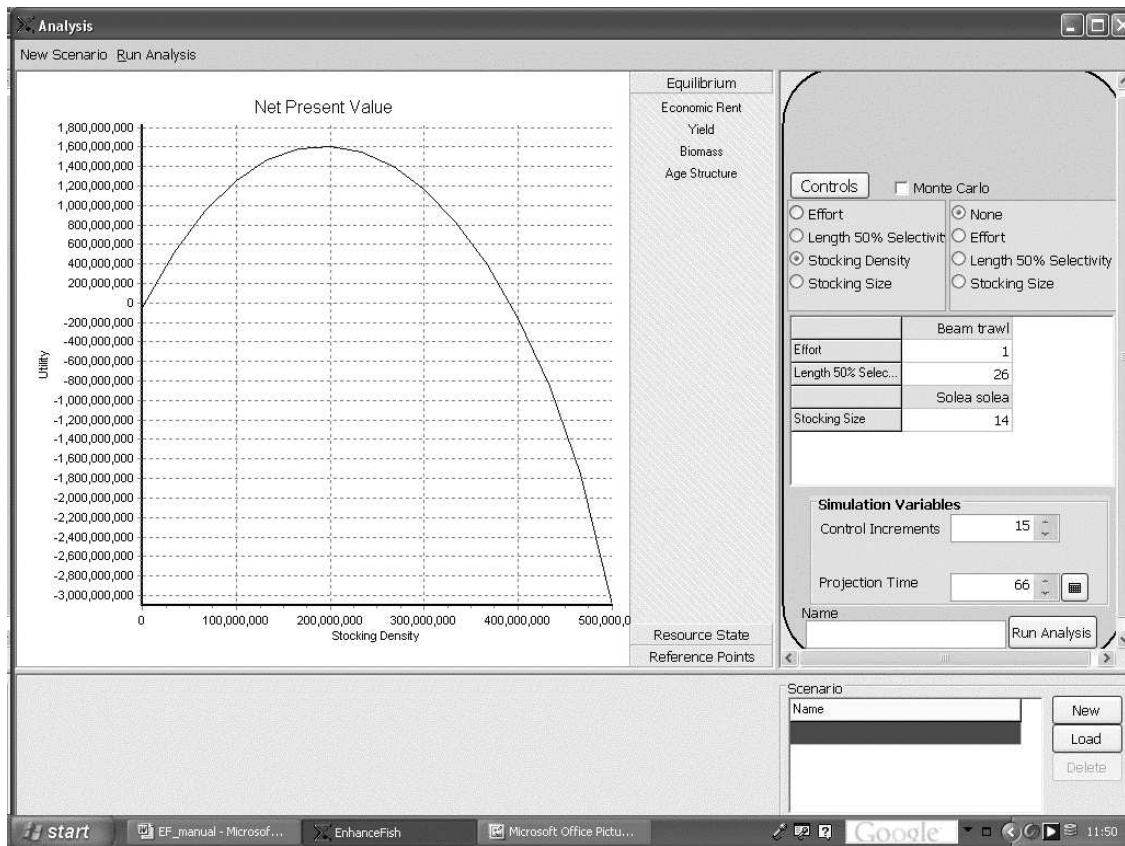


Figure 13. Analysis page

3.7.2 Running analyses: deterministic predictions

You can run a variety of analyses by simulating responses in

- Yield from different stock components,
- Biomass of different stock components,
- Age structure of different stock components,
- Resource rent, and
- Net present value

to changes in

- fishing effort,
- gear selectivity,
- stocking density, and
- stocking size.

To run an analysis, set the control(s) you want to be simulated in the analysis panel. You can choose up to two controls to be simulated simultaneously. The selected control(s) will be varied from the minimum to the maximum values

defined in the control setup page (Step 3). You can return to the control setup page by clicking on the orange 'Controls' button at the top of the analysis panel.

In the analysis panel, there are also two variables that control how the simulations are run. 'Control Increments' is the number of increments between the maximum and minimum control for which simulations are carried out. The more increments there are, the longer it will take to complete the simulation over the range of controls, but the more accurate the graphs will be. 'Projection Time' is the period the fishery is projected into the future on each simulation. If the projection time is very long, each simulation takes longer to complete and later values may have little influence on the result. If the projection time is very short, decisions will be based only on short term outcomes, which may lead to unsustainable management. The maximum projection time is 500. Also, the software automatically detects equilibrium, so a longer projection time is unlikely to increase running time significantly.

Once you have selected the control(s) you want to simulate, click on 'Run Analysis'. **EnhanceFish** will initially show the net present value (NPV) in the graph area, as shown in Figure 13. You can then select other graphs from the menu to the right of the Graph area. If you have loaded the default North Sea sole case study file (Sole.efa), running an analysis for the stocking density control and selecting 'Yield' from the Graph menu will show the screen as in Figure 14. Note that yield and biomass are always shown broken down into the different stock components (wild type, stocked type, naturally recruited hatchery type, and total). See Section 2.1 for an explanation the stock components.

To run an analysis of two interacting controls, for example to evaluate tradeoffs between stocking and fishing regulations, select two controls to be simulated in the analysis panel. For example, selecting 'Stocking Size' and 'Effort', and clicking 'Run Analysis' with the default North Sea sole file will generate the yield predictions shown in Figure 15. There are clear interactions between stocking density and fishing effort: a high stocking density calls for high fishing effort and vice versa if total yield is to be maximised.

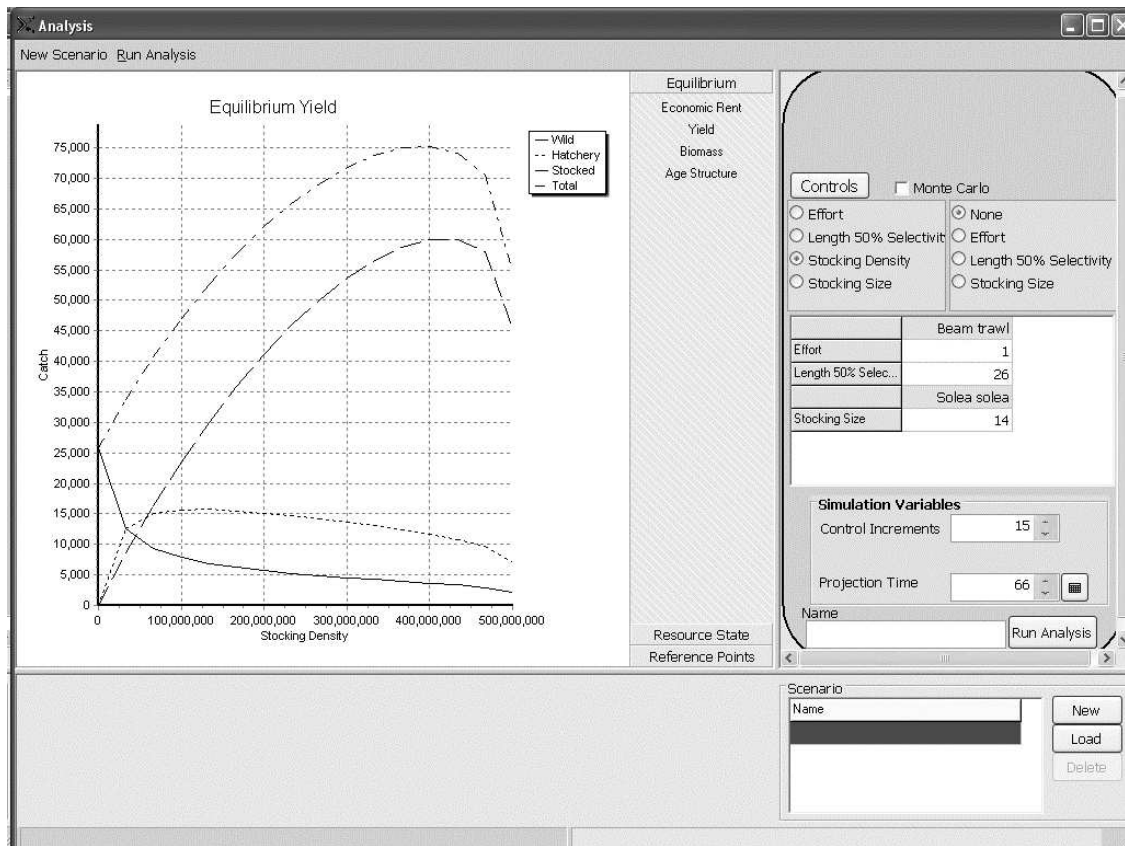


Figure 14. Yield from different stock components and total yield as a function of stocking density for the North Sea sole population under enhancement with hatchery fish at the recruit stage ($L=14$ cm).

Showing results from two interaction controls and multiple stock components in a single graph inevitably leads to a very complex illustration. We will provide greater flexibility to select outputs in the final version of **EnhanceFish**. Alternatively, you can:

- Run the interacting controls step by step, i.e. run the stocking density control several times for different values of fishing effort.
- Export the results to an Excel worksheet and manipulate them to create the graphs you want.

In your analysis, keep the number of simulations and control increments low to speed up exploratory analyses. Also, keep the maximum-minimum range of control(s) wide so that you can see how the simulation behaves. Once you are satisfied with the settings, you can narrow the control range to the area of interest. You may also want to increase the control increments in order obtain more accurate graphs.

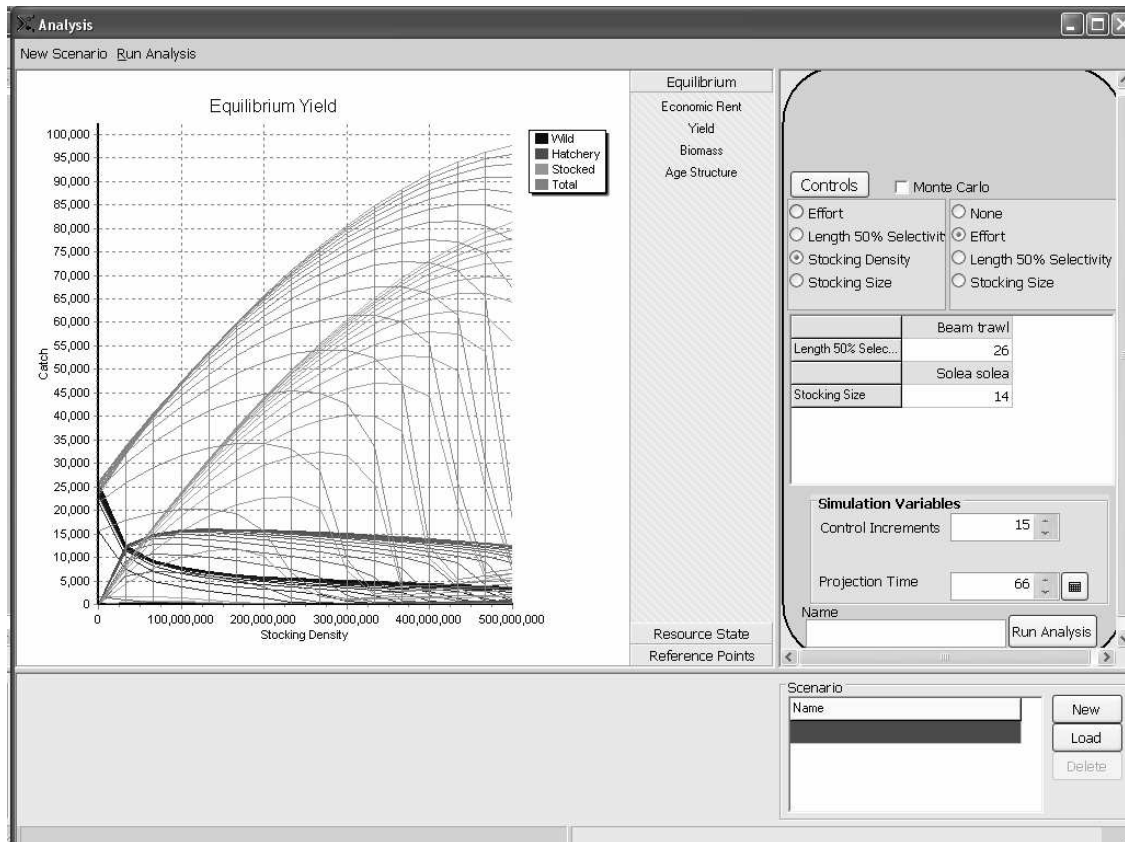


Figure 15. Simulating two controls simultaneously: stocking density and fishing effort.

3.7.3 Saving and manipulating outputs

You can save your complete analysis into the current (*.efa) file by creating scenarios. When you press 'New Scenario', a blank scenario is created and results of the current scenario are saved. We recommend that you save your analyses regularly, in case an error occurs that might force the programme to close.

Analysis results, i.e. the information shown on a graph can be exported from **EnhanceFish** in different formats. To export information, right-click on the graph and select from the menu:

- **Copy data to Excel:** opens an Excel worksheet and imports the data from which the graph has been generated into the sheet. This function only works with certain versions of Excel. If it doesn't work with yours, you can always use 'copy data to clipboard' and then paste the data into Excel.

- **Copy to clipboard:** Copies the graph itself (not the underlying data) to the clipboard. You can paste the graph in many programmes including Word.
- **Copy data to clipboard:** Copies the data from which the graph has been generated to the clipboard. You can paste the data into many documents including Excel worksheets.

3.7.4 Running analyses: Monte Carlo simulations

Both inputs and outputs of the Monte Carlo Analysis are provided by probability density functions (PDFs). PDFs are probability curves, where the area under the curve can be used to calculate the probability of a certain value being true. A PDF provides an estimate of the most likely value for a certain parameter or output, together with a measure of the uncertainty surrounding that value. Uncertainty is indicated by the spread and height of the curve.

Defining PDFs

Before you can run Monte Carlo simulations, you must have defined a PDF for at least one input parameter. PDFs may be set up for all input parameters, in groups linked to the sub-model screens (Figure 16). To set up a probability density function, you need to specify:

- The shape of the distribution: normal or log-normal;
- The mean of the distribution;
- The variance of the distribution;
- The covariance between distributions for individual parameters.

The means are by default the values entered for the parameters on the main screen. The mean or mu parameter for the distribution is on the top line of the grid. The variances and covariances can be entered in the square matrix below. The variances are by default the square-root of the means and off-diagonal covariances are left at zero, which implies the parameters are independent. By increasing or decreasing the covariance values, dependence between parameters can be modelled. The off-diagonal elements of the covariance matrix are automatically copied to the opposite cell across the diagonal to maintain the integrity of the matrix. However, inappropriate covariance values will produce an error as it will not be possible to invert the matrix and the PDF will become undefined.

Parameters can be selected or de-selected from the check box panel at the bottom left of the form. As you select or deselect parameters the mean and covariance matrix grid will automatically update.

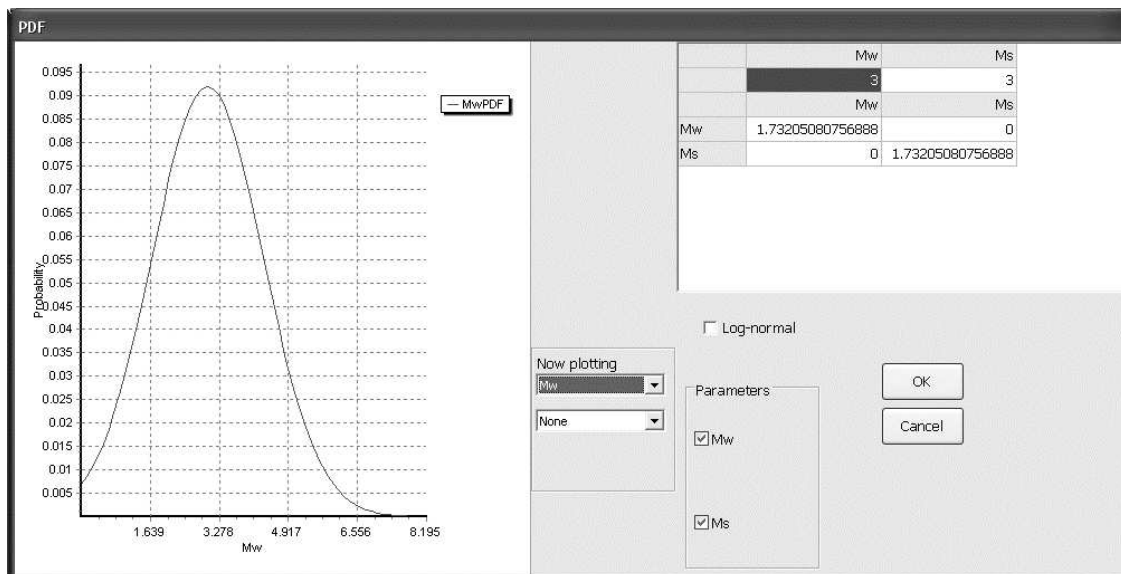


Figure 16. Defining a probability density function

You can choose between normal and log-normal by selecting or de-selecting the log-normal check box. Log-normal operates on the log-scale, so the mean, variances and covariances should also be on the log-scale.

You can view the current PDF in the graph on the left. This will allow you to alter the parameters for the PDF until you see the level of uncertainty you require if you do not have estimates for the variances and covariances. Up to two parameters can be plotted at once. Choose the parameters from the "Now Plotting" panel.

Pressing "OK" keeps the changes you have made, pressing "Cancel" returns the PDF model to its pre-edited state.

Running Monte Carlo simulations

To run the simulations, tick the 'Monte Carlo' box at the top of the analysis panel, then click on 'Run Analysis'. Monte Carlo simulations take a while to run, particularly on older machines. During the simulations, **EnhanceFish** repeatedly scores values for the uncertain parameters from the PDFs, runs the analysis for each set of values, and uses the distribution of results to calculate PDFs for the output variables. The number of simulations to be carried out is set in the analysis panel. The higher the number of simulations the more accurate the

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output PDFs will be, but the longer the analysis will take. It is best to start with a low number of simulations, and increase the number until the output PDFs look smooth and insensitive to further increases in the number of simulations. Figure 17 shows an example of well defined output PDFs. If your PDFs look 'rough' with many little ups and downs rather than the smooth pattern shown in Figure 17, you probably need to increase the number of simulations.

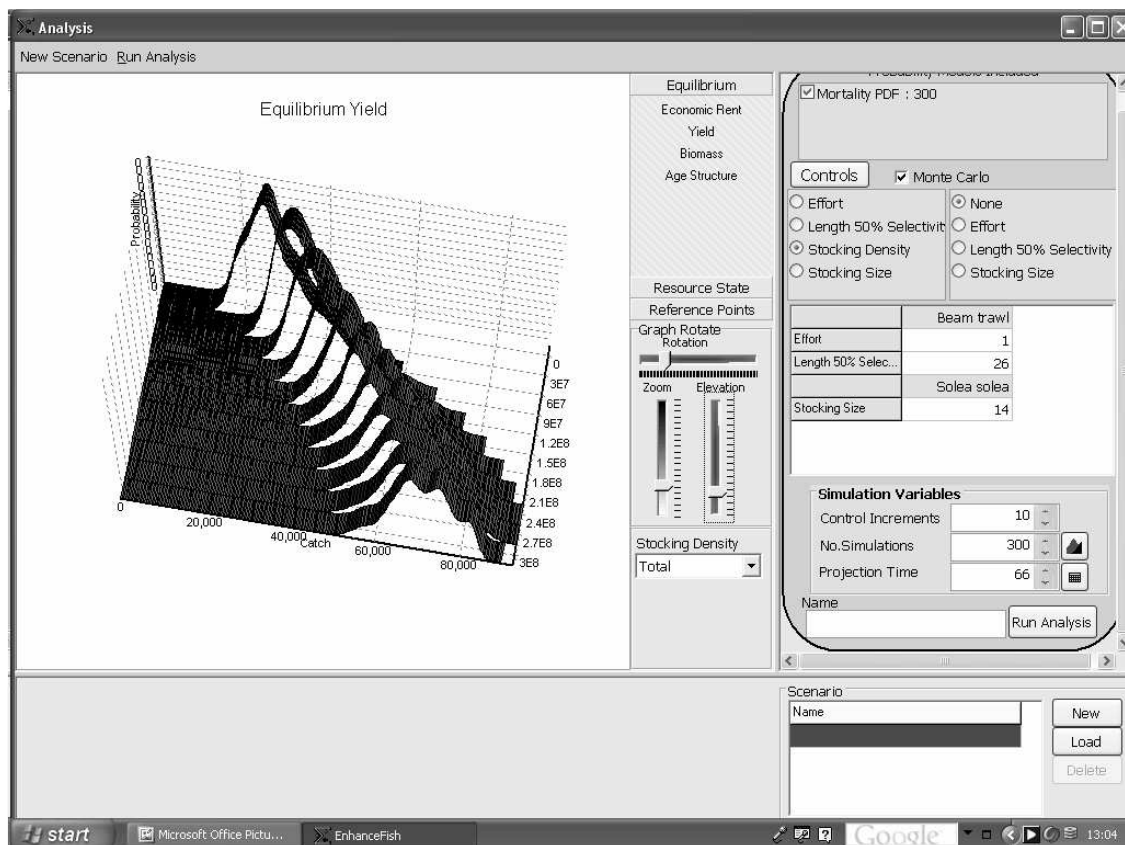


Figure 17. Monte Carlo simulations page

Note that Monte Carlo simulations do not always lead to well-defined distributions for output variables, and that certain input PDFs may make the model crash. This may happen, for example, if an input PDF is so 'flat' that the model occasionally scores extreme values that are biologically or mathematically nonsensical. In such cases, modifying the PDF may alleviate the problem.

4 Conducting analyses

4.1 What to analyse, when and how

By now you should be familiar with the operation of the software, from entering information to running analyses. But what analyses should you carry out, when and how? Essentially, this is the analyst's job to determine. **EnhanceFish** is designed to make the calculations easy, but it can not substitute for the analyst's judgement in determining which analyses are useful in particular circumstances. Here we provide some general guidance, but we emphasize that analysing enhancements is not a case of 'going through the motions' or 'getting the numbers': it requires thought and judgement at every step.

4.1.1 Analyses in different stages of the development of enhancements

Quantitative assessment of biological and economic outcomes is crucial to the rational evaluation of enhancement and alternative or additional management measures, and should be central to any responsible enhancement programme. **EnhanceFish** provides a powerful and general tool for the evaluation of enhancement programmes, from early planning to full-scale operation. Preliminary assessments can and should be carried out before significant investment in experimental research or production facilities, and before any alternative management options are dismissed or delayed in favour of enhancement. Combining population dynamics and bio-economic modelling with participatory planning (see also the **EnhanceFish** Guide) will promote a broad-based assessment of alternatives, and reduce the influence of unrealistic expectations and partisan views on decisions. It is likely that often, preliminary assessments will rule out enhancement as an effective and economically beneficial option. Where this is not the case, further research and development may be justified.

Should a proposed enhancement programme pass the prognostic evaluation and continue to pilot or operational stage, experimental studies may be required to resolve key uncertainties. Experimental studies should encompass monitoring of the wild as well as stocked components of the enhanced population, and be carried out on a large scale to capture the compensatory effects that ultimately determine biological enhancement success. **EnhanceFish** analyses can help to identify the most pertinent uncertainties, and aid the design of experiments to resolve them. Experimental results should then be 'fed back' into the **EnhanceFish** analysis. Close integration of population modelling and experimental management is likely to be the most efficient approach to assessing and developing enhancements.

4.1.2 Compromising over questions and data

In principle, **EnhanceFish** can provide very detailed quantitative predictions for the evaluation of management options, provided that all parameters of the target enhancement are well known. This of course will rarely be the case. There are two approaches to dealing with lack of specific information in analyses:

- Use comparative information from other systems to define approximate values or ranges for parameters.
- Conduct 'partial' analyses of only certain aspects for which good comparative or system-specific information is available

Both approaches have merit, and may be used in combination. As you will see in the next section, comparative information or rules of thumb are available for virtually all of the required parameters. Hence it is possible to run a wide range of analyses even where no system-specific parameter estimates are available. Such analyses will be subject to substantial uncertainty, which can be gauged by sensitivity or uncertainty analysis (e.g. using the Monte Carlo simulation option in **EnhanceFish**).

Often, it is possible to define partial analyses more limited in scope and information requirements than the comprehensive assessments supported by **EnhanceFish** if all parameters are presumed known. Results from such analyses may be subject to much lower uncertainty than the more comprehensive assessments. For example, one can gain a first indication of a species' potential for enhancement by predicting yield and economic rent for a fishery based exclusively on stocking, assuming that recruitment occurs at the stocking size and using an empirical comparative distribution of M_{1H} . This approach cuts out all the uncertainty associated with density-dependent processes, and provides a good indication of potential at 'average' stocking densities. Practical analysis of enhancements may thus involve compromising over the analyses to be carried out and the availability and use of information.

4.1.3 Judging your model

Perhaps the most difficult task in using **EnhanceFish** is to realistically judge your model and its outputs. Experienced fisheries modellers will draw on a wide range of criteria to make such judgements: process understanding, empirical support for parameter and structural assumptions, sensitivity of outputs to assumptions, etc.

New users and management stakeholders not directly involved in the analysis often take either of two diametrically opposed views. Some believe that the model is entirely 'hypothetical' and thus, unrelated to the real world and of little value in decision making. Others almost mistake model results for reality and

uncritically base decisions on them. Both views are wrong. **EnhanceFish** is a theoretical model, which means it uses mathematical process models that have been empirically tested (such as the length-dependent mortality model, Lorenzen 2000). Hence **EnhanceFish** embodies our scientific understanding of the enhanced population: it is not simply 'hypothetical'. On the other hand, there is uncertainty in many parameters and in some structural assumptions of the model. It is unlikely therefore that the real population will behave exactly as predicted. Nonetheless, if the model has been constructed carefully based on realistic assumptions and system-specific or comparative data, it embodies the analyst's best understanding of the population and the management problem. Uncertainties can and should be brought out through sensitivity and uncertainty analysis (e.g. by Monte Carlo simulation). A judiciously constructed and evaluated model is likely to provide the best possible basis for decision making. It is very unlikely that 'just thinking about the problem' without a model, or assuming complete ignorance will lead to better decisions!

Many scientists believe that modelling of enhancements is useful only once all parameters have been measured in the specific fishery and to a high degree of precision. We believe that quite in the contrary, modelling and quantitative analysis are particularly useful in management and development before all relevant parameters are well known. In this way, many costly mistakes can be avoided and the risk of detrimental impacts on wild stocks reduced.

4.2 Getting information on parameter values

This section provides an overview of sources of information, and detailed guidance on setting parameter values.

4.2.1 Overview: sources of information

There are four principal sources of information on parameter values for EnhanceFish analyses:

1. Comparative data and empirical generalisations (rules of thumb)
2. Quantitative fisheries stock assessments of the target population
3. Stocking experiments
4. Monitoring and assessment of the enhanced population (combining (2) and (3)).

There is now a wealth of comparative data and empirical generalisations about key parameters. Comparative studies can provide invaluable a priori information on parameter values including those of the stock-recruitment relationship (Myers 2001), size-dependent mortality in wild and released hatchery fish (Lorenzen

1996a; 2000); density-dependent growth in the recruited phase (Lorenzen & Enberg 2002); and comparative performance of wild and hatchery fish (Fleming & Petersson 2001). Comparative information allows prognostic evaluations to be conducted even in very data-poor situations. Despite large uncertainties, which must be made explicit by providing likely ranges or probability distributions of outcomes, such evaluations will be highly informative for policy decisions.

Existing stock assessments can provide information on model parameters pertaining to the wild target stock. It is beyond the scope of this manual to provide a general overview of stock assessment methods. Please consult Haddon (2001) or Hilborn & Walters (1992).

Stocking experiments allow the direct estimation of growth and mortality parameters in released hatchery fish. See Lorenzen (2006) and Section 5 of this manual for information on how to analyze such experiments to obtain estimates of the **EnhanceFish** growth and mortality parameters.

An overview of comparative information, rules of thumb and approaches to estimation of all **EnhanceFish** biological parameters is given in Table 3. Further details and justifications are provided in the following sections.

4.2.2 Defining the population

As mentioned in Section 2.2.1, **EnhanceFish** assumes that the modelled population is a self-recruiting unit without immigration or emigration, and without any ecological or genetic sub-structure. It also assumes that management actions of stocking and fishing apply to the whole population.

In practice it will rarely if ever be possible to meet these assumptions exactly, except perhaps in the case of small lake populations. Hilborn & Walters (1992) set pragmatic criteria for delineating 'unit stocks' for fisheries management purposes, which may also be used in the context of enhancement:

- The stock should be large enough so as to be self-recruiting (i.e. abundance dynamics should not be determined primarily by immigration and emigration)
- The stock should be small enough not to contain genetically or ecologically different sub-stocks.

Many different kinds of biological information can be useful in delineating the population, including: physical habitat boundaries, migration behaviour, genetic stock discrimination studies, etc. No single approach can conclusively resolve the question and careful judgement is always required.

4.2.3 Life cycle

The cornerstones of the life cycle need to be chosen carefully in the light of existing biological information and the intended size ranges of stocking and harvesting (see Sections 2.1 and 3.3.1). The length at larval-juvenile transition (L_0) and the length at recruitment (L_r) are the lower and upper bounds of the length range during which there is strong density-dependent mortality. In principle, this can be measured through long-term monitoring of abundance at different sizes, but in practice such information is available only for very few populations. Empirical studies show that density-dependent mortality is strongest after the larval stage, but within the first year of life (Myers & Cadigan 1993a,b). For most fish this suggests an L_0 of about 2 cm, and an L_r of 10-25 cm.

4.2.4 Growth

The von Bertalanffy growth parameters L_∞ and K are easily measured in principle, from either length-at-age data or the analysis of length frequency distributions using programmes such as FiSat or LFDA. A complication arises in **EnhanceFish** due to the use of a density-dependent von Bertalanffy growth function where L_∞ is a function of population biomass. Direct measurement will thus provide information on $L_\infty(B)$, where B is the biomass at the time of measurement. The **EnhanceFish** input parameter $L_{\infty L}$ denotes L_∞ at very low biomass (in the absence of intraspecific competition). Where growth has been observed for different levels of Biomass, both $L_{\infty L}$ and g can be estimated directly (see e.g. Lorenzen & Enberg 2002).

A rough rule of thumb can be derived from a comparative study. Figure 18 shows the observed relationships between $L_\infty(B)/L_{\infty L}$ (i.e. $L_\infty(B)$ expressed as a proportion of $L_{\infty L}$) in the populations studied by Lorenzen & Enberg (2002). Biomass is scaled relative to the long-term average population biomass B^* . Note that in these exploited populations, $L_\infty(B^*)/L_{\infty L}$ is approximately 0.93, hence $L_{\infty L} = 1.08 L_\infty(B^*)$. If one assumes that direct measurements of L_∞ correspond approximately to $L_\infty(B^*)$, then this provides a rule of thumb to calculate $L_{\infty L}$. Furthermore, if B^* is known, it is possible by the same rule to calculate a rough estimate of the density-dependent growth parameter $g = (L_{\infty L} - L_\infty(B^*)) / B^*$.

Table 3. Biological parameters and sources of information

Parameter	Explanation	Comparative data and rules of thumb	Direct measurement
Life cycle L_0 L_r a_r	Length at larval/juvenile transition (settlement) Length at recruitment Age at recruitment	2 cm 10-25 cm (arbitrary)	L_0 and L_r are the lower and upper bounds of the length range where density dependence is strong. This is very difficult to do in practice, judgement is usually needed.
Growth $L_{\infty L}$ K g α β	Asymptotic length at $B \rightarrow 0$ Growth rate Density-dependent parameter Coefficient of length-weight relationship Exponent of length-weight relationship	$1.08 L_{\infty B}$ Species specific (check FishBase for $L_{\infty B+}$) Species specific (check FishBase) $(0.08 L_{\infty}(B^*)) / B^*$ Species specific (check FishBase) Species specific (check FishBase)	Fitting to length-at-age data or length-based methods Growth response to variation in biomass (usually long-term data)
Nat. mortality $M_{1,W}$ $M_{1,S}$	Mortality of wild phenotype at $L=1$ cm Mortality of hatchery phenotype at $L=1$ cm	$16.5 (5 - 150) \text{ year}^{-1}$ Distribution: Log-Normal(2.82, 0.87) $66.5 (5 - 500) \text{ year}^{-1}$ Distribution: Log-Normal(4.05, 2.13)	Release-recapture experiments, measurement in unexploited populations
Reproduction L_m p r	Measurement of proportional maturity Relative reproductive performance of stocked fish	$0.66 L_{\infty L} - 1$ $0.2 (0.0 - 1.0)$	Measurement of proportional maturity Relative reproductive performance of stocked fish
Recruitment a^* b^* v	Initial slope of stock-recruitment relationship Asymptotic recruitment level Linear length growth rate	See construction method	Long-term population studies using VPA, catch-at-age methods or direct biomass and recruitment measurements
Fishing F_{∞} L_c q	Fishing effort asymptote Gear selection length Steepness of selectivity curve	$1.0 (0.3-2.0) \text{ year}^{-1}$ Middle of rising arm of catch length distribution -1	VPA or related stock assessment methods, length based methods (FiSat), Analysis if release experiments
Evolution h^2	Heritability of life history traits	$0.1 (0.05-0.2)$	Genetic selection experiments

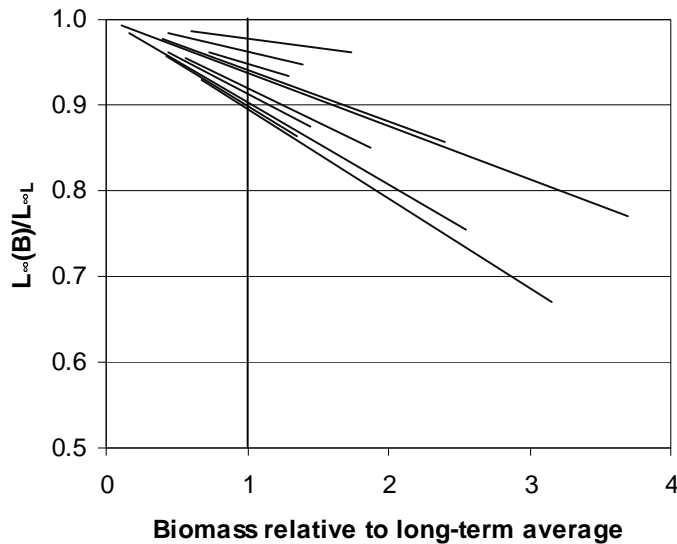


Figure 18. Relationship between $L_{\infty}(B)/L_{\infty L}$ and biomass in 10 fish populations (data from Lorenzen & Enberg 2002).

4.2.5 Natural mortality

Natural mortality throughout the juvenile and adult stages is described by a length-dependent model, where mortality is inversely proportional to length (Lorenzen 2000). The most precise direct estimates of the natural mortality rates at unit length M_1 can be obtained by mark-recapture of wild and released hatchery fish (see Section 5).

Where no data for the direct estimation of M_1 are available, use may be made of comparative data (Lorenzen 1996b, 2000, 2006). Empirical distributions of M_1 in populations of wild and released hatchery fish are shown in Figure 19. Note that the distribution is better defined for wild fish than for released hatchery fish, but both distributions provide a good basis for preliminary assessment. The distributions of M_1 for wild fish is skewed (approximately log-normal) with a median of 16.5 year⁻¹. The cumulative distribution shows that 75% of $M_{1,w}$ values in wild fish are below 30 year⁻¹, while 90% are below 55 year⁻¹. The distribution of $M_{1,s}$ in released hatchery fish extends far to the right of that for wild fish, with a median of 66.5 year⁻¹ and 25% of estimates greater than 175 year⁻¹. Thus post-release performance of hatchery fish may be similar to that of wild fish, but is often much lower. Appropriate PDFs for uncertainty analysis as derived from the data in Lorenzen (1996b, 2000) are Log-Normal(2.82, 0.87) for

wild type fish, and Log-Normal(4.05, 2.13) for hatchery type fish (with Log-Normal(mean, variance)).

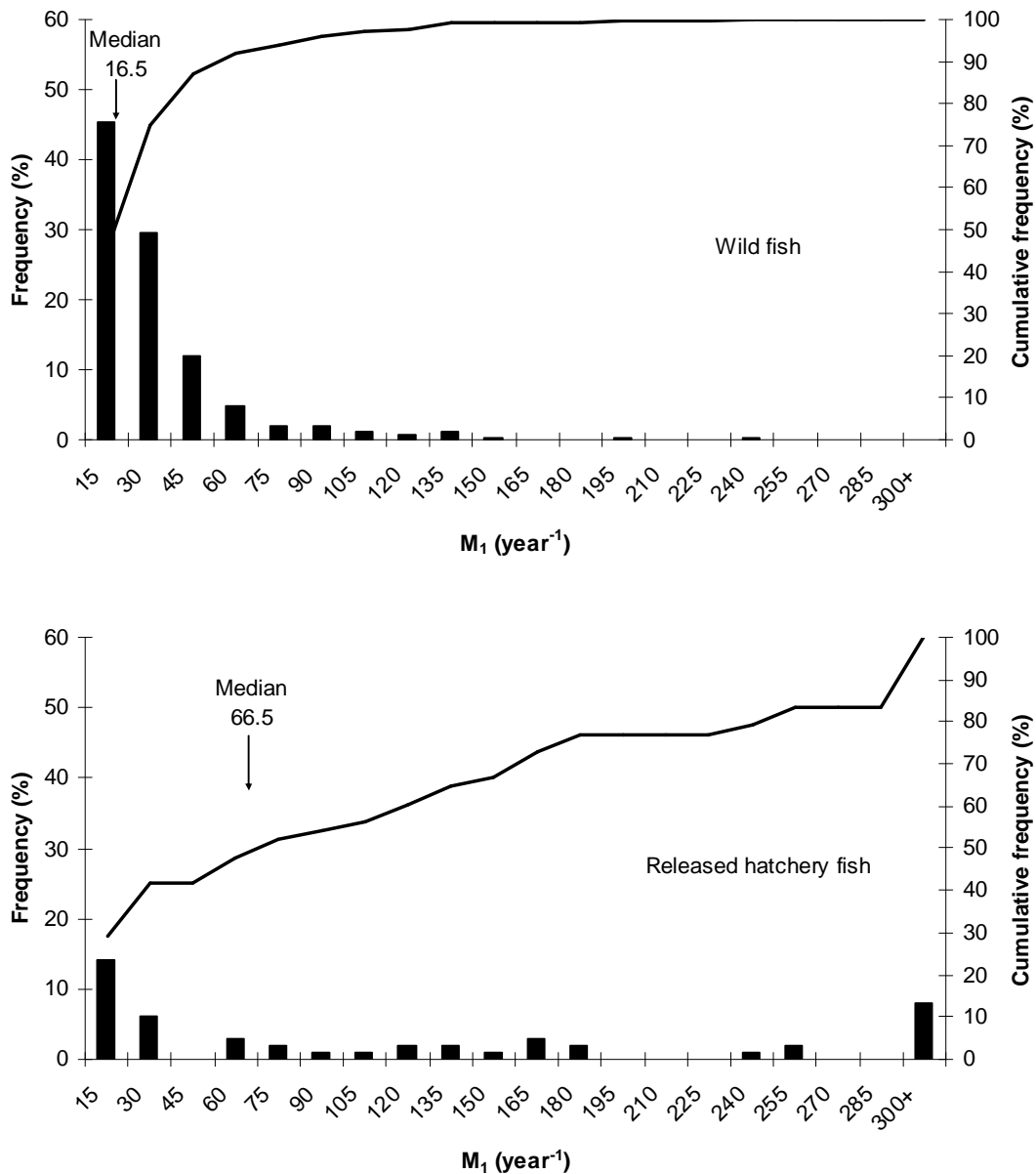


Figure 19. Mortality at unit length M_1 for wild and released hatchery fish

Comparative data on mortality rates in wild and released hatchery fish provide a benchmark against which the performance of released fish can be judged. The distribution of M_1 in wild fish indicates what may be expected if hatchery fish were produced in such a way that their performance in the wild was similar to that of wild fish. It thus provides an 'upper limit' of what may be achievable with

the best genetic and developmental management under hatchery conditions. Conversely, the distribution of $M_{1,S}$ in released hatchery fish allows to measure performance against what has been achieved in other enhancement programmes.

For prognostic evaluations in the absence of specific mortality data, we recommend to use the median $M_{1,S}$ as a default value.

Finally, a reminder that the mortality model used in **EnhanceFish** is length-dependent, and thus different from the constant mortality model used in most conventional stock assessment methods. The natural mortality rate used in conventional assessments applies to the recruited stock only, i.e. to relatively large fish.

4.2.6 Recruitment

The stock-recruitment relationship can be estimated directly only from long time series of data on spawning stock biomass and the level of recruitment. Such data are commonly derived from virtual population analysis (VPA) or related methods. Whilst stock-recruitment relationships are well known for many of the major fish stocks in temperate waters, no such information is available for the vast majority of tropical fish stocks. The stock-recruitment relationship is a key element of the **EnhanceFish** model and must be defined, even in culture-based fisheries where there is no natural recruitment (see Section 3.4.6).

EnhanceFish provides a tool for construction of a stock-recruitment relationship “guesstimate” for use in very data-poor situations – see Section 3.4.6.

4.2.7 Maturity

The proportional maturity curve can be estimated directly from observations of maturity at length. Where such observations are not available, a good rule of thumb is provided by the life history invariant $L_m = 0.66 L_\infty(B^*)$ (Beverton 2002).

4.2.8 Fishing

The parameters of the logistic fishing mortality model (F_∞ , L_c and q) can be estimated directly from release experiments, or from stock assessment methods such as VPA or length based methods (FiSat, LFDA).

Where no suitable data for such analyses are available, length frequency samples of catches can provide a rough estimate of L_c (as the middle of the rising arm of

the length distribution). Fishing mortality in the fully exploited length range (F_{∞}) typically ranges between 0.3 and 2 year⁻¹ in most fisheries. Fishing mortality of course is influenced by management at least in principle, and in initial appraisals of enhancement proposals it may be sufficient to explore the response in yield and economic performance to different levels of fishing mortality rather than focusing on any particular value.

4.2.9 Evolution

Heritability is the change in a quantitative trait due to selection within one generation, relative to the selection differential between the current and the optimal trait value. Heritability of morphological traits is generally around 0.2, that of fitness traits tends to be lower at between 0.01 and 0.1 (Mousseau & Roff 1987).

4.3 What to analyse and how

What analyses to conduct and how? This will depend on the management context. **EnhanceFish** analyses should form part of a wider process of management decision making, and it is during this process that management options and evaluation criteria would be determined, and decisions made. The **EnhanceFish** tool is merely a means for predicting the outcomes of alternative management options, in order to provide information useful to decision making.

4.3.1 The analysis process

An **EnhanceFish** analysis typically involves the following steps:

- (1) **Define the management goal.** This should be done through a participatory process with stakeholders.
- (2) **Define the management options.** Options will typically include continuation of current management ('do nothing'), and changes in fishing, stocking, or habitat management. Identification of options should be done through a participatory process with stakeholders.
- (3) **Define criteria by which to judge how well an option meets the goal.** Criteria may include yield, economic revenue and rent, impacts on wild population abundance, and derived quantities such as fisher's income. Definition of criteria should be a participatory process, but the analyst will have to take an active role to ensure the main criteria can actually be quantified and evaluated using **EnhanceFish**.

- (4) Predict the outcomes of different options using **EnhanceFish**. We have described how to set up such analyses in Section 3.
- (5) **Interpret the results and evaluate the uncertainties associated with them.** As the analyst, don't just 'get the numbers'. Make sure you understand why the predicted outcomes are as they are. This may require you to vary certain model parameters in order to understand the influence of particular processes on results. Once you understand the results, explore how sensitive they are to uncertainty. You can do that manually by varying parameters within realistic ranges, or by Monte Carlo simulation.
- (6) **Synthesize results for communication to stakeholders.** Once you have understood the results and associated uncertainties, synthesize this information for stakeholders. This may involve graphs, a decision table (see Table 4, Section 4.4.1) and a brief written or oral synthesis and explanation.
- (7) **Rank management options.** Establish an overall ranking of management options based on their performance in terms of the criteria established at the outset. This should be done with stakeholders.

4.3.2 How to model different management options

Once different management options have been identified, how do you represent them in the model?

Fishing regime

The fishing regime is determined by overall fishing effort and gear selectivity. Both factors are part of the management controls implemented in **EnhanceFish**.

Stocking regime

The stocking regime is determined by overall fishing effort and gear selectivity. Both factors are part of the management controls implemented in **EnhanceFish**.

Quality of stocked fish

Various aspects of the quality of stocked fish can be manipulated during hatchery production, and may have a major impact on enhancement outcomes. In **EnhanceFish**, the quality of stocked fish is reflected in their natural mortality rate (M_{1H}) and relative reproductive performance rp . The very best hatchery management practices may give rise to stocked fish that approach wild fish performance so that $M_{1H}=M_{1W}$ and $rp=1$. In general, the performance of

hatchery fish will be substantially lower than that of wild fish, and the implications of this are easily explored by varying the two parameters.

Habitat management

Enhancement is often used or considered in situations where natural fisheries production has declined due to habitat loss or degradation. In such cases, habitat restoration may be a management option – either on its own or in combination with changes in the fishing and/or stocking regime. Whilst **EnhanceFish** does not include explicit habitat parameters, it implicitly models the carrying capacities of pre-recruit and recruited habitat through density dependent parameters. Pre-recruit (juvenile) habitat capacity equals the maximum average recruitment parameter b^* of the stock-relationship. Carrying capacity of the recruited (adult) habitat is determined by the density-dependent growth factor g . If $g=0$ then the carrying capacity of the recruited habitat is infinitely high (not a very realistic assumption, but standard in most fisheries models). The greater g , the lower is the carrying capacity of the recruited fish habitat. It is thus possible to model the impact of habitat creation or restoration by changing the b^* and g , though it may not be known exactly how a particular habitat management measure influences the se parameters.

4.4 Example analyses

We provide three case studies to illustrate how **EnhanceFish** may be used in very different situations:

1. The **North Sea sole** case study explores the potential for enhancement in a very well-studied wild population.
2. The **Thmorda reservoir** case study is a partial analysis, using an only partially specified model to explore whether intensive fishing for small fish presents a problem for the viability of a culture-based fishery.
3. The **Ubolratana reservoir** case study explores enhancement potential in a wild population under very data-poor conditions.

4.4.1 North Sea sole

Background

The North Sea sole (*Solea solea*) stock supports a valuable beam trawl fishery (Figure 20). The fishery has been routinely monitored and assessed for over forty years. The stock is considered overfished, with yield marginally below

maximum sustainable yield (MSY) but spawning stock biomass (SSB) is estimated at only 20% of unexploited SSB (ICES 2003).

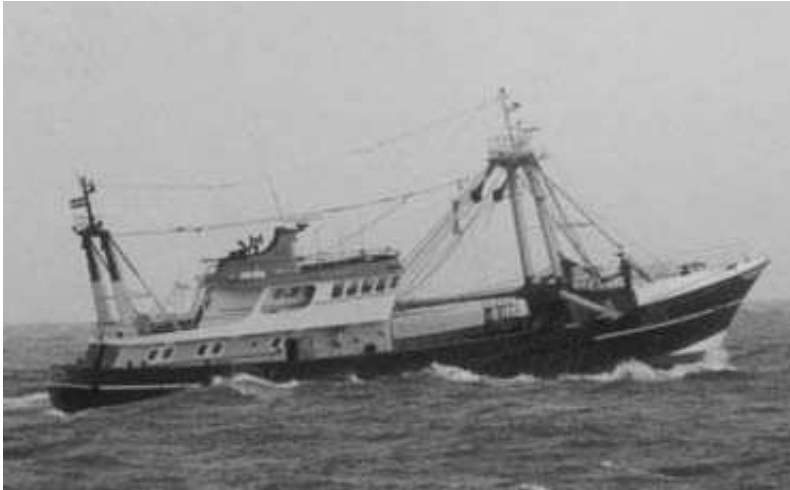


Figure 20. Beam trawler used for sole fishing in the North Sea

Sole has long been considered as a candidate species for stock enhancement. Culture technology posed some initial difficulties but is now well developed, and laboratory experiments have been carried out to assess behavioural attributes of hatchery fish relevant to post-release survival. No experimental releases of sole have been documented.

Aim of analysis

The aim of our analysis is to establish whether enhancement of the North Sea sole fishery could potentially be economically beneficial, without causing significant harm to the natural stock. The options to be considered include continuation of current management, a reduction in fishing effort, enhancement through stocking, or a combination of effort regulation and stocking. The relevant indicators include economic rent from the fishery, and yield and biomass of the wild, stocked, and hatchery components of the population.

Model setup

Regular stock assessments by a working group of the International Council for the Exploration of the Sea (ICES) provide estimates for most of the input parameters required for **EnhanceFish**. The parameter values are given in Table 2 (Section 3.4), and can be loaded from the 'Sole.efa' file included in the **EnhanceFish** setup.

There is, however, considerable uncertainty about the true natural mortality rate. Because natural mortality is difficult to estimate in exploited populations, most stock assessments use a “guesstimate” of the parameter. The North Sea sole assessment, upon which most of the parameter values used here are based, assumes a constant $M=0.1 \text{ year}^{-1}$ in all recruited age groups (ICES 2003). Estimates of most derived quantities such as stock biomass, recruitment and fishing mortality are conditional on the natural mortality rate assumed. To construct a baseline scenario close to the ICES assessment, we use a size-dependent natural mortality of $M_1=3 \text{ year}^{-1}$ (M at $L=1 \text{ cm}$) so that $M=0.1 \text{ year}^{-1}$ at $L=30 \text{ cm}$. This baseline natural mortality rate is, however, very low compared even to the wild population median of $M_1=16.5 \text{ year}^{-1}$ (Section 4.2.5). Hence we conduct an uncertainty analysis in order to establish how sensitive the results of the baseline model are to levels of natural mortality that are more in line with comparative empirical data on M_1 .

Results

We start by assessing the current exploitation status of the wild population. In the controls menu, set the fishing effort to range from 0.01 to 2.0, and the new value of stocking density to 0. In this way, you will be able to explore the response of the natural population to different levels of fishing. Then return to the analysis page and set the controls to be simulated to ‘Effort’ and ‘None’. Then click on ‘Run Analysis’. **EnhanceFish** will now show the equilibrium economic rent in the graph area, as shown in Figure 21.

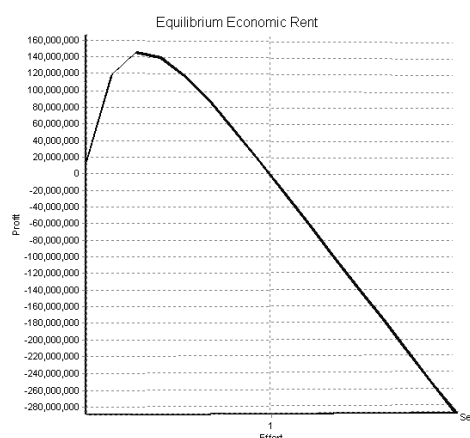


Figure 21. Equilibrium economic rent of the North Sea sole fishery without enhancement.

As you may recall, economic rent is the difference between the total revenue from the fishery (yield times unit price) and the total costs of inputs (in this case, fishing effort times the cost of fishing at $E=1$). In the North Sea sole case study,

the cost of effort has been set so that fishing at the current effort ($E=1$) generates approximately zero economic rent. This is often the case in open access fisheries where effort is attracted into the fishery until all economic rent is 'dissipated'. You can see from the graph that economic rent would be maximised by fishing at only about one third of the current (default) effort level, and that the maximum economic rent would be about 145,000 US\$.

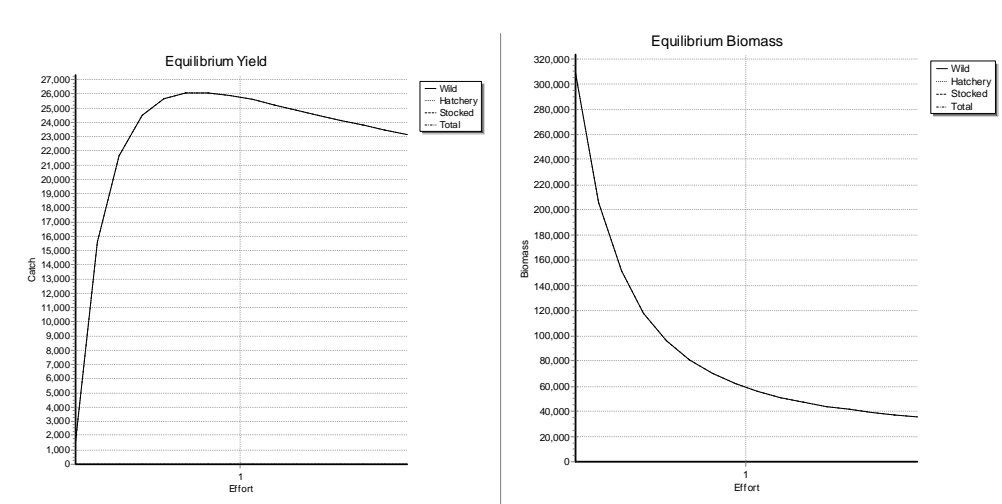


Figure 22. Equilibrium yield and biomass of the North Sea sole fishery without enhancement.

Now select the 'Yield' graph from the drop-down menu to the right of the graph area (see Figure 22). It shows that the fishery is overfished at the current effort level (i.e., yield could be increased by reducing effort). The maximum yield would be achieved by reducing effort by about 25%, but the gain in yield would not be very substantial. Now look at equilibrium biomass (click on the 'Biomass' graph). Biomass at default effort is only about 20% of unexploited biomass, quite a low proportion (less than 40% are usually regarded as problematic). You may also want to look at the equilibrium age structure of the population at different levels of effort. This is of interest for several reasons: old and large fish are thought to be particularly important spawners, and population size structure also has ecosystem level implications. As you can see in Figure 23, fishing at $E=1$ radically reduces the abundance of fish older than about 2 years as compared to an un-fished population (approximated by $E=0.01$). These analyses of the wild population give us a baseline against which to compare the predicted outcomes of enhancement.

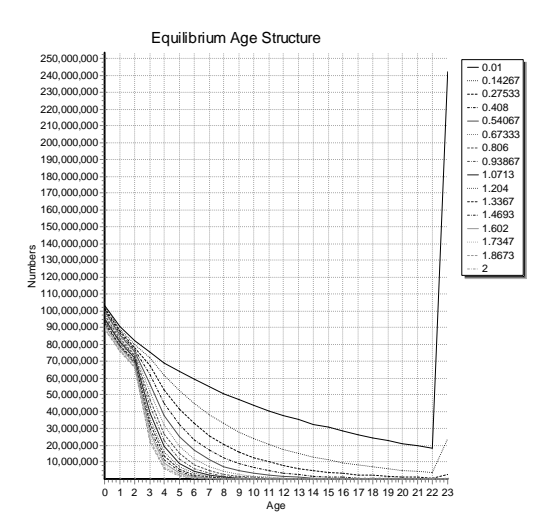


Figure 23. Age structure of the North Sea sole stock for different levels of fishing effort.

Now, let's see how the fishery will respond to enhancement. Set the controls to be simulated to 'Stocking Density' and 'None'. Then click on 'Run Analysis' again. The first graph to appear by default will show economic rent plotted against stocking density (for a constant effort $E=1$). The graph (Figure 24) suggests that the greatest economic rent from stocking (given the current level of fishing effort) would be 165,000 US\$, achieved at a stocking density of about 240 million. This is marginally more than the economic rent that would be generated by reducing fishing effort to about one third of the default level, without enhancement (see above).

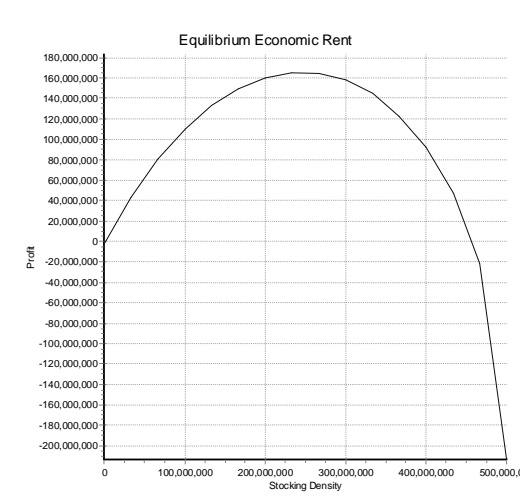


Figure 24. Economic rent in the enhanced North Sea sole fishery as a function of stocking density, for $M_{15} = 3 \text{ year}^{-1}$.

What about yield, and impacts on the wild population component? Select 'Yield' and 'Biomass' from the drop-down menu to obtain the graphs shown in Figure 25. Both graphs now show the yield or population biomass total, and its breakdown into the wild, stocked and hatchery type components (see Section 2). Total yield increases up to a stocking density of about 400 million, and so does the yield derived directly from stocking. Yield based on the wild population component declines rapidly with increasing stocking density. Yield from naturally recruited hatchery-type fish increases initially, peaks at a stocking density of about 50 million and then declines slowly as stocking density increases further. The biomass of population components shows a similar pattern to yield, with the exception that total, stocked and hatchery type biomass increase monotonously. Increasing stocking density always increases total, stocked and hatchery type biomass, but density-dependence in the recruited population increasingly depresses growth so that more and more biomass is composed of fish below the gear selection length. At a stocking density of about 460 million, asymptotic length of the growth function declines to below gear selection length, resulting in a steep decline in yield and increase in biomass (which is no longer removed by fishing). Overall, the results indicate that releasing sole recruits will increase overall yield, but depress the natural population and its contribution to the fishery through compensatory density-dependent processes.

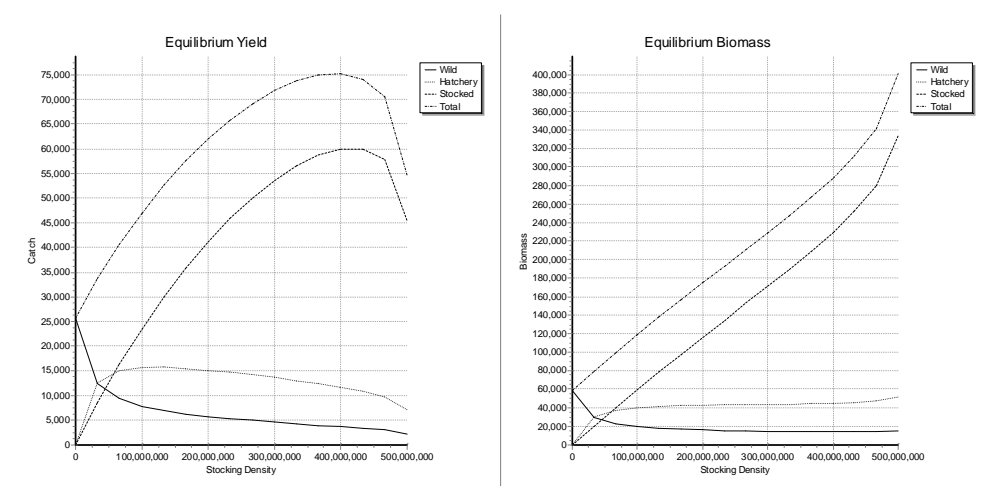


Figure 25. Yield and biomass of North Sea sole under enhancement with hatchery fish at the recruit stage ($L=14$ cm), for $M_{1s} = 3 \text{ year}^{-1}$.

So far we have assumed that hatchery fish will be released at the length at recruitment, i.e. at the end of the juvenile life stage subject to density-dependent mortality. What about stocking smaller seed fish? Set the new stocking density to 240 million in the 'Stocking Density' control panel, and select the controls to be simulated as 'Stocking Size' and 'None'. Then click on 'Run Analysis' again. Total yield is predicted to increase almost exponentially with the stocking size. This reflects the combined action of size and density-dependent mortality in pre-recruits. When stocked at 2 cm the juveniles are subject to very high 'baseline' mortality, plus the full strength of density-dependent mortality which acts during the juvenile phase from 2 to 14 cm length. Clearly, stocking of small seed fish will be ineffective. Note that impacts on the wild population component increase throughout the stocking size range, with displacement being complete initially but only partial when larger fish are stocked.

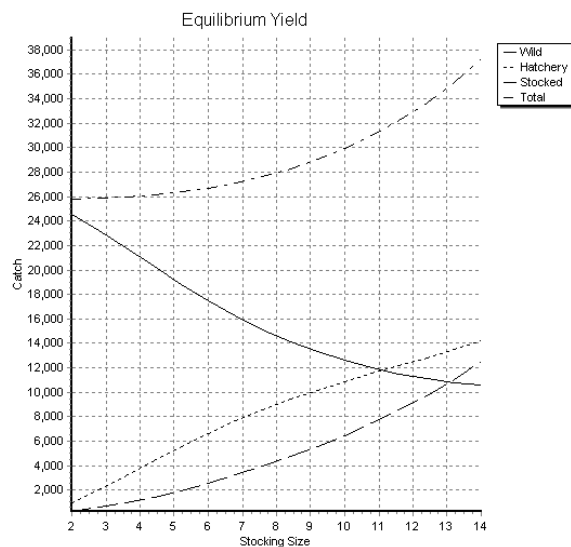


Figure 26. Analysis of stocking size in the North Sea sole fishery for $M_{15} = 3 \text{ year}^{-1}$.

To understand how stocking and fishing regimes interact, and to find the combined optimum in terms of economic rent, can simulate both control variables together. Set the controls to be simulated to 'Stocking Density' and 'Effort', and run the analysis. The output for economic rent is a three dimensional graph of rent plotted against both control variables (Figure 27). Use the 'Rotate', 'Elevation' and 'Zoom' graphics controls to the right of the graph to look at it from different angles. You can see that stocking density and fishing effort interact strongly in determining rent, and that the overall maximum rent of 187,000 US\$ is achieved at a stocking density of 170 million recruits combined with an Effort of 0.6. Even under enhancement, rent would be maximised at a lower fishing effort than the current level (Effort = 1).

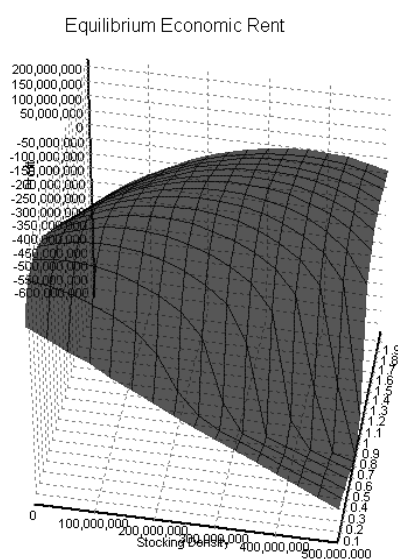


Figure 27. Interaction between fishing effort and stocking density in determining economic rent from the North Sea sole fishery for $M_{1s} = 3 \text{ year}^{-1}$.

The analysis so far has assumed that wild and stocked fish are subject to the same natural mortality rate ($M_1 = 3 \text{ year}^{-1}$), which corresponds to rate assumed in the ICES assessment (see model setup above). How would the predictions change if we assumed that stocked fish natural mortality was equal to the median $M_1 = 16.5 \text{ year}^{-1}$ for wild fish? (Note that this is still very much a 'best case scenario' given that the median for stocked fish is substantially higher at $M_1 = 66.5 \text{ year}^{-1}$). Changing the stocked fish mortality at M_{1s} does not affect the results for fishing regulation in the absence of enhancement (Figure 21-23). Yield and economic rent for enhancement at current fishing effort are shown in Figure 28. The impact of enhancement on total yield is predicted to be marginal, and economic rent declines more or less linearly with increasing stocking density. Clearly, enhancement is not economically beneficial if we assume a stocked fish natural mortality in line with expectations based on empirical data.

We can take the uncertainty analysis further by running Monte Carlo simulations using a probability density function (PDF) for the stocked fish natural mortality. If we assume a log-normal PDF with mean 2.82 and variance 0.87 (the estimated distribution of wild fish M_1 , Section 4.2.5), this generates the total yield PDF shown in Figure 29. Clearly, the likelihood of achieving a substantial increase in yield even at a stocking density of 500 Million recruits is quite low.

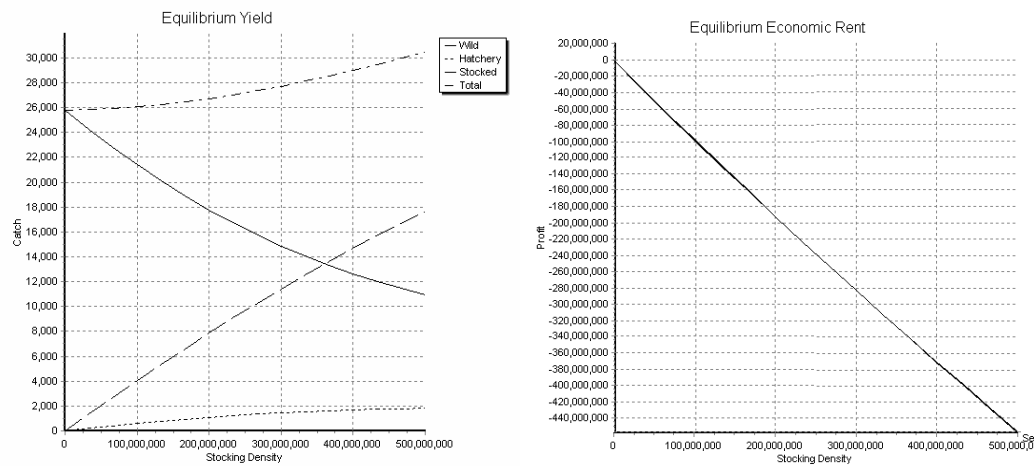


Figure 28. Yield and economic rent from North Sea sole enhancement assuming $M_{1H} = 16.5 \text{ year}^{-1}$.

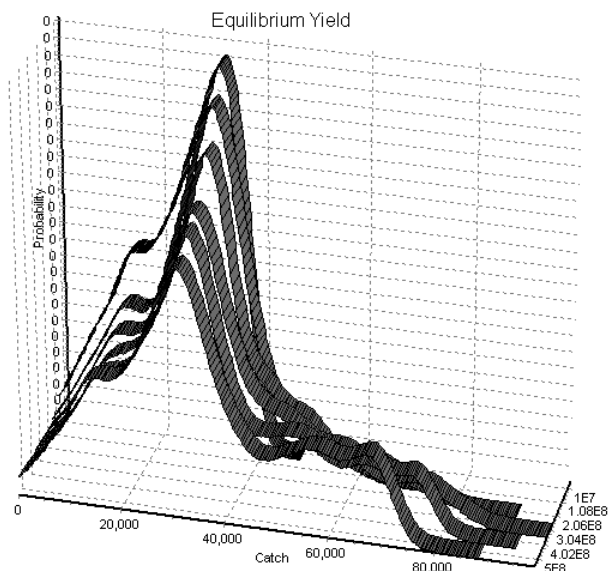


Figure 29. Uncertainty analysis of stocked fish natural mortality.

Results from the analysis can be synthesized in a decision table such as that shown in Table 4. The decision table shows the predicted outcomes of different management options in terms of selected criteria such as yield and economic rent. It should incorporate representation of key uncertainties, such as the natural mortality rate of stocked fish in our current example.

Table 4. Decision table for North Sea sole enhancement

Option \ Criterion	Yield		Economic rent	
	M_{IH}=3.0 year⁻¹	M_{IH}=16.5 year⁻¹	M_{IH}=3.0 year⁻¹	M_{IH}=16.5 year⁻¹
Current fishing effort, no enhancement	26,000	26,000	0	0
Reduce fishing effort by 66%, no enhancement	21,000	21,000	145,000	145,000
Current fishing effort, enhance with 240 Million recruits	68,000	27,000	165,000	<u>-240,000</u>
Reduce effort by 40 %, enhance with 170 Million recruits	53,000	26,500	187,000	<u>-160,000</u>

Conclusions

Overall the potential for North Sea sole enhancement is very limited. If we assume a natural mortality rate in line with the wild type natural mortality rate used in the current stock assessment, enhancement would be technically and economically feasible. However, the maximum economic rent generated with enhancement would be only marginally greater than the rent achievable with effort limitation alone. If we assume a natural mortality rate more in line with empirical distributions, even for wild type fish, enhancement would not be economically viable at all.

4.4.2 Thmorda reservoir

Background

Thmorda reservoir in Cambodia is a shallow irrigation reservoir with a surface area of 80-100 ha. The reservoir is fished by 15 families of full-time fishers, plus several hundred families who engage in fishing on a part-time basis. Virtually all species and the full size range of fish are exploited, and the annual catch varies

between 13 and 13 tons. The silver barb *Barbodes gonionotus* was historically present in the reservoir but has disappeared some years ago. The Cambodian department of Fisheries is considering the potential for establishing a culture-based fishery for *B. gonionotus* in Thmorda, and has carried out a release experiment (Figure 30).



Figure 30. Stocking *B. gonionotus* fingerlings in Thmorda reservoir (Photo: Ouk Vibol)

Aim of analysis

The aim of the analysis is to assess whether a *B. gonionotus* culture-based fishery will be economically viable at all, and whether current fishing practices (intensive exploitation of virtually all sizes of fish) pose a problem for the development of a culture-based fishery. Useful criteria include yield and gross revenue. Because fishing is carried out for a wide range of wild species which will continue to provide the mainstay of the fishery, we can initially ignore the cost of effort.

Model setup

The Cambodian department of fisheries has conducted a release experiment to establish the potential for developing a culture-based fishery for *B. gonionotus* in Thmordar. A total of 15,000 fingerlings of an average length of 9 cm were released, and their growth and recapture monitored over 7 months. The analysis of these data was carried out with the **EnhanceFish** auxiliary data tools described in Section 5. The resulting parameter estimates are given in Table 5, and can be loaded from the 'Thmorda.efa' file included in the **EnhanceFish** setup.

Table 5. Model setup for the Thmorda fishery

Parameter	Values	Basis
Life cycle L_0 L_r a_r	2 cm 9 cm 1	Essentially arbitrary. L_r was set to the stocking size, so that there is no density-dependence in mortality after stocking.
Growth $L_{\infty L}$ K g α β	61 cm 0.45 year^{-1} 0 1×10^{-8} 3	Release-recapture experiment (see Section 5). Density-dependence in growth not considered.
Nat. mortality $M_{1,W}$ $M_{1,S}$	71 year^{-1} 71 year^{-1}	Release-recapture experiment (see Section 5)
Reproduction L_m p r	40 cm -1 1	$0.66 L_{\infty L}$ Arbitrary – note that the stock-recruitment relationship implies there is virtually no recruitment.
Recruitment a^* b^*	10 100	Set so that maximum natural recruitment is negligible relative to stocking
Fishing F_{∞} L_c Q	1.7 year^{-1} 1.7 -2.7	Release-recapture experiment (see Section 5)
Evolution h^2	0	Arbitrary – note that the stock-recruitment relationship implies there is virtually no recruitment.

Results

Predicted equilibrium yield and gross revenue of the culture-based fishery are shown as a function of fishing effort in Figure 31. At the current level of effort ($E=1$) and stocking density (15,000 fingerlings), the culture-based fishery will yield a total of 0.9 t and an economic rent of 1200 US\$. Interestingly, both yield and economic rent are predicted to increase with increasing fishing effort. This implies that the current fishing pattern is not an impediment to developing a culture-based fishery, and that even a moderate increase in effort could be sustained.

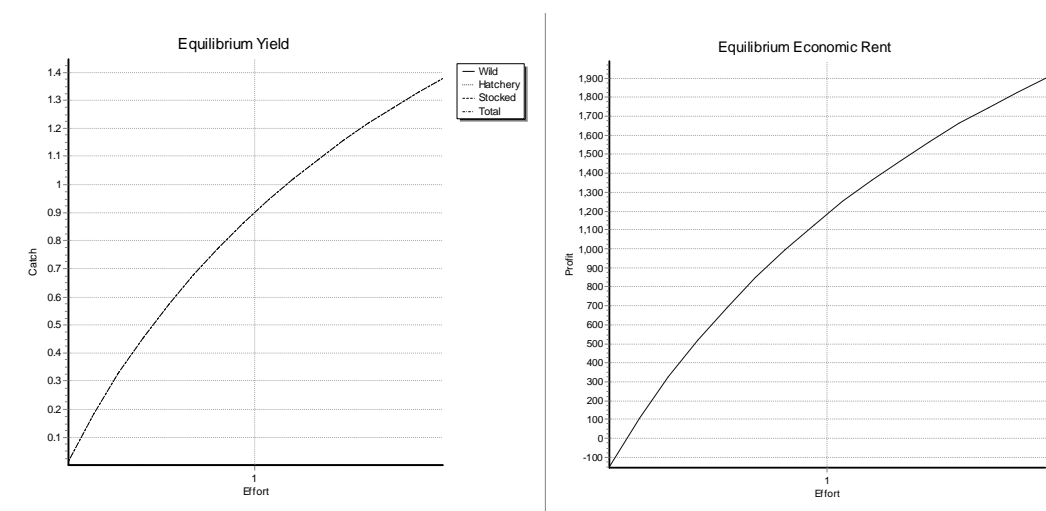


Figure 31. Equilibrium yield and gross revenue of the culture-based fishery in Thmorda reservoir.

Conclusions

Overall this initial result suggests that development of a culture-based fishery for *B. gonionotus* is economically advantageous and would not conflict with the existing capture fishery. Given that *B. gonionotus* was previously present in Thmorda, the species is likely to re-establish a self-recruiting population so that overall benefits may well be higher than those projected here on the basis of stocking alone.

4.4.3 Ubolratana reservoir

Background

Ubolratana is a large (25,000 ha), shallow hydroelectric reservoir in Northeast Thailand. It supports a productive fishery based on some 85 species, exploited by about 1500 full time fishers (Figure 32). The Thai Department of Fisheries is considering enhancing the stock of an indigenous fish, the cyprinid *Henicorhynchus siamensis*. The *H. siamensis* fishery currently yields about 110 t per year. A slow decline in yield has been observed, and attributed to overexploitation. Enhancement is being considered as a way of increasing yields.



Figure 32: Processing fish at Ubolratana reservoir (Photo: Thai Department of Fisheries).

Aim of analysis

The aim of the analysis is to establish the biological and economic potential for enhancing *H. siamensis* stock. Criteria include yield and economic revenue.

Model setup

Population parameters of The *H. siamensis* in Ubolratana have been estimated from length frequency data using the FAO FiSat package. The stock recruitment relationship is unknown, but the 'SRR Estimate' function has been used to generate a plausible relationship (Figure 33, see also Section 3.4.6). The parameter values used in the **EnhanceFish** analysis are shown in Table 6, and can be loaded from the 'Ubolratana.efa' file included in the **EnhanceFish** setup.

EnhanceFish Manual (Beta version)

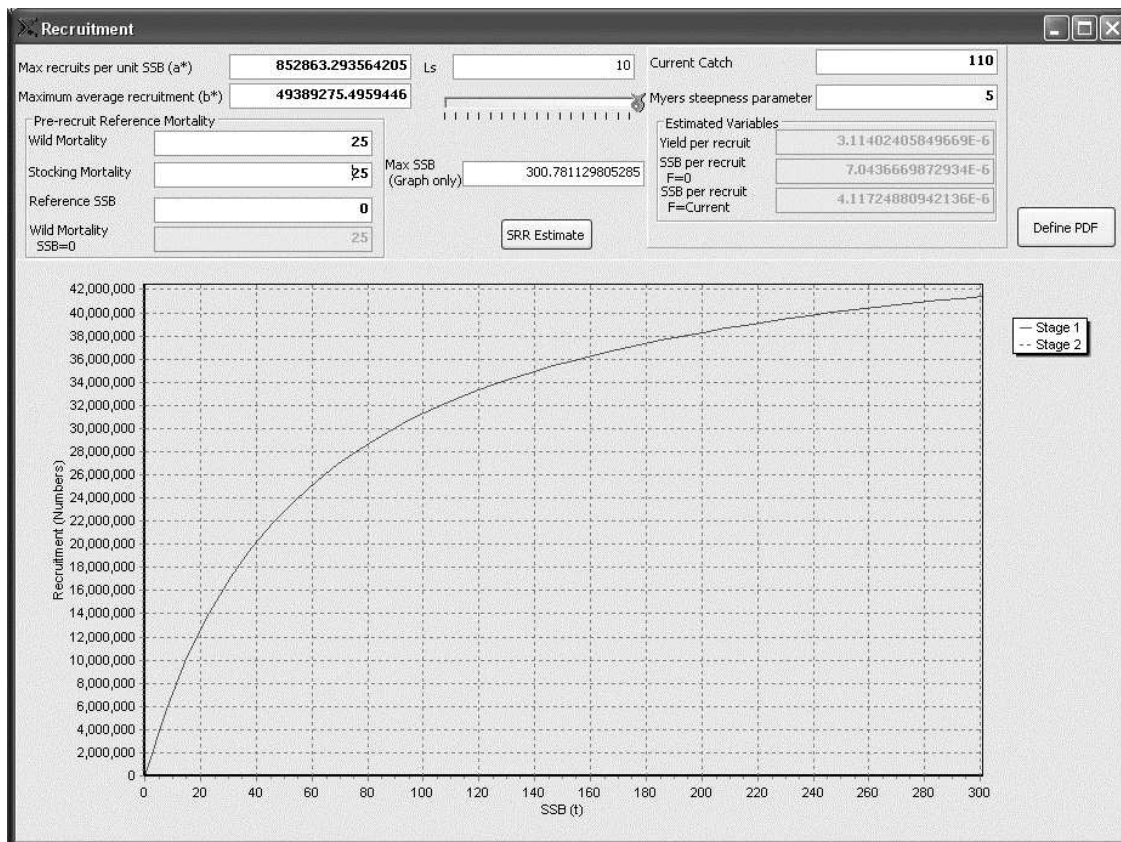


Figure 33. Obtaining an SRR estimate for *H. siamensis* in Ubolratana

Results

The analysis starts with an assessment of the capture fishery (Figure 34). This shows that the fishery is not currently overexploited: higher yield and gross income could be obtained if fishing effort was increased.

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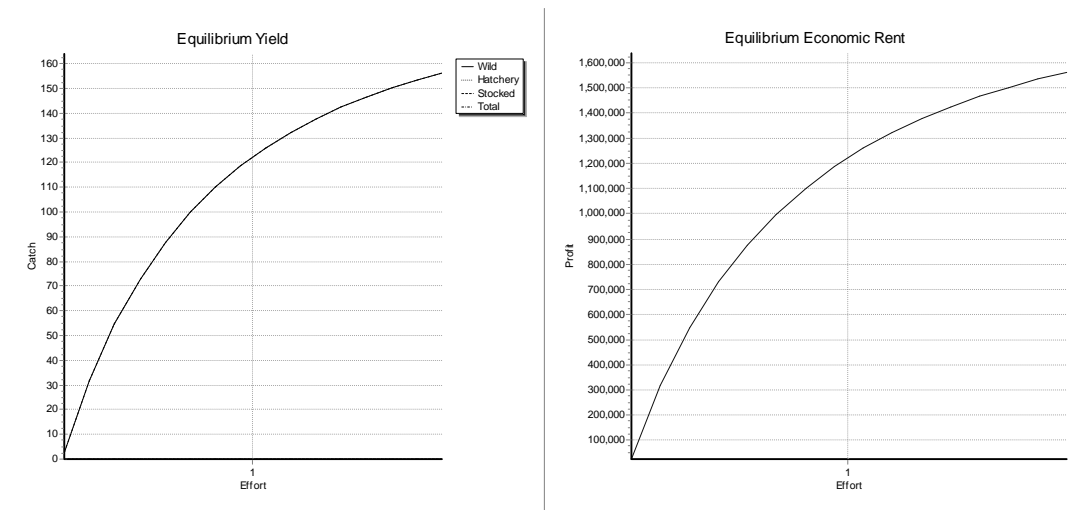


Figure 34. Wild population yield and gross income from fishing as a function of fishing effort

Table 6. Model setup for the Ubolratana fishery

Life cycle		
L_0	2 cm	Gear selectivity and assumption that density dependent mortality occurs below 10 cm.
L_r	10 cm	
a_r	1	
Growth		
$L_{\infty L}$	25 cm	FiSat analysis of length frequency data. $1.08 L_{\infty B}$
K	0.6 year^{-1}	FiSat $(0.08 L_{\infty}(B^*))/B^*$
g	0	
α	5.5×10^{-9}	Length-weight relationship.
β	3	
Nat. mortality		
$M_{1,W}$	25 year^{-1}	Set so that M in recruited stock corresponds to FiSat estimate based on Pauly's empirical formula.
$M_{1,S}$	25 year^{-1}	
Reproduction		
L_m	14 cm	Direct measurement Assumption
p	-1	
r	1	Assumption
Recruitment		
a^*	852063	SRR estimate based on growth, mortality and maturity parameters, a current catch of 110 t, and Myer's $\tilde{a} = 5$.
b^*	49389275	
Fishing		
F_{∞}	1 year^{-1}	FiSat analysis of length frequency data.
L_c	12	
q	-1	
Evolution		
h^2	0.2	Comparative data.

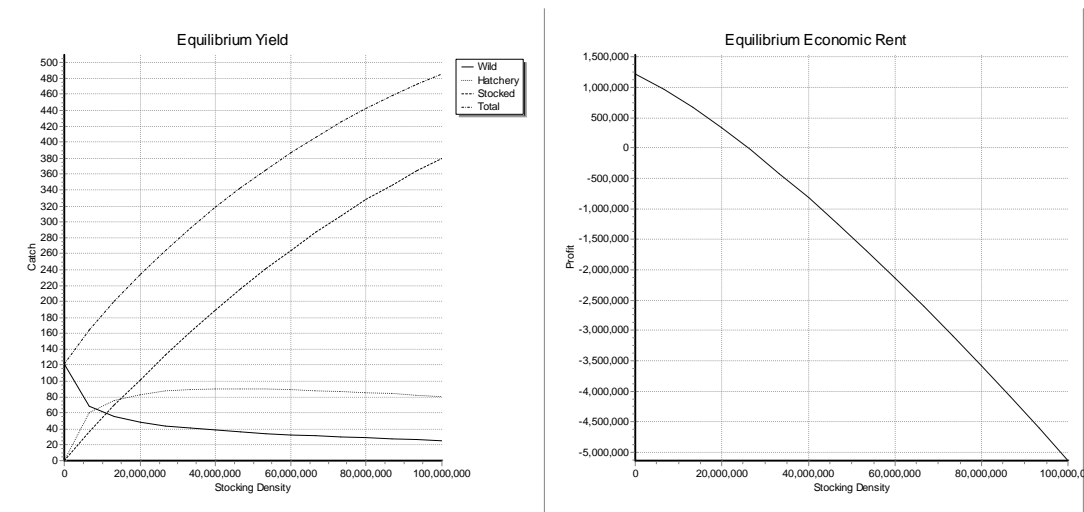


Figure 35. Impact of stocking on yield and economic rent from the fishery

In a second step, the potential for stocking hatchery fish at a length of 10 cm is explored (Figure 35). It is predicted that stocking can increase yield substantially, despite some displacement of wild by stocked and hatchery-type fish. Most importantly, however, the predicted economic rent from the fishery declines with increasing stocking density throughout. This shows that the cost of stocking grossly exceeds the expected benefit.

Conclusions

Stock enhancement of *H. siamensis* in Ubolratana would not be economically viable.

5 Data tools for analyzing release experiments

EnhanceFish is associated with auxiliary data tools currently implemented in an Excel workbook (EnhanceFishDataTools.xls), which may be downloaded from the **EnhanceFish** website. The tools may be used to estimate growth and mortality parameters from release experiments.

Release experiments typically involve the stocking of individually or batch-marked fish. Recaptures of marked fish in the fishery are recorded over a period after release. Data on individual recaptures normally comprise the date and place of recapture, and the length and/or weight of the fish. Often this information is reported in aggregated form: as the number and mean length or weight of fish recaptured within consecutive periods of duration Δt (e.g. months, quarters or years) after release. The analysis approach presented here is designed for such aggregated data. It is the temporal pattern of size and recaptures after release that contains information on population dynamics, hence the temporal dimension of the data must be preserved (where data are aggregated into overall totals, the analysis can not be carried out).

The analysis tools use maximum likelihood estimation. Maximum likelihood estimation works by calculating the likelihood of the data given a model and its parameter values. Initial parameter values are determined visually 'fitting' the model to the data, and maximum likelihood estimates are then obtained by searching for the parameters that maximize the likelihood of the data. For convenience the goodness of fit is expressed as the negative log likelihood L , so that likelihood is maximized by minimizing L . The parameter values that minimize L may be found using the SOLVER tool in Excel. Confidence limits for model parameters can be constructed from their likelihood profiles (Hilborn & Mangel 1997).

The release experiment tools are illustrated here with data from the *B. gonionotus* release experiment in Thmorda reservoir, Cambodia (see Section 4.3.1). In the experiment, 15000 fingerlings of *B. gonionotus* were released in the reservoir, where the species was absent at the time of stocking. Growth and recapture of the released cohort were monitored through catch surveys of the reservoir fishery. Whilst the fish were not marked, the species was absent at the time of stocking and hence all captures of *B. gonionotus* in the months following release were assumed to be from the released cohort.

5.1 Growth parameter estimation

The setup of the growth parameter estimation tool is shown in Figure 36. Length measurements were aggregated into a mean length for each month after release. These data (time since release, and mean length during the month) have been entered into the red area (cells B14 to C21). Predicted length is calculated in cells D14 to D21, based on a von Bertalanffy growth model and the parameter values in the yellow area (cells B6 to B7). The model was then fitted by minimizing the negative log likelihood L in the blue cell (E6) using the Solver tool.

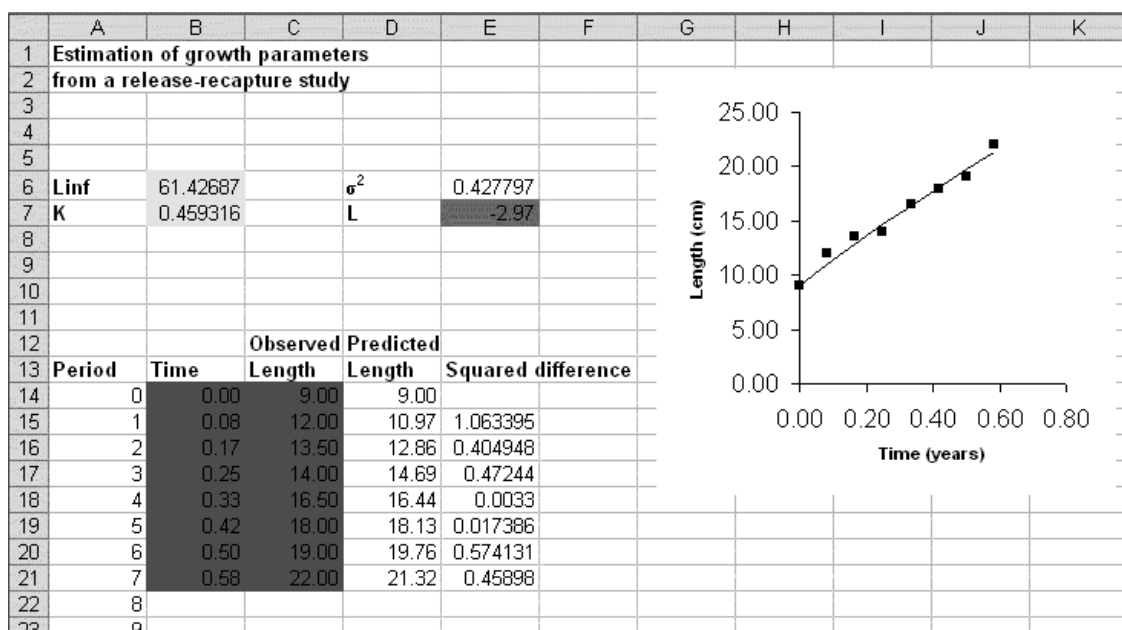


Figure 36. Spreadsheet for estimating growth parameters from a release-recapture study

The solver tool comes as a standard component of most recent Excel versions, but may need to be 'added in' before first use. Go to 'Tools', and if Solver does not appear in the drop-down menu click on 'Add ins' and add the Solver. Upon opening the Solver tool, the menu will look as shown in Figure 37.

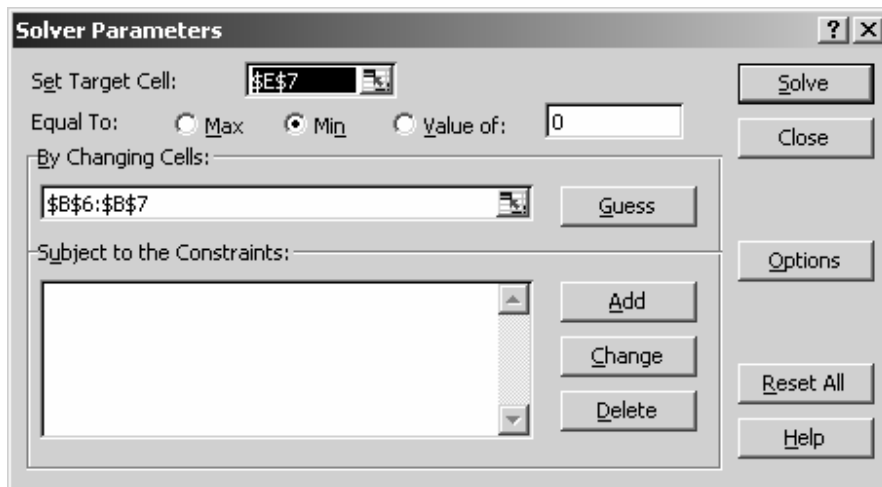


Figure 37. Excel Solver menu.

The target cell is E7, the negative log likelihood L which we'd like to minimize by changing cells B6 and B7 where the parameter values are given. Make sure to set the 'Equal to' selector to 'Min' and click on 'Solve'. The Solver will now search for the parameter values that minimize L . You may like to try this out by changing the parameter values from the best estimates, and re-fitting the model.

To apply this data tool to a new data set, simply enter the new data in the place of the Thmorda data. Then find approximate growth parameters by changing the values until the graph shows a reasonable fit. Finally, use the solver tool to find the best estimates. Sometimes the numerical search does not work well when the starting values are very different from the best estimates. If this is the case, try running the search again from a different set of starting values.

5.2 Natural and fishing mortality

The population analysis is based on modelling the probability of recapturing marked fish over time, and fitting the model to observed recapture data. The setup of the growth parameter estimation too is shown in Figure 38. Note that, because mortality is length-dependent, the worksheet includes a growth model using the parameters determined in the previous analysis (Section 5.1.1). Release and recapture data are entered in the red areas: number released (G23), time since release (B27 to B35), and number recaptured (H27 to H 35). Model parameters are set up in the yellow area (B11 to B16), and L calculated in the blue cell (L21). Note that this tool uses a multinomial error model in the calculation of L . As before, the model was fitted by minimizing the negative log likelihood L using the Solver tool.

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The mortality model has six parameters:

- M_1 : Mortality rate at unit length
- F : Fishing mortality rate in the fully exploited length range
- L_c : Gear selection length
- p : Steepness of the selectivity curve
- l : tag loss rate (rate at which tags are lost over time)
- q tag reporting rate (proportion of tags recovered that are actually reported)

In the example used here, the released fish were not tagged and hence the tag loss and reporting rates are inapplicable. The rates have been fixed at 0 and 1 respectively, and are not estimated from data.

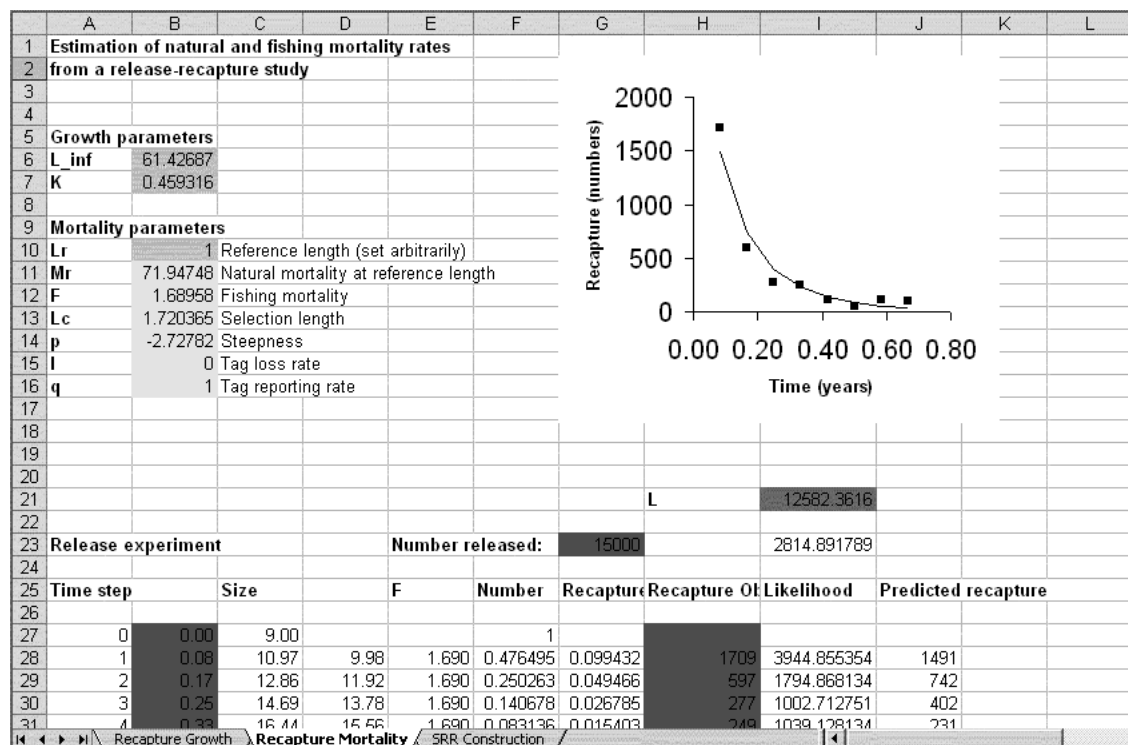


Figure 38. Spreadsheet for estimating mortality parameters from a release-recapture study

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Appendix: Mathematical details of the *EnhanceFish* model

A1 The population model

The ***EnhanceFish*** model is essentially based on the model developed in Lorenzen (2005), but incorporates some modifications.

Maturity model

The proportion mature $Q(a,t)$ is given by

$$Q(a,t) = \frac{1}{(1 + \exp(p(L_m - L(a,t))))} \quad (\text{A1.1})$$

where L_m is the length at 50% maturity and p describes the steepness of the maturity curve.

Growth model

Density-dependent growth is described by a simple extension of the von Bertalanffy growth function with asymptotic length $L_\infty(B)$ a function of population biomass B

$$L_\infty(B) = L_{\infty L} - g B \quad (\text{A1.2})$$

where $L_{\infty L}$ is the asymptotic length in the absence of competition ($B \rightarrow 0$), and g measures the strength of density-dependence.

Growth is described by the density-dependent von Bertalanffy model defined in equation (A1.2), starting with a constant length at recruitment $L(1,t)$. All population components are assumed to share the same growth pattern. A discrete time model to predict mean length $L(a,t)$ of age group a at time t from mean length of the cohort in the previous year $L(a-1,t-1)$ is given by:

$$L(a,t) = L_{\infty B} - (L_{\infty B} - L(a-1,t-1)) \exp(-K) \quad (\text{A1.3})$$

where $L_{\infty B}$ is the asymptotic length at biomass density B (Equation A1.2).

Mortality model

Natural mortality is modelled as an inverse function of length:

$$M(L) = M_1 \frac{1}{L} \quad (\text{A1.4})$$

where $M(L)$ is the natural mortality rate at length L , and M_1 is the natural mortality rate at unit length.

Gear model

Gear selectivity and proportional maturity are described by length-dependent logistic functions. Fishing mortality is given by

$$F(a, t) = \frac{F_{\infty}}{(1 + \exp(q(L_c - L(a, t))))} \quad (\text{A1.5})$$

where F_{∞} is the fishing mortality at fully selected length, L_c is the length at 50% gear selection and q describes the steepness of the selectivity curve.

Recruitment model

The stock recruitment relationship is given by

$$N_r = \frac{a^* S}{1 + b^* S} \quad (\text{A1.6})$$

where N_r is the number of recruits, S is spawner biomass, a^* is the maximum number of recruits produced per unit spawner biomass (the product of larval production and subsequent survival) and b^* describes the degree of density-dependence in recruitment. This may be partitioned into a three-stage model with density-independent larval production

$$N_0 = f S \quad (\text{A1.7})$$

and two consecutive phases of potentially density-dependent survival according to a Beverton-Holt relationship, e.g. for the first stage:

$$s_1 = \frac{N_1}{N_0} = \frac{a_1}{1 + b_1 N_0} \quad (\text{A1.8})$$

The parameters f , a_1 , b_1 , a_2 , and b_2 of the three-stage model are related to a^* and b^* by

$$a^* = f a_1 a_2 \quad (\text{A1.9})$$

and

$$b^* = f b_1 + f a_1 b_2 \quad (\text{A1.10})$$

The three-stage model thus has three free parameters, which are however constrained within certain ranges given that a_1 and a_2 are survival rates and thus must be between 0 and 1.

Unpacking the stock-recruitment relationship

Unpacking of the stock-recruitment relationship is carried out as follows. Length growth in the pre-recruit stage is described by a linear growth rate v . Pre-recruit mortality at reference SSB (SSB^*) is described by the same size dependent (length-inverse) model as in the recruited stock, but the mortality rate M_1 can be set to a different value from that used in the recruited stock. Survival at SSB^* during the two stages is calculated as:

$$s_1(SSB^*) = \left(\frac{L_0}{L_s} \right)^{\frac{\mu_1}{v}} \quad (\text{A1.11})$$

$$s_2(SSB^*) = \left(\frac{L_s}{L_r} \right)^{\frac{\mu_1}{v}} \quad (\text{A1.12})$$

Then:

$$f = \frac{R(SSB^*)}{SSB^* s_1 s_2} \quad (\text{A1.13})$$

Density-dependence is allocated to the two phases according to:

$$d = \left(\frac{L_s - L_0}{L_r - L_0} \right) \quad (\text{A1.14})$$

This allocates density-dependence in proportion to the stage's length interval. The density-dependent parameters are then obtained by:

$$b_1 = \frac{d a^*}{f b^*} \quad (\text{A1.15})$$

$$a_1 = s_1 (SSB^*) (1 + b_1 N_0 (SSB^*)) \quad (\text{A1.16})$$

$$b_2 = \frac{\frac{a^*}{b^*} - f b^*}{f a_1} \quad (\text{A1.17})$$

$$a_2 = \frac{a^*}{f a_1} \quad (\text{A1.18})$$

Population dynamics

We assume that fishing occurs in discrete events once a year, and that natural mortality is size-dependent and acts continuously between the fishing events. Population numbers N_I of the different components ($I=W, H, S$) are given by

$$N_I(a,t) = N_I(a-1,t-1) \exp(F(a-1,t-1)) \left(\frac{L(a-1,t-1)}{L(a-1,t-1) + L_\infty(B)(e^k - 1)} \right)^{\frac{M_{1,I}}{L_\infty K}} \quad (\text{A1.19})$$

where F is the fishing mortality rate, and $M_{1,I}$ is the natural mortality rate at unit length. Catch at age $C_I(a,t)$ is given by:

$$C_I(a,t) = N_I(a,t) (1 - \exp(-F(a,t))) \quad (\text{A1.20})$$

Total biomass B , spawner biomass S and Yield Y of the population components are given by

$$B_I(t) = \sum_a \alpha L(a,t)^\beta N_I(a,t) \quad (\text{A1.21})$$

$$S_I(t) = \sum_a Q(a,t) \alpha L(a,t)^\beta N_I(a,t) \quad (\text{A1.22})$$

$$Y_I(t) = \sum_a \alpha L(a,t)^\beta C_I(a,t) \quad (\text{A1.23})$$

where α and β are parameters of the length-weight relationship.

Natural juvenile production J up to the stage at which hatchery fish are released is described as follows. Survival of naturally spawned juveniles to the stage at which hatchery fish are released is given by a Beverton-Holt type survival function s_1 dependent on total larval production:

$$s_1 = \frac{a_1}{1 + b_1 f (S_W + r(S_H + S_S))} \quad (\text{A1.24})$$

where f is the larval production per unit of spawner biomass, and r is the reproductive performance of the hatchery and stocked components relative to the wild phenotype ($0 \leq r \leq 1$). Natural selection is assumed to act during the first juvenile stage, described by transition of a proportion h^2 (heritability) of larvae produced by the hatchery and stocked components to juveniles of the wild component. The numbers of wild and hatchery juveniles J_W and J_H are thus given by:

$$J_W = f s_1 (S_W + r h^2 (S_H + S_S)) \quad (\text{A1.25})$$

$$J_H = f s_1 r (1 - h^2) (S_H + S_S) \quad (\text{A1.26})$$

Survival from release to recruitment is subject to the second Beverton-Holt survival function s_2 , dependent on the combined abundance of naturally produced juveniles ($J_W + J_H$) and stocked fish R .

$$s_2 = \frac{a_2}{1 + b_2 (J_W + J_H + R)} \quad (\text{A1.27})$$

Recruitment into the different population components at age 1 is then given by:

$$N_W(1, t) = s_2 J_W \quad (\text{A1.28})$$

$$N_H(1, t) = s_2 J_H \quad (\text{A1.29})$$

$$N_S(1, t) = s_2 R \quad (\text{A1.30})$$

where R is the number of hatchery fish released. This formulation allows release at any juvenile size or stage to be represented by a particular combination of before- and after release survival functions as defined by SSR unpacking.

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A2 Analysis of release experiments

Release experiments typically involve the stocking of individually or batch-marked fish. Recaptures of marked fish in the fishery are recorded over a period after release. Data on individual recaptures normally comprise the date and place of recapture, and the length and/or weight of the fish. Often this information is reported in aggregated form: as the number and mean length or weight of fish recaptured within consecutive periods of duration Δt (e.g. months, quarters or years) after release. The analysis approach presented here is designed for such aggregated data (Lorenzen 2006).

Growth model

Both natural and fishing mortality rates are size-dependent, and it is thus necessary to model growth as a basis for modelling the mortality processes. Growth is often well described by a von Bertalanffy model predicting mean length $l(t_i)$ at time t_i from mean length of the cohort at the time of release $l(t_0)$:

$$l(t_i) = l_{\infty} - (l_{\infty} - l(t_0)) \exp(-K t) \quad (\text{A2.1})$$

where l_{∞} is the asymptotic length and K is the growth rate.

As data have been aggregated over intervals of time, mean length during each interval is used to fit the model to data, and calculate the length-dependent natural and fishing mortality rates for that interval. Mean length $\bar{l}(t_i)$ during the interval preceding t_i is given by

$$\bar{l}(t_i) = \frac{l(t_{i-1}) + l(t_i)}{2} \quad (\text{A2.2})$$

The maximum likelihood estimate of the growth parameters l_{∞} and K is obtained by minimizing the negative log likelihood L of the observed length data given the model. Assuming a normal error distribution, denoting the observed mean length in interval t_{i-1} to t_i as x_i , and ignoring an additive constant the log likelihood is L given by:

$$L = \frac{n}{2} \log \left(\frac{\sum_{i=1}^{i_{\max}} (x_i - \bar{l}_i)^2}{n} \right) \quad (\text{A2.3})$$

The parameter values that minimize L may be found using numerical search routines such as the SOLVER tool in Excel. Confidence limits for model parameters can be constructed from their likelihood profiles (Hilborn & Mangel 1997). Likelihoods of independent data sets predicted by the same model can be combined. Thus, if several independent releases have been conducted and the resulting data are predicted by a joint model, the negative log likelihoods L of all experiments given the joint model may be combined additively.

Population model

The population analysis is based on modelling the probability of recapturing marked fish over time, and fitting the model to observed recapture data. It broadly follows established methods for analysing recapture data (Lebreton *et al.* 1992; Julliard *et al.* 2001), but incorporates the size-dependent mortality model and is formulated specifically for fitting to aggregated data. Assuming that recapture monitoring covers the full area of distribution, the probability of a marked fish being recaptured and reported in any particular period depends on the natural and fishing mortality processes that have acted since the time of release, the rate at which tags are lost from live fish, and the proportion of recovered tags that are reported.

Both natural and fishing mortality rates are size dependent. Following the results of Lorenzen (1996, 2000), natural mortality is assumed to be inversely proportional to length:

$$M(\bar{l}) = M_r \frac{l_r}{\bar{l}} \quad (\text{A2.4})$$

where $M(\bar{l})$ is the natural mortality rate at mean length, and M_r is the mortality rate at reference length l_r . The relationship between size and fishing mortality depends on the gear types used in the fishery, but is often well described by a logistic function of length:

$$F(\bar{l}) = \frac{F_{\infty}}{(1 + \exp(q(\bar{l} - l_c)))} \quad (\text{A2.5})$$

where F_{∞} is the fishing mortality at fully selected length, l_c is the length at 50% gear selection and q describes the steepness of the selectivity curve (Gulland 1981).

Using the size-dependent natural and fishing mortality models and assuming that tag loss is a size-independent rate process, the probability $Q(t_i)$ of a tagged fish surviving to time t_i and retaining its tag can be calculated from $Q(t_{i-1})$ by:

$$Q(t_i) = Q(t_{i-1}) \exp(-(M(\bar{l}) + F(\bar{l}) + \phi) \Delta t) \quad (\text{A2.6})$$

where ϕ is the rate of tag loss. This model assumes that all captured fish are retained rather than re-released, as is the case in most commercial fisheries. Finally, the probability $P(t_i)$ of a tagged fish being recaptured and reported in period t_{i-1} to t_i is given by:

$$P(t_i) = \rho Q(t_{i-1}) \frac{F(\bar{l})}{(M(\bar{l}) + F(\bar{l}) + \phi)} (1 - \exp(-(M(\bar{l}) + F(\bar{l}) + \phi) t)) \quad (\text{A2.7})$$

where ρ is the probability of a tag recapture being reported. Using this model it is possible predict the probability of a tag being reported for all periods monitored.

Parameter estimation is again by maximum likelihood. For each period, the probability $P(t_i)$ of a tag being recaptured and reported is given in equation 7. The probability of a tag not being reported at all equals one minus the sum of the probabilities $P(t_i)$ for all periods monitored. It is thus straightforward to calculate the negative log likelihood L of the observed data:

$$L = -\sum_{i=1}^{i_{\max}} C(t_i) \ln(P(t_i)) - \left(R - \sum_{i=1}^{i_{\max}} C(t_i) \right) \ln \left(1 - \sum_{i=1}^{i_{\max}} P(t_i) \right) \quad (\text{A2.8})$$

where R is the number of tagged fish released, and $C(t_i)$ is the number of recaptures actually reported in the period t_{i-1} to t_i . The maximum likelihood estimate of the model parameters is obtained by finding the parameter values that minimize L through numerical search.

The population model described here is relatively complex. It contains a total of six free parameters (M_r , F_{∞} , q , l_c , ϕ and ρ), which may be difficult to estimate from data sets that are small or of low contrast. It may thus be necessary to fix certain parameters a priori at values estimated in independent studies. The tag loss rate ϕ in particular can be estimated independently using double-marked fish (Seber 1982).

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