

Software for predicting deposition of wastes arising from fish farms – March 2008

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Other models available: AutoDEPOMOD (automated version of DEPOMOD used regulation of Scottish sites); MERAMOD (Eastern Mediterranean Sea Bass, Sea Bream), BenOss (sewage discharges)

Training courses for these models where the user learns how to use the model using their own data, can be organised. Please note, contouring software is not supplied with any of these models.

Overview

DEPOMOD is a particle tracking model developed at Scottish Association for Marine Science which predicts the dispersion of particulate wastes from fish farms (Cromey *et al.*, 2002a, 2002b). DEPOMOD has been developed from a model, BenOss, also developed at SAMS and used by SEPA and water companies to assess the dispersion of discharges from long sea outfalls (Cromey *et al.*, 1998). The use of DEPOMOD for predicting dispersion from an existing or a proposed farm is beneficial to both the farmer and the regulator, allowing various scenarios to be tested to aid the decision making process. The model forms part of the regulatory process in Scotland (www.sepa.org.uk/aquaculture) and has been tested in other countries for this purpose.

DEPOMOD has a structure made up of the following components: grid generation, particle tracking, resuspension and benthic response. A sub-model GaBoM (Growth and Biomass Model) is also available for predicting feed input throughout a growing cycle. The model runs on a pc-based Windows 95TM platform or later. Users should read the model output section below and note a contouring package is not included with DEPOMOD.

DEPOMOD has the following modelling capabilities:

- Prediction of solids flux ($\text{g solids m}^{-2} \text{ bed yr}^{-1}$) of waste food and faecal material and several benthic indices arising from an operational farm at any stage of the growing cycle
- Prediction of the total deposition of waste material ($\text{g solids m}^{-2} \text{ bed}$) arising from a single release
- Prediction of the total deposition and sediment concentration ($\text{g kg}^{-1} \text{ sediment}$) of the active ingredient of in-feed medicines

Some example scenarios indicating how DEPOMOD may assist in consultation exercises:

- Assessing the potential impact of a farm throughout a growing cycle or if biomass consent is increased

- Site selection process for a new farm can be assisted by examining proposed positions and biomass levels
- Prediction of the dispersion of particulates during use of in-feed medicines

Verifying model predictions (model validation) has been undertaken in three stages. Validation of initial deposition of material from the farm was undertaken with sediment trap studies. A field trial and modelling study was then undertaken to assess the resuspension of particulate tracer from the sea bed. The benthic response model was then developed to establish semi-empirical relationships between predicted solids accumulation and several benthic indices measured at fish farms.

Validation of DEPOMOD consisted of three stages:

i. Validation of the particle tracking stage with sediment traps. To validate near-field, sea surface to sea bed particle tracking algorithms, a 24 hour sediment trap study was undertaken at the two sites. For the dispersive site, model predictions of flux ($\text{g m}^{-2} \text{d}^{-1}$) generally agreed well with field data and an accuracy of $\pm 20\%$ was achieved. At the depositional site, an improved accuracy of $\pm 13\%$ was achieved. An extensive sensitivity test of the model input data used was undertaken and found the most sensitive parameter in the model to be particle starting position in the pen, which was subsequently defined in the model as random. Some sensitivity of horizontal dispersion coefficients and current speeds was also found.

ii. Validation of the resuspension model via a tracer study. To validate the DEPOMOD resuspension model, a UV fluorescent particle tracer was selected with similar settling characteristics to salmonid faeces and food. Tracer was introduced to the seabed (water depth ~ 30 m) and sediment samples taken on days 0, 3, 10, 17 and 30 to measure the horizontal and vertical distribution of tracer in sediments. The bulk of the deployed tracer initially deposited in an area 25 m radius from the release point and was observed to steadily decrease to zero over a period of 30 days. Redeposition of tracer in the study area was minimal where low concentrations were measured at a distance of up to 200 m from the release point in the direction of the residual current. The validated model generally gave good predictions of total mass budgets ($\pm 7\%$ of total tracer released) particularly where tracer concentrations were high near the release point.

iii. Validation of the benthic module. Semi-empirical quantitative relationships between predicted solids accumulation ($\text{g m}^{-2} \text{yr}^{-1}$) and observed Infaunal Trophic Index (ITI) and total abundance have been established using data from several fish farm sites. Envelopes of Acceptable Precision (EAP) have also been established. These allow predictions of indices to be obtained where the width of the EAP reflects natural variability of the benthic data measured for duplicate samples. Data are also given for Shannon Weiner, Evenness and number of species but no predictive relationships have been established due to the variability with these indices in the sea loch environments studied.

Sensitivity analyses were undertaken on the main model variables and model parameters and assessed for sensitivity on predictions of solids accumulation and ITI. The most sensitive variables in the model were current speed, horizontal dispersion coefficients used in the random walk model and grid cell resolution. These results

demonstrated the need for accurate and reliable current measurements in order to obtain realistic predictions from the model. The sensitivity of the model to horizontal dispersion coefficients also demonstrates the importance of these measurements, which are severely lacking for sea loch environments.

General data requirements for modelling of steady state solids accumulation with DEPOMOD ($\text{g m}^{-2} \text{yr}^{-1}$)

The following data are desirable for the set up of DEPOMOD:

- 1.1 current velocity data for an area close to the fish farm site (include information on heights of instruments above bed, total depth of water column at mooring, position of mooring, time (e.g. GMT) and direction formats (e.g. degrees true or magnetic))
- 1.2 some knowledge of the vertical structure of the water column; shear in the water column can be represented in DEPOMOD by setting up layers in the model represented by different current velocity records
- 1.3 horizontal and vertical dispersion coefficients for the area⁺
- 1.4 bathymetry of the area of interest either from a site survey or from an Admiralty chart of the area
- 1.5 number and dimensions (length, width and depth) of pens and the proposed/existing positions of these pens
- 1.6 feed input data (kg food d^{-1} for the whole farm) and mean fish size for the intended scenarios
- 1.7 information on water content and digestibility of the food to be used at the stage of the growing cycle to be modelled*
- 1.8 food and faecal settling velocity data from measurements undertaken by SAMS and literature values*

*=DEPOMOD defaults available

⁺=DEPOMOD recommended values available

The following data would be useful for assessment of site characteristics and interpretation of model results:

- 2.1 benthic macroinvertebrates present at the proposed site and the value of some benthic indices (e.g. Species, Total abundance, Biomass, Infaunal Trophic Index, Shannon Weiner) for sampling stations at the site
- 2.2 sediment type and characteristics for the proposed/existing site

General data requirements for modelling of total deposition from a single release (g m^{-2})

As for data points 1.1-1.8 above, but with the exception of 1.6 which requires the following:

- 3.1 feed input data for the whole release period (kg food per unit time)

General data requirements for modelling of total deposition (g m^{-2}) or sediment concentration (g kg^{-1}) of in-feed medicines

As for data points 1.1-1.8 above and the additional information:

- 4.1 Concentration of active ingredient on medicated feed ($\text{g ingredient kg}^{-1}$ food)
- 4.2 Excretion of active ingredient by fish (e.g. 90% excreted)
- 4.3 Mass and total period of time for which medicated feed is being used (e.g. 100 kg pen^{-1} over 7 days)

Model Output

Predictions are given in an ASCII text data file showing predictions for the grid and for sampling stations. Predictions are also given in a x, y, z ASCII file which can be used in a contouring package for visual display. A contouring package is NOT included with DEPOMOD.

Model distribution

There are more than 100 license holders of DEPOMOD in 14 different countries (Figure 6).

Current model development

The benthic module is being tested with different indices under the ECASA project (www.ecasatoolbox.org.uk) and a biochemical component is also being developed.

Other related models available

MERMOD version 1.4 – Validated for sea bream and sea bass farms in the Eastern Mediterranean, this model can be used for prediction of solids flux and benthic effects (e.g. benthic descriptors such as species, abundance, biomass, etc). Released January 2004 (www.ecasatoolbox.org.uk).

AUTODEPOMOD version 2 – This is an automated piece of software used specifically by the Scottish regulator SEPA and others to determine maximum biomass and sea lice treatment consents at farms. It integrates Surfer for Windows™, Excel™ and DEPOMOD. Released June 2005.

BenOss – Used for prediction of flux and benthic effects from sewage outfalls and is still used despite a long period elapsing since its release in 1995.

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Project participants and funding

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Project participants

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Scottish Salmon Growers Association (now Scottish Quality Salmon)
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Chris Cromey, Map and Marine Limited is the sole distributor of the models.

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Further details available from:

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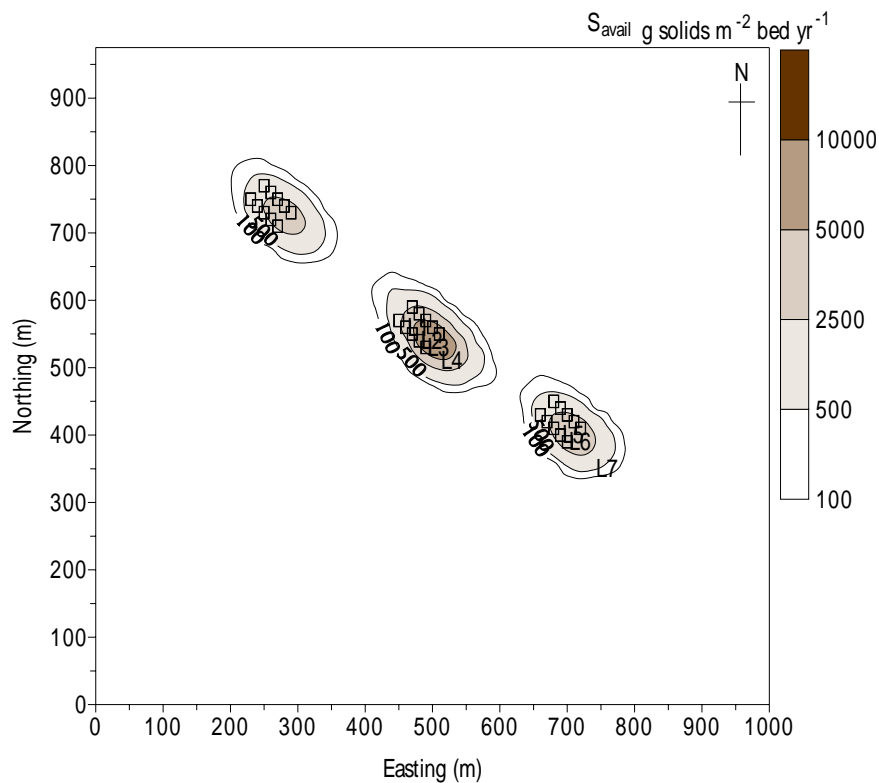


Figure 1. Predicted solids accumulation (S_{avail}) for Site A showing sampling stations L1–L7 (cage centres shown as \square). Plot generated with Surfer for Windows™.

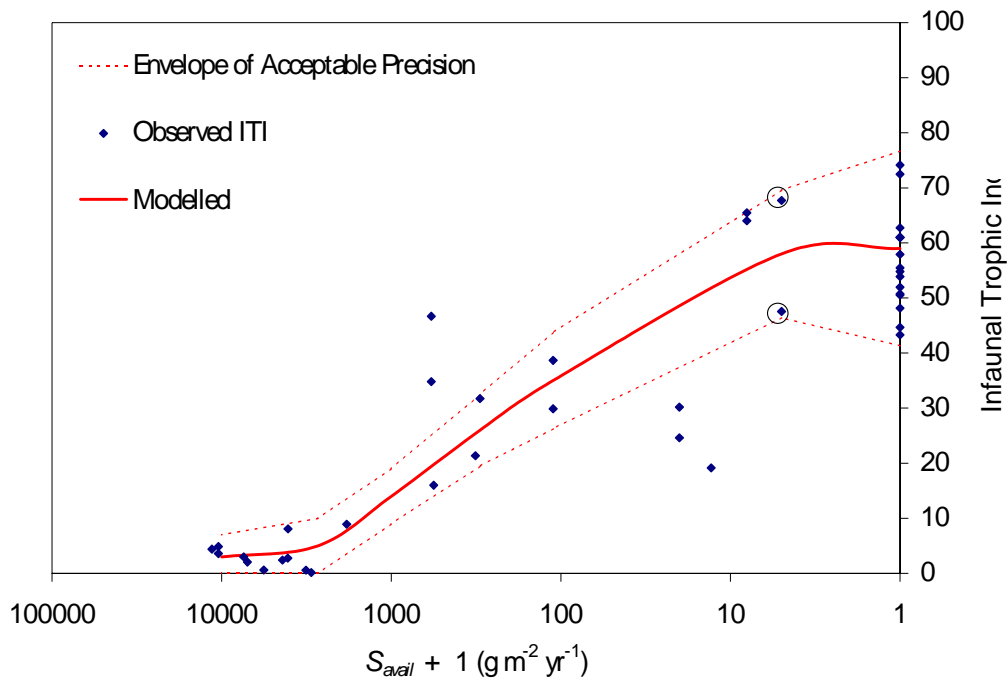


Figure 2. Modelled solids accumulation (S_{avail}) plotted against observed Infaunal Trophic Index. Circles demonstrate the variation in the benthic composition of

duplicate grabs and the Envelope of Acceptable Precision is defined to take account of this natural variation (Table 20) (88% in EAP, n = 42 stations).

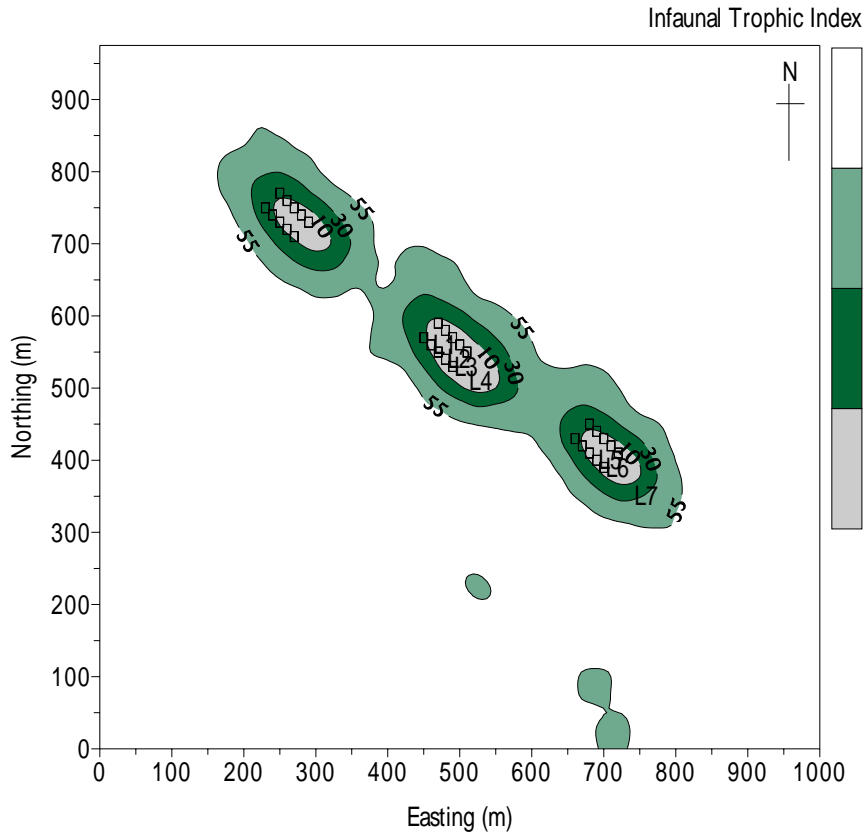


Figure 3. Predicted Infaunal Trophic Index for Site A showing sampling stations L1–L7 (cage centres shown as □). Plot generated with Surfer for Windows™.

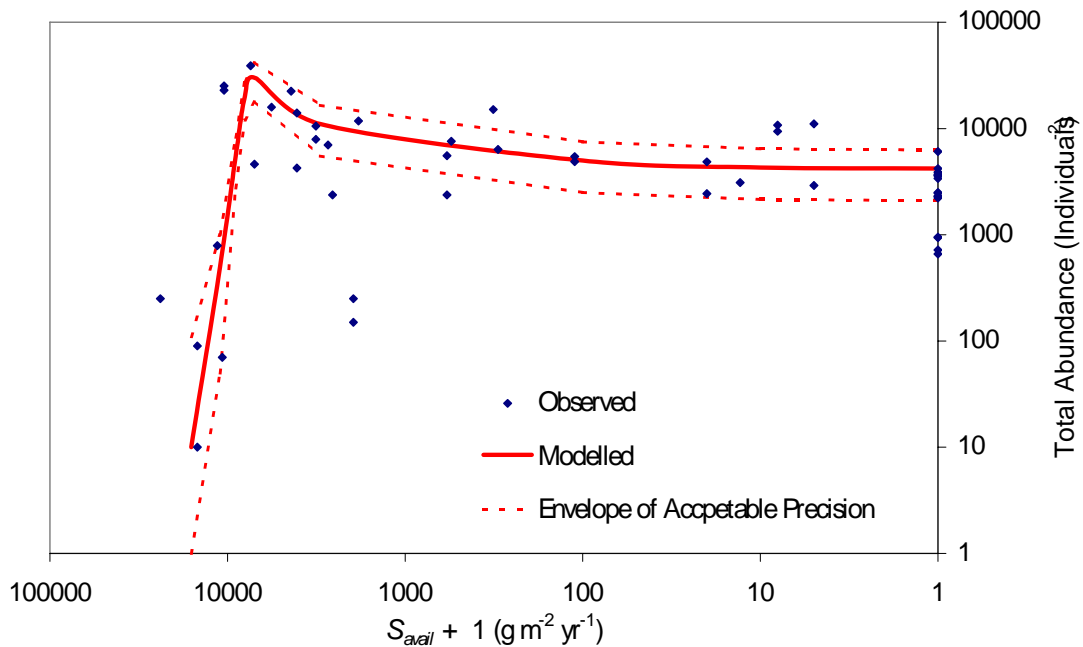


Figure 4. Modelled solids accumulation (S_{avail}) plotted against observed total abundance. Envelope of Acceptable precision is shown by the dashed line (68% in EAP, $n=50$).

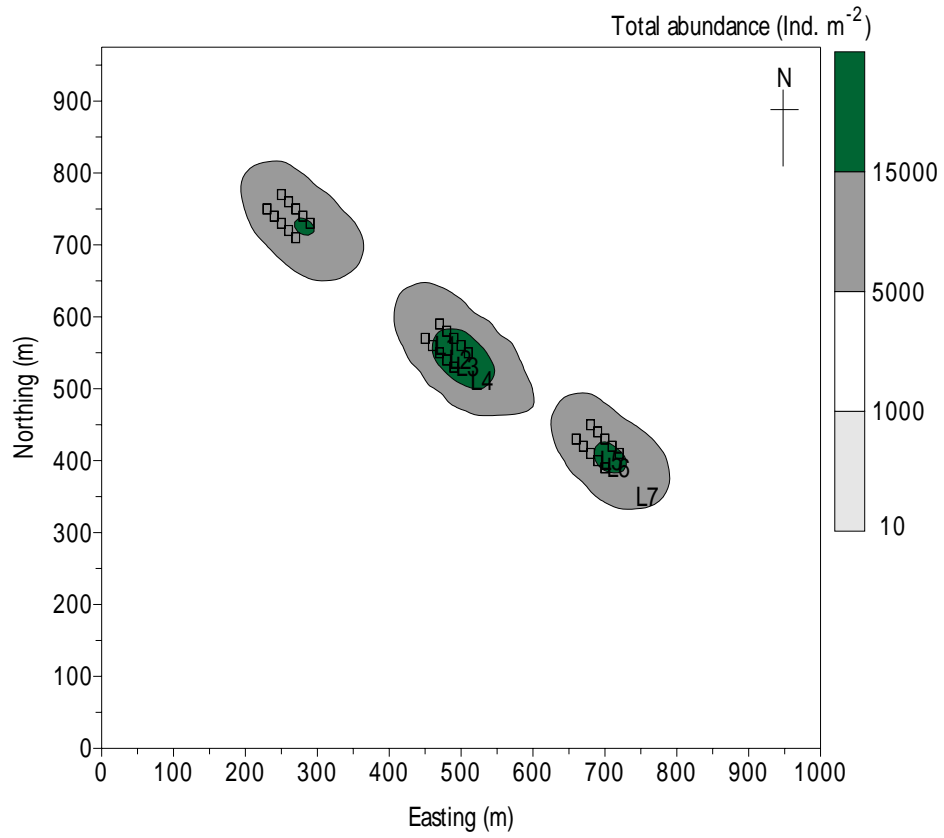
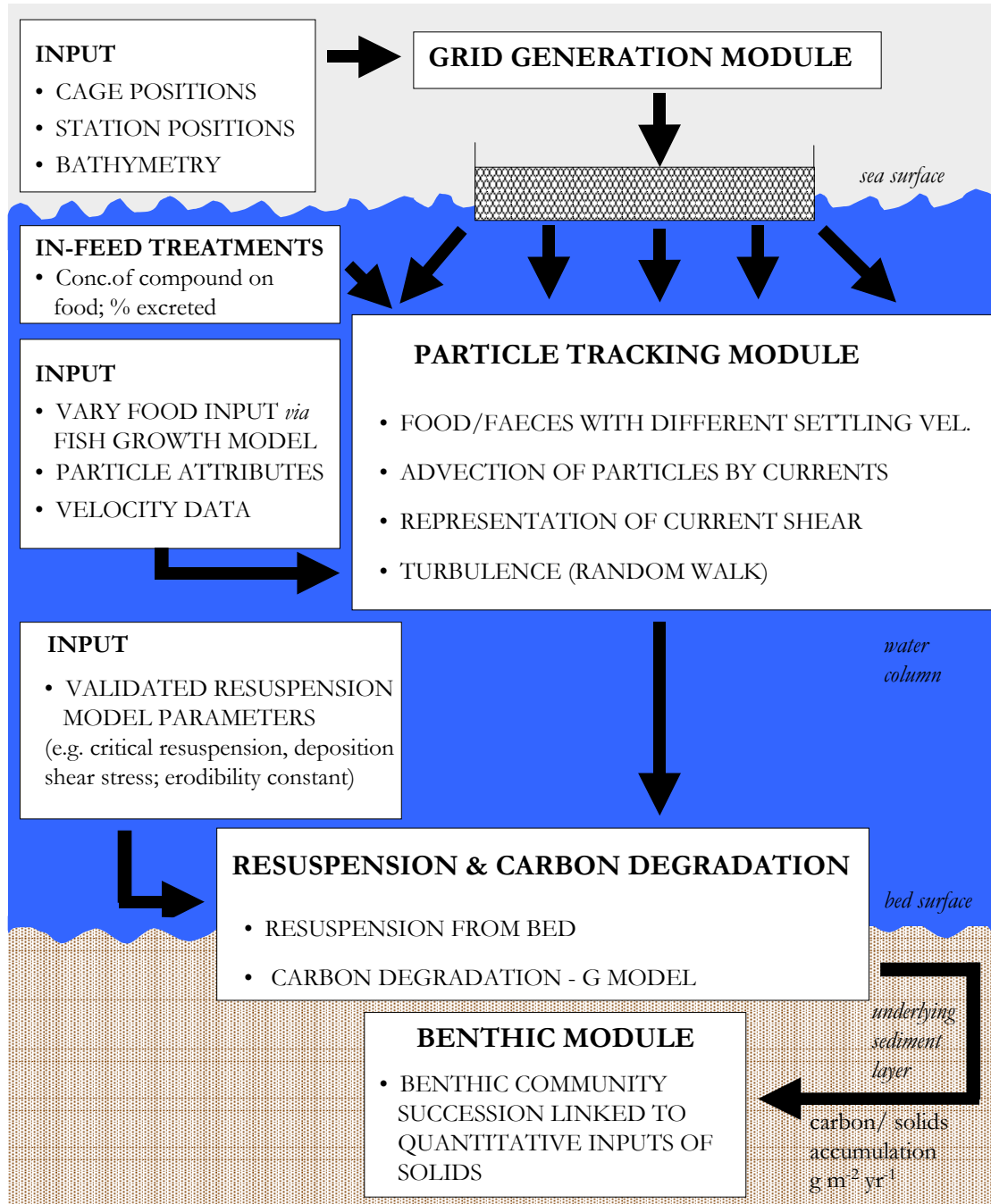
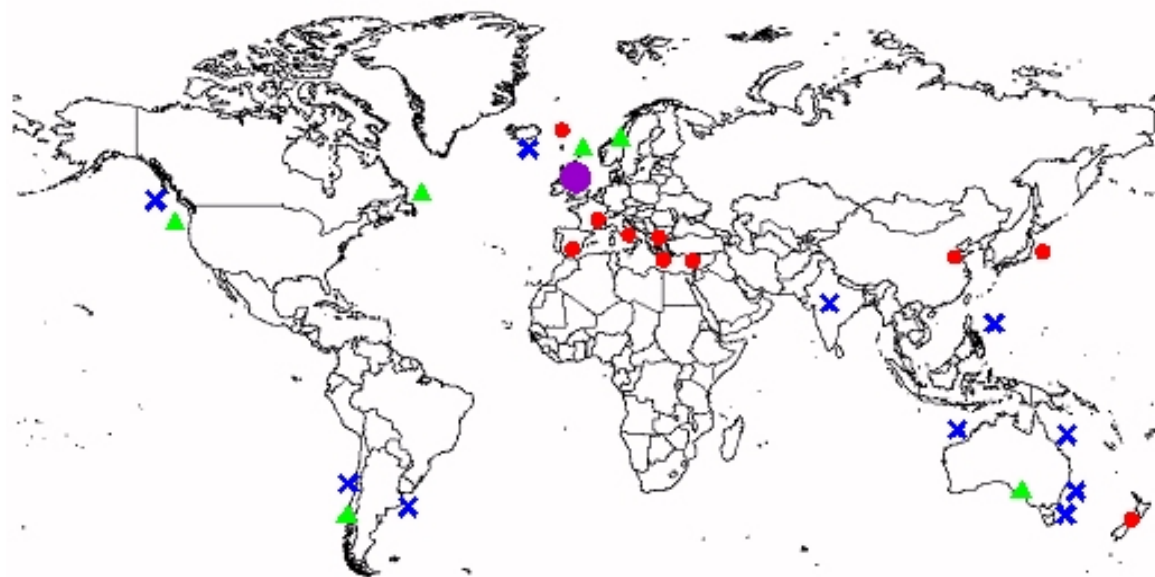


Figure 5. Predicted total abundance for Site A showing sampling stations L1–L7 (cage centres shown as □). Plot generated with Surfer for Windows™.

DEPOMOD MODULES FOR MODELLING THE EFFECTS OF DEPOSITION FROM MARICULTURE





● <3 licences; ▲ 3-5 licences; ● 5+ licenses; ✕ regular enquiries only

106 licenses in 15 different countries (65 % commercial)

Help line – approx 100 enquiries p.a. (75 % email, 25 % phone)

Figure 6. DEPOMOD and MERAMOD model license holders.