Same-Risk-Area Assessment Model (SRAAM)
User's manual. Version 2.0

DTU Aqua
National Institute of Aquatic Resources

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Preface

This user's manual describes the installation and use of the Same-Risk-Area Assessment Model (SRAAM), which has been prepared by DTU Aqua for the Danish Environmental Protection Agency and funded by
The Danish Maritime Fund (DDMF).

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1.   Short description of the tool

1.1 Background

The Ballast Water Management Convention (BMWC) entered into force on
September 8, 2017. The primary objective of the BWMC is to prevent the spread of marine invasive species via the ships' ballast water. Therefor the BWMC requires ballast water to be treated before discharged into the marine environment. In some cases, however, national authorities may grant exemptions to the BWMC. This requires a risk-assessment to be carried out. In the G7 guideline of the BWMC there is an option for an area-based risk-assessment, a so called Same-Risk-Area (SRA). An SRA is a marine area between two or more countries within which ships are exempted from the BWMC's requirement to treat ballast water. An exemption based on an SRA will only apply to ships operating exclusively within the SRA and is granted for a 5 year period. Typical types of shipping may include ferries, supply ships and similar types of short sea shipping operators. The exemption does not apply to ships that occasionally or frequently enter or leave an SRA.

The main prerequisite for an SRA is that the risk of natural spread of invasive species inside an SRA is high, and that the contribution of ballast water mediated transfer of marine invasive species does not contribute significantly to the overall risk. The rationale is that if the risk of natural spread is high the marine invasive species may spread within the SRA due to natural processes within a given time frame. In other words, if the risk remains more or less unchanged it doesn't matter if the ballast water is treated or not, and an SRA may be considered by the respective national authorities. Because natural spread is the key parameter of the SRA risk-assessment, some sort of estimate of the natural spread of marine invasive species is required for supporting decision makers.

The Same Risk Area Assessment Model (SRAAM) has been developed to support decision makers in the risk assessment process of identifying a possible SRA. The SRAAM provides a number of outputs and tools to analyze the natural dispersal of marine invasive species in a given area, but the final risk assessment still needs to be carried out by scientific staff and decision makers and rely on expert judgement and decisions. For information on how to address the SRA risk assessment we refer to Stuer-Lauritsen et al. (2016), Stuer-Lauritzen et al. (2018) and Hansen et al. (2018).

1.2 SRAAM Overview

In short the SRAAM tool is a software tool that calculates dispersal trajectories of agents representing individual marine pelagic life stages, i.e. life stages that occur as suspended in the water and hence subject to drift. Dispersal trajectories are calculated based on existing hydrographic data produced by hydro-dynamic models describing the physical environment (e.g. ocean currents), and based on biological parameters that affect the dispersal of an organism. The simulated agent trajectories are used to analyze the connectivity of the study area considered and the study area may subsequently be subdivided into well-connected sub-areas using data clustering techniques.

The SRAAM relies on existing 3D hydrographic data available and the current version of SRAAM supports a number of hydrographic model data formats. More will be added and may already be available on request (contact ftho@aqua.dtu.dk or asc@aqua.dtu.dk). The formats currently supported include:

- HBM (North Sea and the Western Baltic Sea)
- POM (The North Sea)
- NEMO (Mediterranean)
- NCOM (Caribbean)

The hydrographic data parameters used for simulating agent trajectories include current speed, current direction, salinity and water temperature. The biological parameters that can be set for the agents include the duration of the pelagic life stages (referred to as PLD or Pelagic Larvae Duration), which may vary from a few hours to several months (or the entire life cycle for fully pelagic organisms), the positioning and/or vertical migration of the organism in the water column, habitat preferences/requirements, settling behavior (for benthic species with limited pelagic life stages) and environmental tolerance limits to salinity and water temperature. The results from the agent dispersal calculation are stored in a result file that keeps track of the start and end positions (X,Y and Z) of each agent (For visualization and animation purposes additional time steps can be stored.), and the minimum and maximum salinity and temperature experienced during the pelagic stage (used for agent querying – see the connectivity analysis section 2.6.3).

The connectivity analysis is then carried out first by specifying a sub-division of the study area into a 'connectivity grid' representing a number of regular shaped subareas (e.g. 20x20 grid, 50x30 grid etc.) and secondly by populating an connectivity adjacency matrix by counting the number of agents with start and end positions connecting each pair of sub-areas in the 'connectivity grid'. The connectivity adjacency matrix can be translated into a connectivity probability matrix representing connectivity as probabilities instead of absolute numbers. In biological terms the connectivity probability represents the probability that an organism starts its pelagic life stage in one area (e.g. as an larvae) will end up (~settle) in any of the other areas within the extent of the connectivity grid.

The connectivity probability matrix can be further analyzed using cluster analysis, to identify clusters (~assemblies) of sub-areas where the connectivity between sub-areas within the clusters are high, and where the connectivity to neighboring clusters are low. These clusters are here referred to as "hydrographic regions" (as proposed by Vincent et al. (2014)), and the delineation together with metrics on the within and between cluster connectivity probabilities are the primary outputs of the SRAAM tool, to support the risk assessment for identification of a Same-Risk-Area (SRA). The individual steps involved in the generation of hydrographic regions using the SRAAM tool are shown in Figure 1.
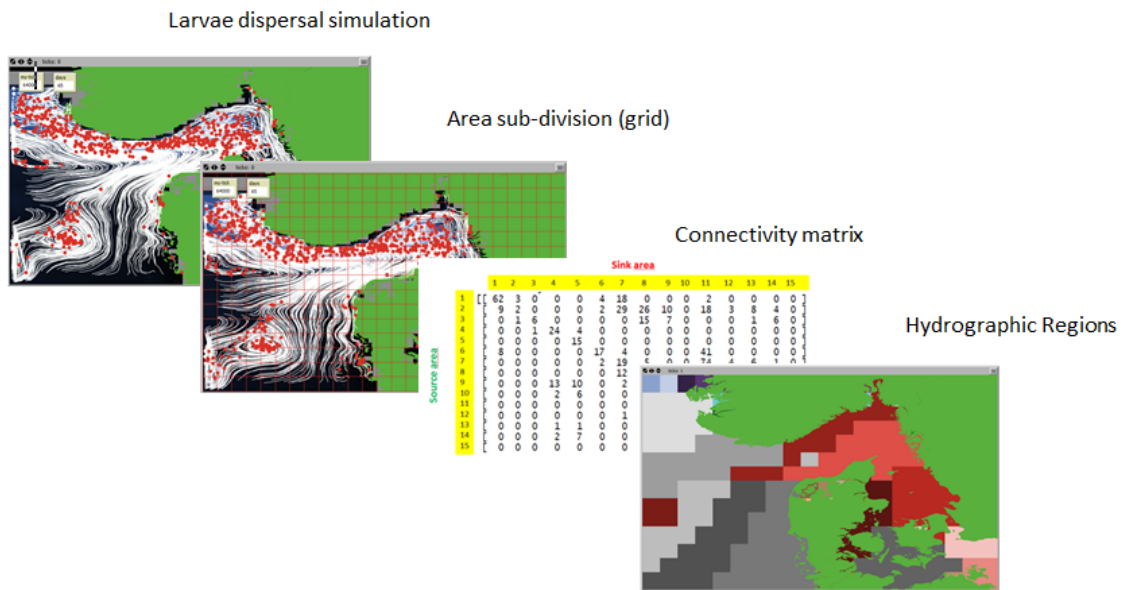
Figure 1. Individual steps supported by the SRAAM tool: 1. Larvae dispersal simulation based on existing hydrographic data. 2. Area subdivision, - dividing the model domain into a regular grid. 3. Calculation of a connectivity probability matrix. 4. Cluster analysis for dividing the model domain into hydrographic regions representing regions with high connectivity within each region, and low connectivity between regions.

The animation of simulated larvae trajectories is mostly an option available for visualizing the dispersal patterns and drivers in the system analyzed, and should only be done using simulation results for relatively limited number of agents, e.g. ~ up to max 10 000 agents for 1 year simulation with stored time step interval of 1 day, due to pc-processing time and memory, and optimal visualization.

The SRAAM tool utilizes a combination of 3 freeware/open source software:

- **Netlogo** is one of the most popular software for Agent-Based / Individual-Based Modeling (Wilensky, U. 1999). NetLogo is used as the SRAAM user interface for setting up simulations and analyzing simulation results.

- **R** is a popular software package for statistical and mathematical data analyses and processing (R Core Team 2013). Most of the data pre- and post-processing in SRAAM is handled using R scripts and a Netlogo extension linking Netlogo with R.

- **IBMlib** is a modelling system (~model library) specifically developed for linking agent-based simulations to simulated 3D hydrodynamic data (Christensen 2008, Christensen et al. *in review*). It is used in SRAAM as the calculation engine for the agent-based simulations.

2. User interface

2.1 User interface overview

The SRAAM user interface is generated in Netlogo 5.3.1 using standard Netlogo interface components and the Netlogo extension "xw" (~"Extra widgets") supporting multiple tabs for user interface customization. An overview of the primary tab is shown in Figure 2.

All SRAAM user inputs are organized in 3 standard Netlogo tabs and 5 tabs specific for SRAAM user inputs. The 3 standard Netlogo tabs include:

- "Interface"
- "Info"
- "Code"

The tabs specific to SRAAM include 5 additional tabs

- "1. Agent Release Settings"
- "2. Dispersal Parameters"
- "3. Simulation Settings"
- "4. Connectivity Analysis"
- "5. Cluster Analysis"

The numbers 1-5 indicate the order of the typical workflow.
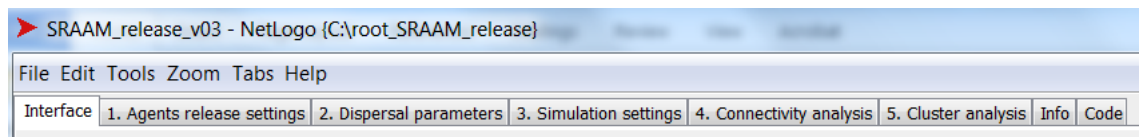
Figure 2. The SRAAM user interface in Netlogo is organized in to a number of tabs.

The standard Netlogo tab "Interface" is the main tab of Netlogo. This is where the "World view" is located which is a 2D map display (see Figure 3). In SRAAM the "World view" represents the extent of the geographical world to be analyzed, ideally identical to the extent of the hydrographic data set used for dispersal modelling, or a subarea here-off. It is possible to add shape files representing land or another polygon feature to be displayed within the world view extent. SRAAM functionalities that interact directly with, - or that set the extent/zoom of, - the world view, are all located in this tab to the left of the "Word view".

The Standard Netlogo tab "info" is for adding information of the spedific netlogo file. Useful for including documentation embedded in the *.nlogo file.

The standard Netlogo tab "code" holds all the SRAAM code executed when interacting with the individual tabs.

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The SRAAM specific tabs are ordered from 1 to 5 to reflect the typical order of required user input, i.e. setting the parameters and input for the dispersal simulation and subsequent simulation execution (1-3), calculation of the connectivity matrices based on the dispersal simulation results (4) and finally delineating hydrographic regions based on the generated connectivity matrices (5). The required input and procedures are described in detail in the proceeding sections.

In addition to the SRAAM specific user interface components the standard Netlogo user interface supports a number of standard functions for displaying, editing and programing agent based model and agent based model results. To get acquainted with the standard Netlogo user interface, please refer to the Netlogo Dictionary:
file:///C:/Program Files/NetLogo 5.3.1/app/docs/index2.html.

Or visit the Netlogo homepage:
https://ccl.northwestern.edu/netlogo/
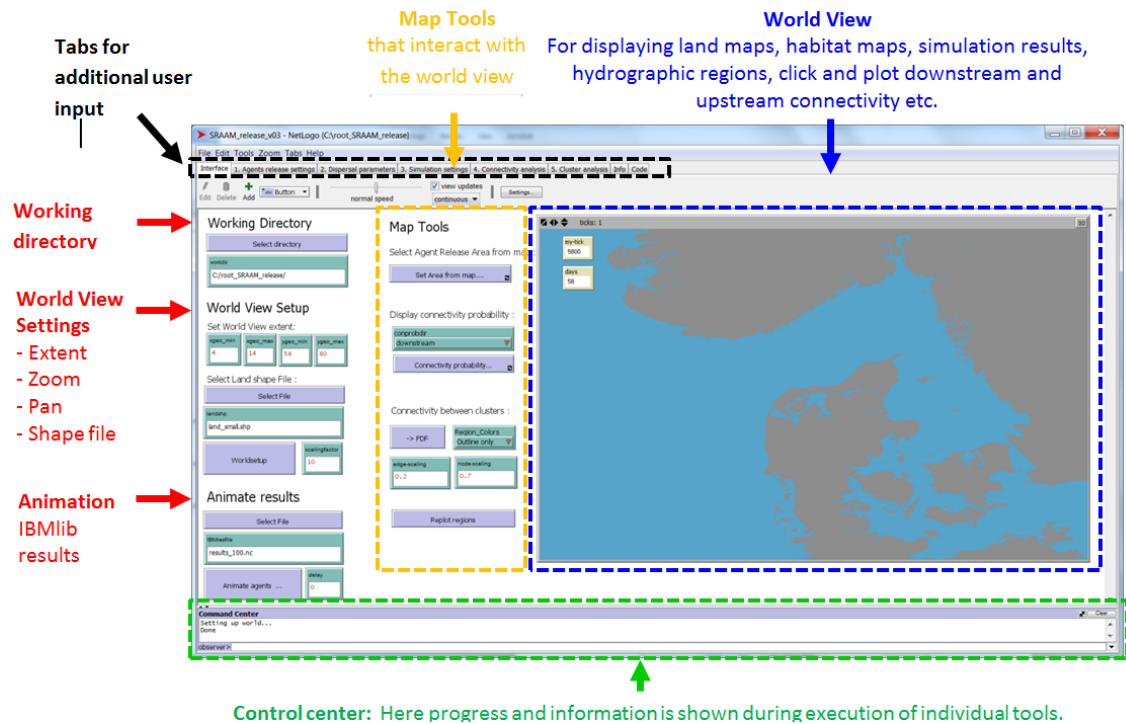
Figure 3. The SRAAM tool Graphical User-Interface showing the Netlogo "interface" tab which is the main tab. This is where the 2D map interface, the so called "World view", is located. The "World View" (Blue) extent has to be setup to represent the geographical extent (or parts) of the area covered by the hydrographic data to be used for the agent dispersal simulation. Tools that interact directly (Orange) or indirectly (Red) with "World view" are located to the left. In the top section of the interface (Black) the user has access to the SRAAM specific tabs for user input. In the bottom section (Green) the Netlogo control center is located. This is where progress and information is shown during execution of individual tools.

In addition to these tool specific sections, - the lower part of the "interface" tab consist of the Netlogo "control center". Here progress and information during SRAAM tool execusions are shown. Also if some error may occur.

2.2 The "Interface" tab

The main tab in Netlogo is the "interface" tab. This is where the 2D map display referred to as the "World view" is located. The main tab is divided in to 4 main headings supporting user input:

- Working directory
  For setting the working directory where all generated files are stored and where the hydrographic data set needs to be located (see later)

- World view setup
  For setting up the "World view" extent and specifying a shape file for land boundaries.

- Animate results
  For animation of dispersal simulation results.

- Map tools
  These are tools that interact directly with the "World view" by e.g. clicking or pointing with the mouse curser.

2.2.1 Working directory
The working directory has to be set for SRAAM to function properly. You can select any directory location either by using the "Select directory" button, or by typing the path manually into the "workdir" input box. Notice that the path has to be specified using forward slash. To select a working directory click on the "Select directory" button:
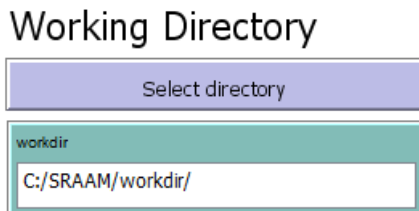
A windows explorer window will open. Select the working directory and click "open":
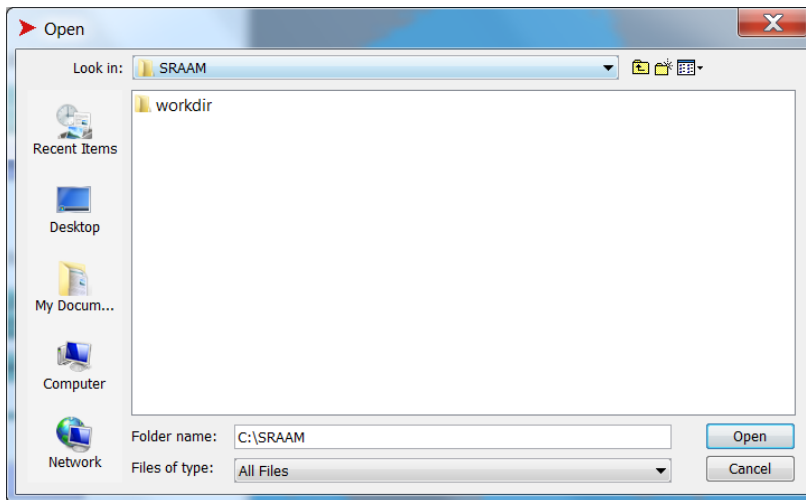
The only requirement is that the working directory include a subfolder name "IBMrun" where the hydrographic data sets are stored. In the IBMrun-folder each hydrographic data set must be stored in individual sub-folders named depending on the hydrographic data format:
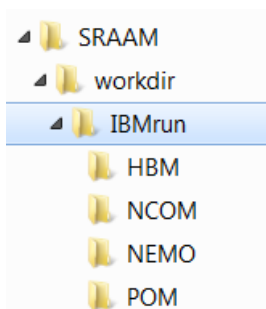
In the "IBMrun" directory the IBMlib executable files have to be stored "IBMrun_connect_... .exe". The available IBMlib executables are:

- IBMrun_connect_HBM .exe
- IBMrun_connect_POM.exe
- IBMrun_connect_COARDS.exe
- IBMrun_connect_HDboot.exe

The latter "IBMrun_connect_HDboot.exe" is an IBMlib version that supports a dataset comprising a single time-step of ECOSMO data for the NorthSea and the western Baltic Sea. (4-14 degree east, 54 – 60 degree north). It is used for demonstration purpose only, and can execute simulations within seconds or minutes. The IBMrun_connect_HDboot.exe does not require a subfolder for storing hydrographic results. Instead 3 files has to be located in the IBMrun-directory, - the 3 files are outlined in red below:
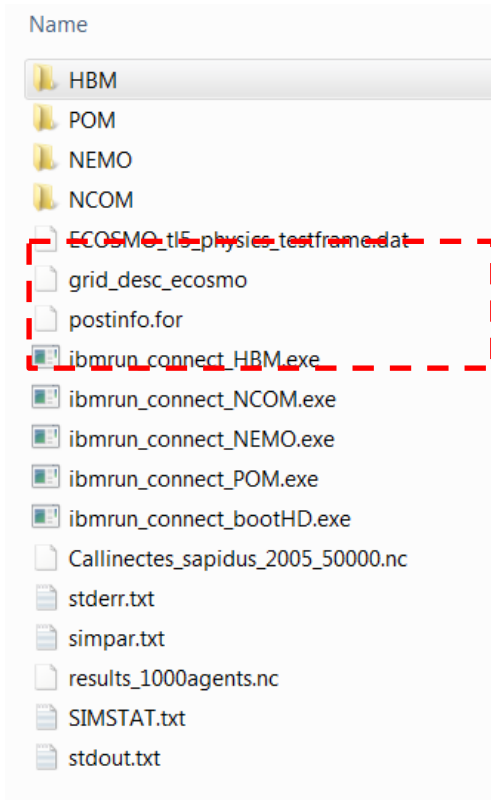
2.2.2 World view setup

Before any visualization of larvae dispersal trajectories or delineation of hydrographic regions can be done, the World View needs to be setup to cover the model domain, or a part of the model domain.

The settings include:

- Set World View extent
- Select Land Shape File
- Scaling factor
- World setup

Set World View Extent

The World View Extent is set by specifying minimum and maximum for the X and Y coordinates respectively (xgeo_min, xgeo_max, ygeo_min, ygeo_max). The extent should cover the extent of the hydrographic data set to be used, or a subarea hereof. To zoom into an area, the 4 parameters will have to be changed manually. Every time changes has been made, the "World Setup" button must be activated.

Select Land Shape File

The land GIS file must be an ESRI shape file (*.shp) with land areas represented as polygons. If the file name including the "shp"-extension is written manually without the path in the "landshp" input box, the shape file set is assumed to be located in the working directory. If you choose a file from another location using the "Select File" button, a prescript "…/'filename'" will be included in front of the file name to indicate the file is not located in the working directory.

Scaling factor

The scaling factor is used as an easy option to set the visual extent of the World View within the graphical user interface. E.g. if the scale factor is doubled the extent of the world view is doubled in both the X and Y direction. This is useful e.g. when zooming into a small area (by changing the min and max values of the X and Y coordinates of the World View extent) where a small World View extent should be accompanied with an increase in the scaling factor. NOTICE! If you by accident type a very large scaling factor the program may freeze.

World setup

This button executes the world view setup based on the settings set for the World View extent, Scaling factor, and specified land shape file.

For more options controlling the World View the Netlogo World View customization can be accessed by right click within the World View extent and select "edit" from the pop-up menu. For details please refer to the Netlogo documentation.

2.2.3 Animate results

Once an IBMlib simulation has been successfully executed, the results can be animated in the world view. The IBMlib stores results in a NetCDF data format (with the file extension ".nc") with a user specified time step frequency (see "Simulation setting" section). Animation of the results displays the dispersal trajectories for all simulated agent time-step-by-time-step with the current location represented by a point (red) and with the trajectories shown as a line (yellow).

Because IBMlib results may include unlimited number of agents, animations should only be attempted for limited data sets: Depending on the PC an upper limit may be a simulation with a maximum number of agents of 50 000, covering a simulation period of up to 1 year, and with daily or weekly time step between stored results. If there is a need to display larger data files one option could be to store only the last time step in the IBMlib simulation. This way the end positions of larger data files can be displayed.

The settings in the animation section include:

- Select file
- Setting the "delay" – parameter
- Launch "Animate agents"

Animate results
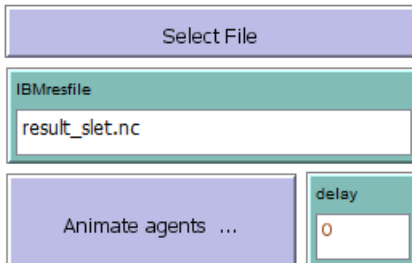
Select file

To select a IBMlib result file, click on the "Select file" button or write the name of the file manually in the "IBMresfile" text input box. The file must be a NetCDF file (*.nc)

If the file name including the "nc"-extension is written manually without the path in the "IBMresfile" input box, the file set is assumed to be located in the sub-directory "IBMrun" in the working directory. If you choose a file from another location using the "Select File" button, a prescript "…/'filename'" will be included in front of the file name to indicate the file is not located in the working directory.

When a new IBMlib simulation is successfully executed the "IBMresfile" text input box is automatically updated with the latest results file.

Delay-parameter

The "delay" parameter input box is an option for controlling the speed with which the agent trajectories are animated in the World View. The default value is "0". For small result files, e.g. including 100-1000 agents the animation may be very fast, almost instantaneous, and setting the "delay" paramter to 0.00001, 0.0001 0r 0.001 will slow down the animation. If the animation takes too long or if the animation should be interrupted for some other reason, the animation can be interrupted using the Netlogo "Halt" function located in the "Tools" menu.

Animate Agents

To animate the agent trajectories of the IBMlib result file, click on the "Animate Agents…" button. A progress bar will be displayed while IBMlib results are loaded into Netlogo:
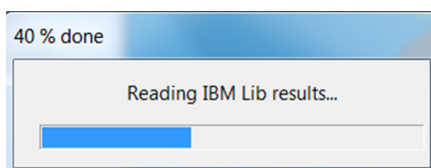
Agent trajectories are subsequently animated in the World View, see Figure 4. For keeping track of the time step displayed during the animation two small info boxes are shown next to the upper left corner of the World View,- counting the number of ticks as the product of number of agents and the number of timesteps ("my-tick") and the number of days ("days") from the onset of the animation, respectively:
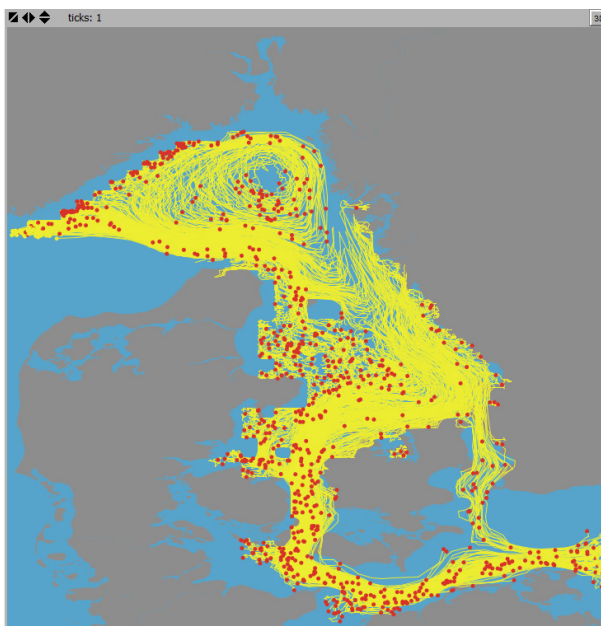
Figure 4. Example of an animation of agent trajectories from a IBMlib simulation. Current agent positions is shown as a "red" dot and where the individual trajectories prior to the "current" position is shown as a yellow line track. Background colors: Grey = Land. Blue = water.

2.2.4 Map tools

The Map tools are tools which support user interaction with the World View. Therefore the different tools are placed here in the "Interface" tab next to World View, but may serve very different purposes, and support SRAAM functionalities otherwise organized in the SRAAM specific tabs 1 – 5.

The tools include:

- Select agent release area from map
- Display connectivity probabilities
- Connectivity between clusters
- Replot regions

Select Agent Release Area from map

Prior to the execution of a IBMlib simulation initial positions of agents (~release positions) have to be set. Agent release settings are set in the "1. Agent Release Settings" tab manually by specifying X Y coordinates for a release area, or by specifying a habitat map representing an outline of a species specific habitat for agent release. As an additional feature to specify X Y corner coordinates, this tool support a World View interactive selection of a lower left and upper right sets of corner coordinates by simply pointing and clicking in the world view.

The tool is activated by clicking on the "Set area from map…" and while activated (button appears black), first the lower left corner is selected, then the upper right corner:

Select Agent Release Area from map :

Set Area from map....

User Message

CLICK on map and SELECT the lower-left and Upper-right corner of the spawning area !

OK   Halt
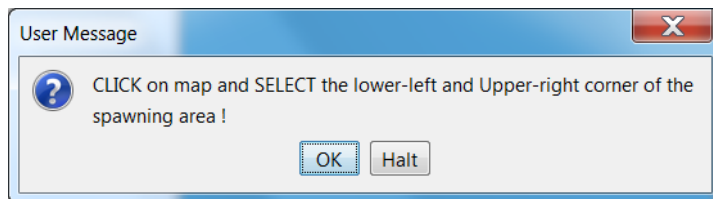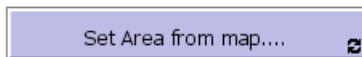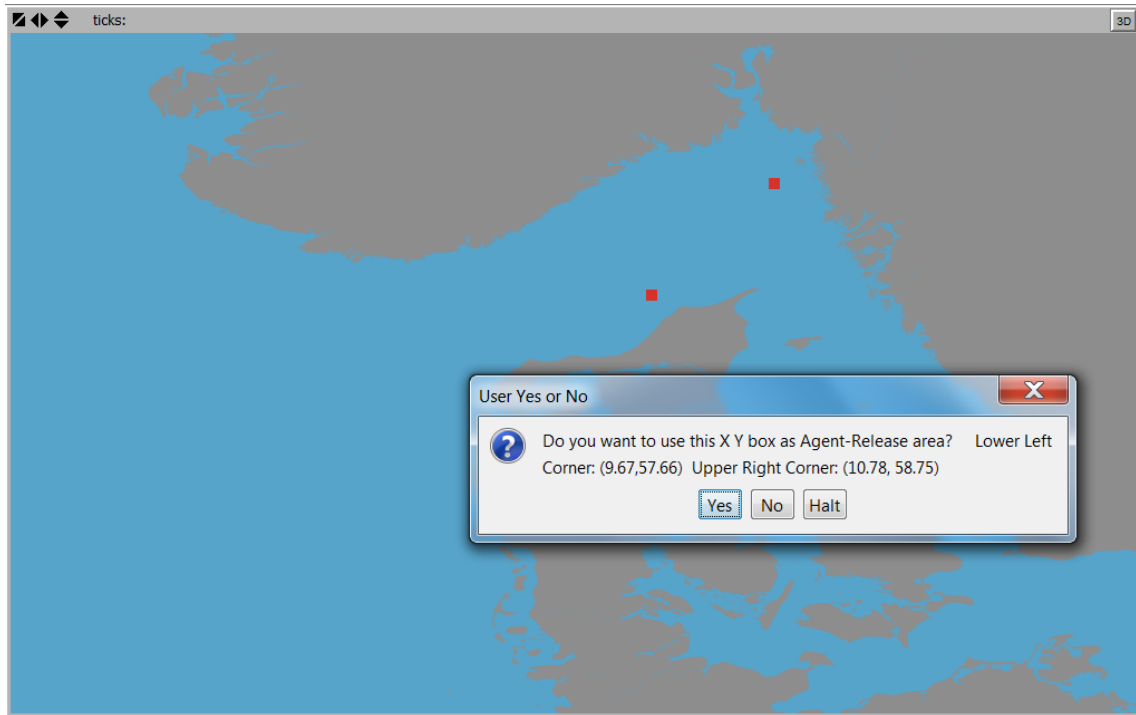
Figure 5. The Map tool "Selelct Agent Release Area from map" where the user points at the lower left and upper right corner coordinates of the Agent Release Area (red squares) and subsequently prompts the user for accepting the input.

Once selected the user is prompted for accepting the input. Once accepted the corner coordinates input boxes in the "1. Agent Release Settings" tab are updated.
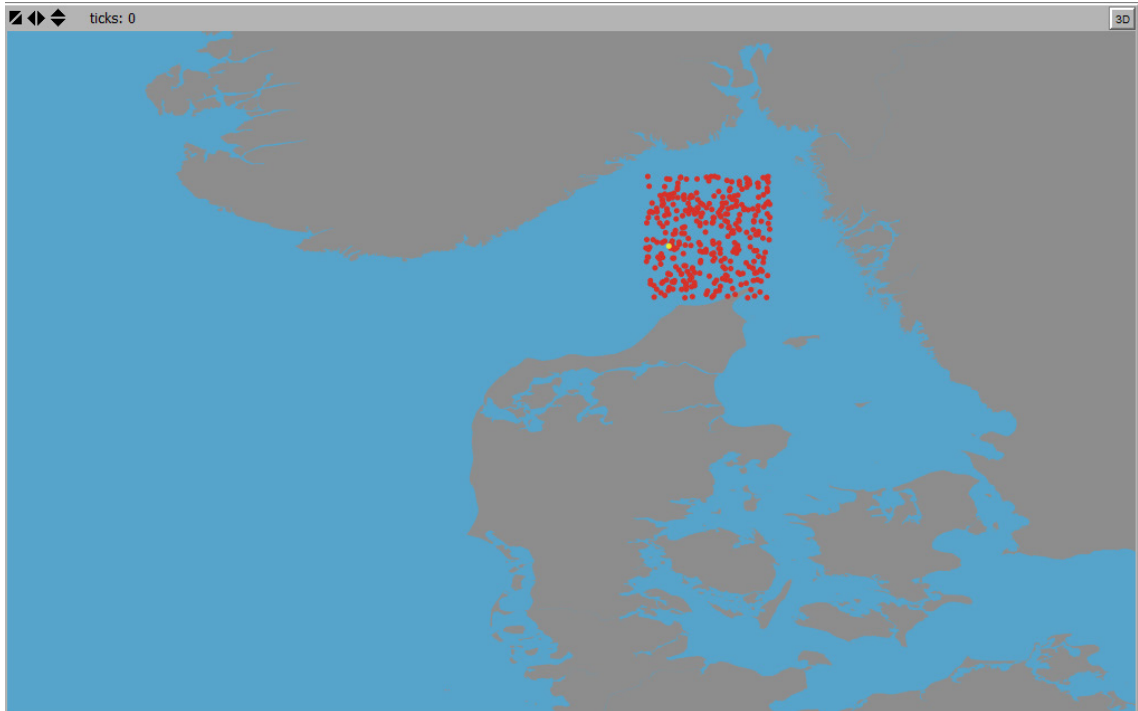
Figure 6. The initial positions of agents (~agent release positions) of a simulation based on the corner coordinates set using the Map Tool "Select Agent release area from map…" – see Figure 5.

Display connectivity probability

This tool is included to explore the connectivity output from the connectivity analysis in more detail. It is a click-and-plot tool, where a click at a specific location in the World View, will display the corresponding "downstream" or "upstream" connectivity for that specific location in the connectivity grid (see section "Connectivity Analysis" for details on connectivity analysis and connectivity grid). "Downstream" connectivity refers to the probability that an agent with an initial position corresponding to the selected grid cell in the connectivity grid will disperse to and end up in any of the other grid cells in the connectivity grid. The "Upstream" connectivity refers to the opposite direction, i.e. the probability that an agents that ends up in the user specified grid cell in the connectivity grid, originates from any of the other grid cells in the connectivity grid.

"Downstream" and "Upstream" connectivity are selected from the pull down menu. Then press the "Connectivity probability…" –button, and left click using the mouse cursor in the desired location in the World View.
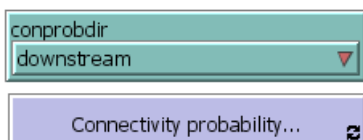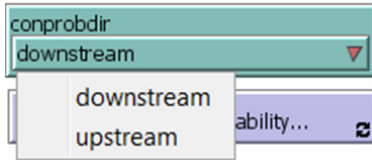
An example of "Downstream" and "Upstream" connectivity plots is shown in Figure 7. The Minimum and maximum probability values of the graduated color legend is shown in the Netlogo command center, e.g.:

```
Max value of color legend: 0.0702811
Min value of color legend: 0
Done
```

To retrieve the exact value for each connectivity grid cell right click on the cell and from the Netlogo pop-up menu choose "inspect patch …." to access the patch values associated with the specific location.
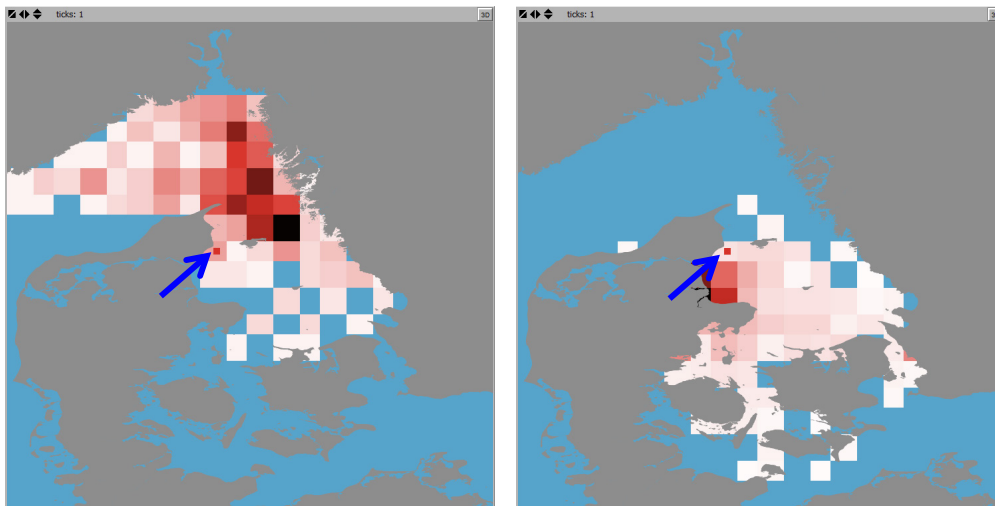
Figure 7. Examples of "Downstream" (left) and "Upstream" (right) connectivities using the click-and-plot tool "Display Connectivity probability…". Click positions indicated by blue arrows. Grey = Land. Blue = Zero values. Red graduated colors = connectivity probabilities. Downstream connectivity legend max color (black/dark red) = 0.07. Upstream connectivity legend max color (black/dark red) = 0.26.

Connectivity between clusters

This tool is included to provide a more informative plotting representation of the hydrographic regions derived from the cluster analysis (for details see the cluster analysis section). The tool uses a graph representation of the hydrographic regions and their connections exported to a pdf-format (see Figure 8).

The centroids of each region are indicated with numbered circles representing the graph nodes. Numbers represent the coherence (or "self-recruitment") of each region in percent, i.e. the fraction of agents that have both their initial and their end positions in the same region. Lines

between nodes represent graph edges and indicate the direction (arrows) and probabilities (line thickness) of the connectivity between regions. Two plot layouts are available, one displaying regions as hollow polygons with colored outline, and on displaying regions as filled colored polygons. Edge thickness and node-sizes can be modified using the "Edge-scaling" and "node-scaling" parameters.

The tool uses the latest output from the Cluster Analysis for plotting (See Cluster Analysis section).

To export the hydrographic regions from the latest cluster analysis, simply press "-> PDF" button.

To select one of the two possible layouts select from the "Regions Colors" pull down menu, and select between "Filled" or "Outline only".

Thickness of the graph edges and size of the graph nodes are set in the "edge-scaling" and "node-scaling" input boxes.

Connectivity between clusters :
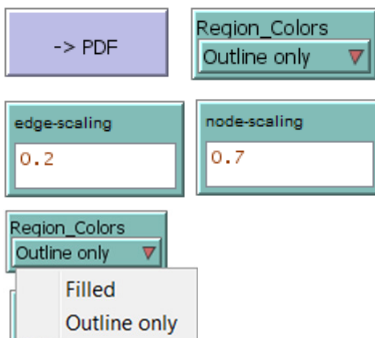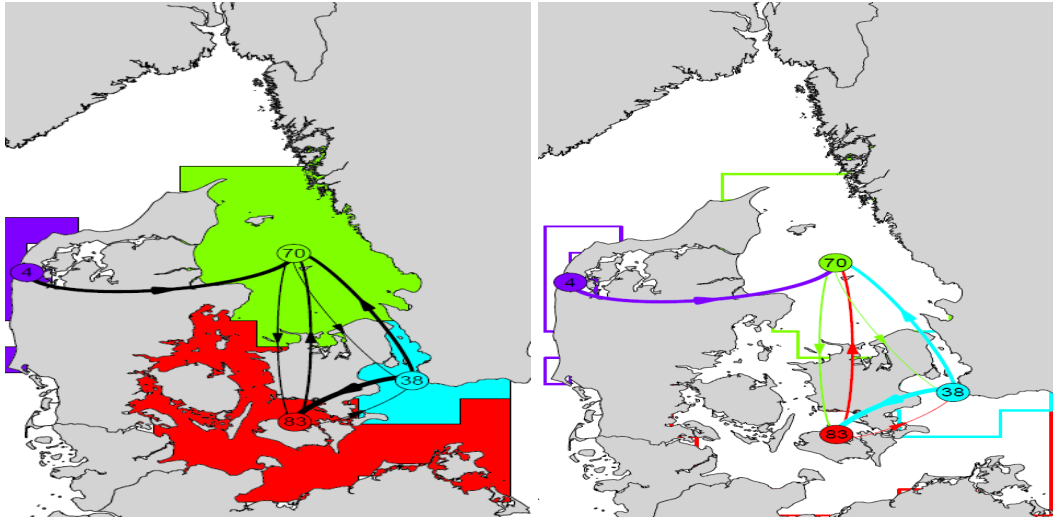
Figure 8. Examples of the output of the Map tool "Connectivity between clusters" represented as graphs. Each cluster or hydrographic region is assigned a unique color. The centroid of each region is indicated with a numbered circle representing the graph nodes. Numbers represent the coherence (or "self-recruitment") in percent, i.e. the fraction of agents that have both their initial and their end positions in the same region. Lines between nodes represent graph edges and indicate the direction (arrow) and probability (line thickness) of connectivity between regions. The two plot show the same data, but the 2 different layouts.

Replot regions

The last Map tool is an option for replotting the hydrographic regions from the last cluster analysis.
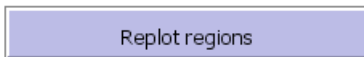
2.2.5 World View

Detail description of the World View and customization apart from what has been described in the previous sections, please refer to the Netlogo documentation.

2.2.6 Command center

The Netlogo "control center" is located the bottom of the user interface. Here progress and usefull information during SRAAM tool execusions are shown.

2.3 The "Agent Release Settings" tab

The "Agent Release Settings" tab is where parameters and inputs are set for specifying how agent are "released" in the simulation.

The tab include:

- Select how to release agents
- Release area coordinates
- Release habitat map
- Agent release depth interval
- Agent release time
- Number of agents

Agents Release settings

Select how to release agents :

Agents release
Specified corner coordinates ▼

Agents Release Depth Interval:

Min depth (m)	Max depth (m)
0	0

Release Area coordinates:

x1	y1	x2	y2
8.983	54.308	13.817	59.992

Agents Release Time:

Start time	End time
2009 03 02 0	2009 03 02 0

Release Habitat map:

Select a habitat file	Display

Number of agents:

No. of agents
1000

Habitat input file
select file ...

2.3.1 Select how to release agent

Agents can be released in the model domain in two ways. Either by specifying corner coordinates of the lower left and upper right corner of a rectangular release area, or by specifying a habitat map.

Agents release
Specified corner coordinates ▼
Select...
Specified corner coordinates
Habitat map

2.3.2 Release area coordinates

Release coordinates can be set manually by typing in the lower left and upper right corner coordinates in x1, y1, x2 and y2 input boxes, or by using the tool "Select release area from map…" located in the "Interface" tab (see section 2.2.4). The latter will automatically update the input boxes accordingly.

Release Area coordinates:

x1	y1	x2	y2
8.983	54.308	13.817	59.992

2.3.3 Release habitat map

To specify a habitat map for agent release, click on the "Select a habitat file" –button and select a habitat map file. The file must be an asci grid with the value 1 representing habitat, and a "no data" value (-9999) representing no habitat. Notice that the resolution of the habitat grid may affect input data processing time, so optimally use a relatively low resolution (a few grid cell as possible still representing the habitat detail level necessary).

Release Habitat map:

Select a habitat file	Display

Habitat input file
hab_simple_3_areas.asc

To show the habitat map in the World View, click the "Display" button and the "interface" tab will be launched and the habitat map shown with light green color in the World View (see Figure 9). If the habitat map does not show, check the coordinate extent of the habitat asci grid and that the grid values have the right format.
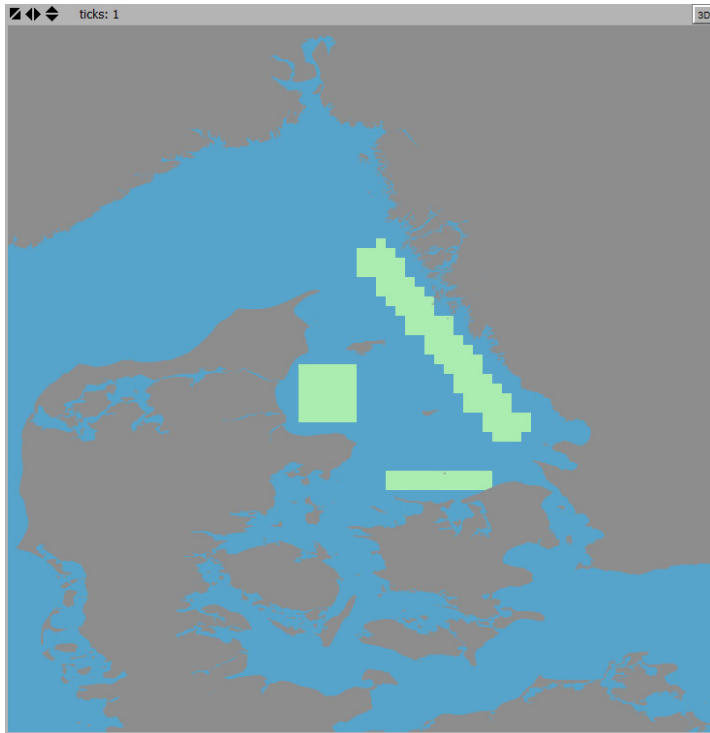
Figure 9. Display of an ascii habitat map (green) used for agent release.

When using a habitat map the start position of each agent is selected randomly among habitat grid cells, and also the position inside a grid cell itself is selected randomly in space. The time of release is selected randomly from the release time interval specified (see section 2.3.5)). All random selections are assuming a uniform random distribution in time and space. This option generates a single line for each agent in the IBMlib simulation parameter file "simapar.txt" (see section 2.5). When simulating larger numbers of agents (e.g. >> 50 000) this may slow down simulation time considerably. In such cases the agent release specification in the simpar.txt file can be simplified by preparing the agent release specification using at text editor to edit the simpar.txt file.

The section in the Simpar.txt file for agent release looks like this:

```
! ==============================================================
!          Release dynamics
! ==============================================================
dry_emission_boxes = ignore
!
emitbox =  2009 03 02 0    2009 03 02 0  11.44 56.53 0  11.93 57.12 0  100  par1 5.6  whatever
```

Any number of emitbox-lines can be included and uses the following syntax:

For more information see the IBMlib user manual: https://github.com/IBMlib/IBMlib .

2.3.4 Agent release depth interval

The Agent release depth interval refers to the vertical distribution of the initial position of the agents. To specify an absolute depth interval use negative values. To specify relative depth interval use positive values between 0 and 1. Zero values refer to the surface. Minimum and maximum depths are specified in the "Min depth" and "Max depth" input boxes.

Agents Release Depth Interval:

Min depth (m)	Max depth (m)
0	0

2.3.5 Agent release time

Time interval for agent release is speicified in the "Start time" and "End time" input boxes. The format used is: "YYYY MM DD h"

Agents Release Time:

Start time	End time
2009 03 02 0	2009 03 02 0

2.3.6 Number of agents

The total number of agent be released in the IBMlib simulation is given as an integer and specified in the "No. of agents" input box.

Number of agents:

No. of agents
1000

2.4 The "Dispersal parameters" tab

The "Dispersal parameters" tab is where parameters and inputs are set for specifying how agent are dispersed during in the IBMlib simulation.

The tab include settings for:

- Pelagic Larvae Duration (PLD)
- Settling dynamics
- Vertical distribution range
- Dispersion
- Vertical sinking speed

Dispersal parameters

Pelagic larvae duration:

Days
20

Settling dynamics:

☐ Include Active Settling (within habitat)

Select a habitat file	Display

Habitat input file
select file ...

Age gaining settling competancy (days)
30

Vertical Distribution Range:

Min Depth (m)	Max Depth (m)
0	20

Dispersion:

Vertical (m2/s)	Horizontal (m2/s)
0.001	10

Vertical Sinking speed:

(m/s)
0

2.4.1 Pelagic Larvae Duration (PLD)

The Pelagic Larvae Duration (PLD) is the duration of the pelagic life stage where the organism is suspended in the water column and subject to drift. The PLD is specified in the "Days" input box with the unit "days".

Pelagic larvae duration:

Days
20

2.4.2 Settling dynamics

Settling dynamics is an option to mimic active settling behavior, i.e. a behavior observed in some species where pelagic larval stages at a certain age achieve settling competency, e.g.

coral larvae. When settling competency is achieved, the larvae may settle if exposed to the right environmental cues. Such a behavior can optimize settling so that it happens when the organism is conveyed to an area where habitat conditions are favorable.

To enable settling dynamics the check box "Include Active Settling (within habitat):

To select a habitat file for settling click the "Select a habitat file" button and select a habitat file from any location. If the habitat file is not located in the SRAAM working directory a prefix ".../" will be shown in front of the file name. The habitat file must be an asci grid format (*.asc) similar to the habitat file specified for agent release, see section 2.3.3.

Notice that if a habitat file has been specified in the "1.Agent Release Settings" –tab the "habitat input file" input text box in the "Settling dynamics" section is automatically updated with the same habitat file. For most organisms the same habitat support both spawning and settling. However for some species like many fish species spawning and settling habitats are not identical. Although in SRAAM the settling habitat can be specified as different from the release- (or spawning) habitat, please notice that the clustering techniques available in SRAAM for analyzing the connectivity matrices may not give meaningful results.

The competency age is specified in the input box "Age gaining settling competency (unit: days).

2.4.3 Vertical Distribution range

The vertical position of the simulated agents during simulation can be limited to a vertical distribution range by setting minimum and maximum depths as positive number, in the "Min Depth" and "Max depth" input boxes.

2.4.4 Dispersion

The vertical and horizontal dispersion coefficients are specified in the "Vertical (m2/s)" and "Horizontal (m2/s)" input boxes. The dispersion coefficient can be included in the simulation to represent hydrodynamic processes not resolved by the hydrodynamic data and/or to represent spatial (and random) dispersal due to biological behavioral processes. The vertical dispersion is limited by depth interval specified in the previous section.

Dispersion:

Vertical (m2/s)	Horizontal (m2/s)
0.001	10

2.4.5 Vertical Sinking speed

A vertical sinking speed can be set at se constant speed (m/s) in the "(m/s)" input box. By combining the vertical sinking speed with the vertical dispersion parameter and the depth distribution range, the vertical distribution of agents can be biased towards the upper or lower vertical distribution range.

Vertical Sinking speed:

(m/s)
0

2.4.6 Diurnal vertical migration

Pelagic stages of many aquatic species exhibit more or less pronounced diurnal vertical migration (DVM), e.g. by migrating towards the surface when light disappears at dusk, and towards the deeper parts when light increases during dawn. DVM is not included as an option in the SRAAM user interface, however, IBMlib supports DVM and settings has to be added manually to the IBMlib simulation parameter file "simpar.txt".

active = 2   ! (0=no active swimming, 1=keep within depth min and max, 2=DVM)
swim_depth_min = 0   ! [m] upper confinement level > 0 (active>0)
swim_depth_max = 20   ! [m] lower confinement level (or sea bed, if shallower) (active>0)
swim_speed_light = 0 ! [m/s] swim speed when light, positive down (active = 2)
swim_speed_dark = 0 ! [m/s] swim speed when dark, positive down (active = 2)

2.5 The "Simulation Settings" tab

The "Simulation Settings" tab is where parameters are set for specifying the simulation parameters for the IBMlib simulation.

The tab includes:

- Select hydrographic data format
- Simulation start and end time
- Simulation results storing frequency
- Simulation result file name
- Run simulation

Simulation settings

Select Hydrographic data format:

Select Hydrographic data format:
Stationary_flow_field ▾

Simulation start and end time:

Start_time	End_time	Time step
2009 03 02 0	2009 04 29 0	1800

Simulation results storing frequency:

Storing Frequency
86400

Simulation result file name:
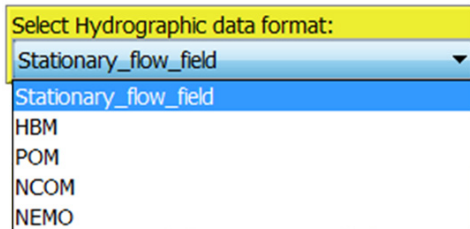
File Name
results_1000.nc

Run Simulation!

Run IBMLib

2.5.1 Select Hydrographic data format

The hydrographic data to be used for the IBMlib dispersal simulation has to be selected from the "Select Hydrograhpic data format" pull down menu. The formats currently available and format discriptions are found in section 3. Apart from the "Stationary_flow_field" the each data set has to be stored in a subfolder with the same name in the IBMrun directory., i.e.. "HBM", "POM", "NEMO" and "NCOM".
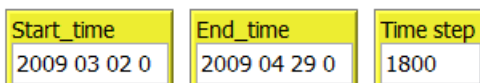
Select Hydrographic data format:

Stationary_flow_field ▼
Stationary_flow_field
HBM
POM
NCOM
NEMO

2.5.2 Simulation start and end time

Simuation start and end time has to specified in the input boxes "Start time" and "End time" respectively. The format used is "YYYY MM DD h". The IBMlib simulation time step must be specified in the "Time step" input box (unit: seconds).

Simulation start and end time:
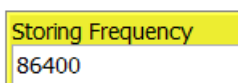
Start_time	End_time	Time step
2009 03 02 0	2009 04 29 0	1800

2.5.3 Simulation results storing frequency

The IBMlib simulation results storing frequency has to be specified in the "Storing Frequency" input box (unit: seconds).

Simulation results storing frequency:

Storing Frequency
86400

2.5.4 Simulation result file name

A file name for the IBMlib results has to be specified in the "File name" input box. The file name must have the file extension ".nc". The file will be saved to the "IBMrun" folder located in the working directory.

Simulation result file name:

File Name
results_1000.nc

2.5.5   Run simulation

To start the IBMlib simulation click on the "Run IBMlib" button.

During the IBMlib execution in addition to the IBMlib result file three files are saved to the IBMrun-folder:

SIMSTAT.txt

The file stores the simulation progress i.e. the number of that completed time steps, and the total number for time steps in the simulation.
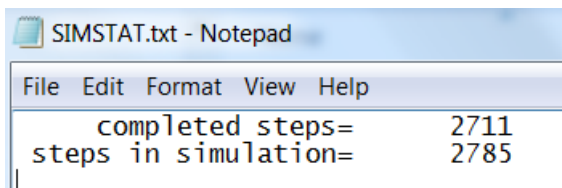
stout.txt

This file is the IBMlib simulation log file. In case IBMlib execution fails to complete, the log file may provide information on when or why the execution stopped.

sterr.txt

Explicit IBMlilb execution errors will be displayed here.

The IBMlib result file is stored in a NetCDF file format . The file include up to 19 variables:

```
19 variables (excluding dimension variables):
  float topolon[nxtop]
      meaning: topography sampling zonal grid
      unit: degrees East
  float topolat[nytop]
      meaning: topography sampling meridional grid
      unit: degrees North
  float topography[nytop,nxtop]
      meaning: topography sampling on grid
      unit: meters below sea surface
  float lon[nparticles,nframes]
      meaning: particles zonal position
      unit: degrees East
  float lon0[nparticles]
      meaning: particles zonal initial position
      unit: degrees East
  float lat[nparticles,nframes]
      meaning: particles meridional position
```

unit: degrees North

float lat0[nparticles]

    meaning: particles meridional initial position

    unit: degrees North

int time[i4,nframes]

    meaning: time corresponding to particles frames

    unit: year, month, day, second_in_day

float depth[nparticles,nframes]

    meaning: particles vertical position

    unit: meters below sea surface

float depth0[nparticles]

    meaning: particles vertical position

    unit: meters below sea surface

byte is_out_of_domain[nparticles]

int is_settled[nparticles]

float age_at_settling[nparticles]

float degree_days[nparticles]

float max_temp[nparticles]

float min_temp[nparticles]

float max_salt[nparticles]

float min_salt[nparticles]

float connectivity_matrix[nsource,ndest]

    meaning: probability of particle transport

    unit: 0 < probability < 1

2.6 The "Connectivity Analysis" tab

The "Connectivity Analysis" tab is where parameters are set for the connectivity analysis. The connectivity analysis requires a subdivision of the study area into smaller areas (a connectivity grid). The IBMlib results are analysed and translated into a connectivity probability matrix that represents the probability that an agent released in on sub-area ends up in any other subarea. If the study area is divided into 20x20 grid, a total of 400 subareas are included, and the connectivity probability matrix will express all pairwise connectivity probabilities,i.e. in a 400x400 matrix.

The tab includes :

- Select a simulation result file
- Set resolution of connectivity grid
- Set Agent Filters
- Create Connectivity Matrix

Connectivity Analysis

Select a simulation resultfile :

Use latest result file	Select a previous file

IBM result input file
Callinectes_sapidus_2005_50000.nc

Set resolution of connectivity grid:

Columns	Rows	
20	20	Display

Create connectivity matrix :

Calculate

Set Agent Filters:

☐ Include only agents settled within habitat

Temperature Min	Temperature Max
0	40
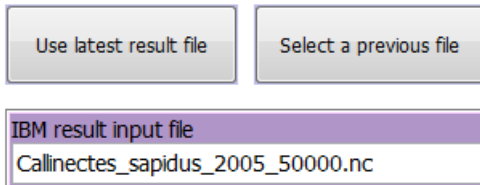
Salinity Min	Salinity Max
0	35

2.6.1   Select a simulation result file

To select the IBMlib result file to be used as input to the connectivity analysis, click on "Use latest result file" to use the latest IBMlib result file generated, or click on "Select a previous file" to select file from any location. The file name will be shown in the "IBMlib result input file" input box. If the file is not located in the IBMrun subdirectory of the working directory, the file name will include a prefix "…/".

Select a simulation resultfile :
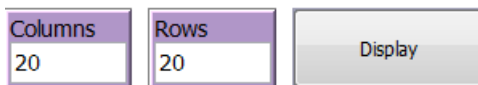
| Use latest result file | Select a previous file |

IBM result input file
Callinectes_sapidus_2005_50000.nc

2.6.2   Set resolution of connectivity grid

The connectivity grid is specified as number of columns and rows in the input boxes "Columns" and "Rows", and will divide any current extent of the World View into the number of rows and columns specified. To show the resulting grid on the current World View extent press "Display" button, see Figure 10.

Set resolution of connectivity grid:

Columns	Rows	Display
20	20	
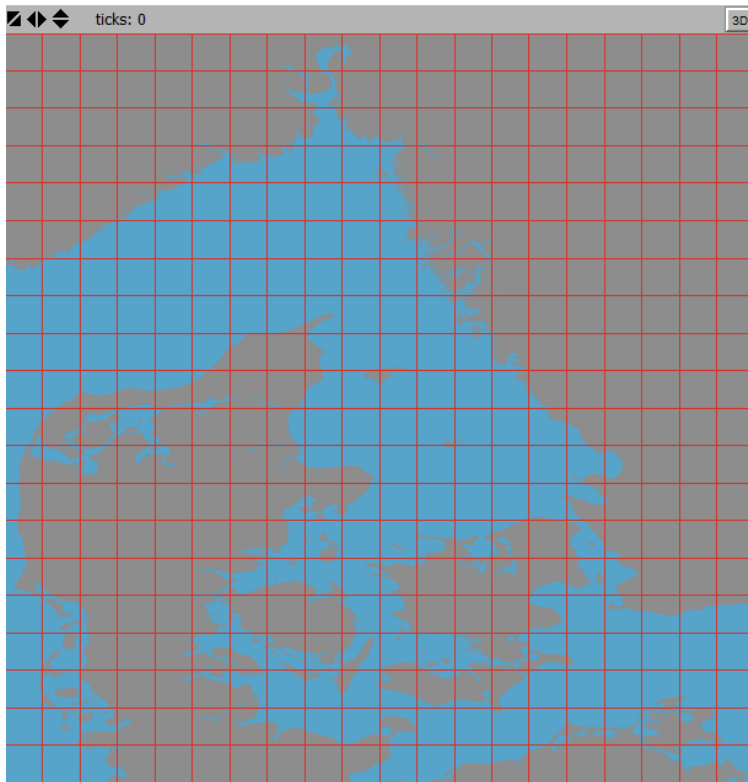
Figure 10. An example of a connectivity grid as specified in the "Connectivity Analysis" tab in the section "Set resolution of connectivity grid". Here the number of columns and number of rows are set to "20". Note that the extent of the connectivity grid is defined by the current extent of the World View.

2.6.3   Set Agent Filters

It is possible to apply filters to the IBMlib result file used in the connectivity analysis.

To include only agents that successfully settle within a settling habitat (as specified in the "Dispersal parameters" tab (see section 2.4.2) mark the check box "Include only agents settled within habitat".

To include only agents that disperse within a given temperature tolerance interval set the minimum and maximum temperature (as degree Celsius) in the "Temperature Min" and "Temperature Max" input boxes.

To include only agents that disperse within a given salinity tolerance interval set the minimum and maximum salinity (as PSU) in the "Salinity Min" and "Salinity max" input boxes.

Note that salinity and temperature filters are based on the minimum and maximum values of salinity and temperature experienced by each agent during the entire simulation. I.e. if the salinity or temperature experienced by an agent exceeds a threshold value in a single time step the agent will be excluded from connectivity analysis.

2.6.4 Create Connectivity Matrix

To calculate the connectivity adjacency and connectivity probability matrices press "Calculate". This may take some time depending on the size of the result file. The agent filter "Include only agents settled within habitat" may be time consuming depending on the resolution of the habitat grid applied. Progress bar will inform on the progress of the individual steps. Note that progress bars may be hidden behind you program interface depending on the PC settings.

Create connectivity matrix :
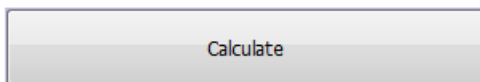
Calculate

The output of the connectivity analysis calculation are stored in a number of csv-files located in the working directory: sourcelist.csv and sourcelist_hab.csv

These comma separated files are used as input for the cluster analysis, see next section.

sinklist.csv and sinklist_hab.csv
These comma separated files are used as input for the cluster analysis, see next section.

conmatnos_colllist.csv
This is a comma separated file storing the connectivity adjacency matrix

conmatprob_collist.csv
This is a comma separated file storing the connectivity probability matrix

NOTICE: if any of the csv-files has been opened by other programs such as spreadsheets or GIS software, the "Calculate" connectivity matrix may return an unspecified error. Close the programs used for opening the csv-files and try again.

To display the density and distribution of initial positions of agents included in the connectivity analysis a grid showing the density of initial positions are shown in the World View when the connectivity matrices calculations are done. The grid is saved to an ascii grid file "ininopar.asc" stored in the SRAAM working directory and can be imported in to a GIS system. The minimum and maximum values of the grid color legend is shown in the command center. To inspect

individual values, right click on the grid cell in the world view, and select "Inspect patch…" from the Netlogo pop-up menu to access patch values.

Figure 11. Example of the grid produced by the connectivity analysis showing the densities of initial positions of agents included in the connectivity analysis. Legend (Minimum value – 2 , Maximum value – 785).

In the control center the connectivity analysis statistics are displayed. Depending on the agent filters settings and the extent covered by the connectivity grid, the final number of agents included in the connectivity analysis may be considerably smaller than the number of agents released originally in the IBMlib simulation. An example is given below:

```
Connectiity analysis statistics:

48273    TOTAL NUMBER of agents in IBMlib result file
48273    Number of agents with START position inside connectivity grid
46741    Number of agents with END position inside connectivity grid
48265    Number of agents within SALINITY and TEMP tolerance
46740    Number of agents in CONNECTIVTY ANALYSIS
Updating world view
Setting up world...
Done
```

2.7 The "Cluster Analysis" tab

The "Cluster Analysis" tab is where parameters are set for the delineation of hydrographic regions using cluster analysis.

The current version of SRAAM supports the clustering method named "Infomap" (Rosvall and Bergstrom 2008). This clustering techniques is based on information theory principles and has been used recently to delineate hydrographic regions in the Mediterranean, see: Vincent et al.(2014). The use of Infomap requires that the connectivity probability matrix is converted into a graph (i.e. as in the context of Graph Theory) where graph nodes represent each sub-area in the connectivity grid, and where pairwise connectivity probabilities are translated into weights of graph edges between nodes in a directed graph ("directed" refers to the connectivity probability from A to B may be different from the connectivity probability from B to A). The tab is prepared to include more alternative cluster techniques in future versions of SRAAM.

The cluster analysis tab provides an option for including multiple generation clustering mimicking the dispersal of organisms through multiple generations and with a given between-generations survival probability. Multiple generation connectivity probabilities are simply calculated by multiplying the connectivity probability matrix by itself a number of times corresponding to the number of generations. The connectivity probabilities between generations can be adjusted assuming a constant survival rate. Note that this way of analyzing the connectivity across multiple generations is a strong simplification and the outcome will be highly dependent on which hydrographic year is used, the number of generations included and the survival rate assumption applied.

The tab includes:

- Multiple generation analyses
- Select Cluster analysis method
- Delineate Regions

2.7.1 Multiple generation analysis

To include multiple generation connectivity in the cluster analysis, specify an integer different from "1" in the "Generations" input box. A between generations survival rate can be specified in the "Survival rate" input box.

Multigeneration analysis:

Generations:	Survival rate
1	0.1

2.7.2 Select Cluster analysis method

The cluster analysis option currently includes only one method "Infomap". The user interface is prepared for adding additional clustering methods. Currently the pulldown menu's show, i.e. "Graphmode", "Delineation method" and "Color legend" are included for information only.

The minimum size of hydrographic regions generated using the cluster analysis method can be set in the "Cluster min Size" input box. The "size" refers to the number for sub-areas or grid cells in the connectivity grid.

Select Cluster analysis method :

Graphmode
directed ▼

Delineation Method
cluster infomap ▼

Color legend
Regions IDs ▼

Cluster Min Size:
1

2.7.3 Delineate Regions

To execute the cluster analysis and delineate hydrographic regions, press the "Delineate Regions" button.

When the cluster analysis finalizes, the delineated hydrographic regions are shown in the World View, see Figure 12.

Figure 12. Hydrographic regions displayed in the World View following the termination of the cluster analysis. This example show 4 regions with unique colors.

To display the hydrographic regions using a graph representation use the "Connectivity between clusters" Map tool (see section 2.2.4) located in the "Interface" tab next to the World View.

A number of outputs of the cluster analysis are saved to the SRAAM working directory and can be used for use in a GIS environment. The outputs include:

hydregids.asc
this is an ascii grid file with values representing the hydrographic regions IDs.

centroids.shp

This is a point shape file representing the hydrographic regions as graph nodes, with geographical positions corresponding to the centroids of areal extent of the hydrographic regions. There are 6 fields in the centroids.shp attribute table:

Id	The ID of the hydrographic region
Lat	The geographical latitude of the node position (~centroid of the region extent)
Long	The geographical longitude of the node position (~centroid of the region extent)
Cohprob	The coherence as probability
Cohnos	The coherence as absolute number of agents
Ininos	The initial number of agents included in the connectivity analysis

edges.shp

This is a line shape file representing the connectivity probability between hydrographic regions as graph edges. Note that the graph representation is directional so that there may be 2 edges between 2 nodes, which cannot be seen using default GIS plotting since the edges overlap. There are 9 fields in the edges.shp attribute table:

Id	The ID of the hydrographic region
From	The "from" ID of the edge
To	The "to" ID of the edge
Weight	The the weight of the edge corresponding to connectivity probability
lat1	The latitude of the "from" node position
long1	The longitude of the "from" node position
lat2	The latitude of the "to" node position
long2	The longitude of the "to" node position
nos	The total number of agents exported from "from" node to "to" node

clconnos.csv

this is a comma separated data file representing a matrix with between cluster connectivities with values representing absolute numbers.

clconprob.csv

This is a comma separated data file representing a matrix with between cluster connectivities with values representing probabilities.

2.8 Tips and tricks

It is possible to work with SRAAM without the use of the user interface

2.8.1 IBMlib execution

The IBMlib execution can be done from a windows command line, or windows batch file for multiple simulations to be executed one by one, e.g.

C:\workdir\ibmrun\ibmrun_connect_HBM.exe simpart1.txt > stdout.txt
C:\workdir\ibmrun\ibmrun_connect_HBM.exe simpart2.txt > stdout.txt
C:\workdir\ibmrun\ibmrun_connect_HBM.exe simpart3.txt > stdout.txt
Etc.

To generate a simpar.txt file open an existing simpart.txt file in a text editor and change the sections accordingly. I SRAAM each time you click "Run IBMlib" a new simpar.txt file is created. Before the IBMlib executes, the user is prompted for if the IBMlib execution should proceed. If "No" the simpar.txt file is generated and located in the IBMrun sub-folder, but without execution. The simpar.txt can then be replicated and edited to create any number of simpar.txt files to support batch execution of IBMlib. Make sure that the "output" filename in each "simpar.txt" file are assigned a unique filename to avoid files to be overwritten. To disable the IBMlib logfile add " > NUL" to the end of the IBMlib command syntax instead of " > stdout.txt".

2.8.2 R-scripts

The individual calculation procedures in SRAAM is carried out using R, by translating the input in the SRAAM user interface to R-scripts that are subsequently executed. The generated scripts are automatically save to the SRAAM working directory. The scripts included are summarized below.

Reading IBMlib results
ncdf2array.r

This script reads all time steps and agent positions of the IBMlib result file (~ NetCDF file). It is used for animation of agent trajectories stored in the IBMlib result file.

Agent release boxes
relhabasc2ibmlib.r

This script is used to create the "Release dynamics" section in the IBMlib simulation parameter file "simpar.txt" when the agent release are based on a user specified habitat file. The script creates one line in the simpar.txt file for each agent where the initial position and initial time is sampled randomly from the spatial habitat extent and the user specified release start and end dates.

Agent settling boxes
sethabasc2ibmlib.r

This script is used to create the "Settlement dynamics" section in the IBMlib simulation parameter file "simpar.txt" when the agent settlement is based on a user specified habitat file. The script creates one line for each grid cell in the habitat ascii grid with values different from "no-value" (= -9999).

Connectivty grid

conmatpolylines.r

The script generates a line shape file (congridlinesxy.shp) with the lines representing the outline of the connectivity grid subdivision. The file(s) is saved to the SRAAM working directory. Notice that the origo of the file is per default (0,0) because the extent is linked directly to the World View setup. To display the shape file correctly in a GIS you need to set the correct origo coresponding the coordinate system applied.

Connectivity matrices

conmat.r

This script calculates the connectivity matrices (absolute numbers and probabilities) based on the IBMlib simulated agent trajectories, the specified connectivity grid and the agent filters. The output of the script include:

Conmatnos_collist.csv   - the connectivity matrix, values representing absolute numbers
Conmatprob_collist.cv   - the connectivity matrix, values representing probabilities

Sourcelist_hab.csv   - list with agent ID, start position X and Y
Sinklist_hab.csv   - list wit agents ID, end positions X and Y

Ininopar.asc   - an Asciii grid with the number of agents included in the connectivity analysis with start positions in each grid cell in the connectivity grid. This is the output shown in the World View after termination of the connectivity analysis.

Cluster analysis

cluster.r

This script performs the cluster analysis based on the connectivity matrices calculated. The script saves the cluster analysis output, the hydrographic regions, as an ascii grid file with numbers representing hydrographic region ID's. The file "hydregids.asc" is saved to the working directiory.

Between clusters connectivity

clconmatrix.r

The script calculates the between clusters connectivity in terms of absolute numbers and probabilities. The output include:

Centroids.shp   - point shape file representing regions as graph nodes (see section 2.7.3)

Edges.shp   - line shape file representing regions connectivity as graph edges (see section 2.7.3)

Clconnos.csv   - between clusters connnectiviy matrix as absolute numbers (see section 2.7.3)

Clconprob.csv   - between clusters connectivity martrix as probabilities. (see section 2.7.3)

Hydrographic regions PDF plot
clcon2pdf

This script creates a graph representation of between clusters connectivity in terms of "nodes" and "edges" representing "hydrographic regions" and "between regions connectivity" respectively. The graph is saved as temporary pdf file and opened in the default pdf viewer or browser.

3.   Hydrographic data formats

The normal way to interface IBMlib with a new hydrographic format is to add a new physical interface layer that couples the data set to IBMlib. This procedure does not require reformatting of the hydrographic data set, but IBMlib can then read data as-provided. Alternatively, one can recast (~translate) a new hydrographic data set into a format corresponding to an already implemented interface; this alternative should be pursued with caution, because (i) recasting may involve numerical truncation and thus accuracy loss and (ii) recasting may be faulty because the translator either have misunderstood the native hydrographic format or the format specification and (iii) some special features of the hydrographic data set may be lost because it can not be represented by the target format. Extensive testing is therefore recommended before actual result generating runs are performed.

IBMlib on this web site comes in 4 pre-compiled versions: (i) at hydrographic testing environment, based on a realistic hydrographic model, (ii) a version reading a generic data format, based on the POM output format, (iii) a version reading COARD-compliant data formats, e.g. NEMO and NCOM output, and (iv) a version reading the HBM data format.

3.1   Bootstrapped testing configuration

In many practical applications of individual-based simulations in marine environments, the simulation is conducted off-line, i.e. hydrographic data is loaded from a precomputed database, which contains hydrographic data for the time period, where the simulation is conducted. The most time consuming part is loading hydrographic data from the database, which often contains TB of data. To speed up the production cycle during a testing phase, it is useful have a testing environment, which limits time-consuming data reading from the hydrographic database. One trick to do this is to recycle a hydrographic time frame (~time step) over and over again, rather than loading a new data frame for each time point; we call this the bootstrapped hydrography mode. In this way, one can test a setup in a setting with a realistic topography and hydrographic variability, but without temporal variability. The precompiled bootstrapped version on this web site is based on the ECOSMO (Schrum et al, 1999; 2006) coupled physical-biogeochemical model, and the SRAAM setup files include a single time frame of hydrography. The testing area is the North Sea/Baltic region with 10 km horizontal resolution, and only the physical variables enabled.

3.2   Generic POM data format

The suggested target format for recasting is based on the POM (Blumberg and Mellor, 1987) output layout, which is relatively simple and transparent; the abundance of regional POM setups also gives a chance that very little data transformation actually has to be done. The format will support many typical usages of IBMlib. The target grid is regular longitude-latitude (with arbitrary user provided longitude-latitude spacing), with vertically sigma-type (with number of layers specified by user), dynamic sea-level elevation and arbitrary topography. Data is stored as daily averaged hydrography data frames with a filename corresponding to the date. The format is stored in netCDF (see http://www.unidata.ucar.edu/software/netcdf/) and consists of:

(1) A grid desciptor file "grid.nc"
(2) A sequence of daily hydrography frames with filename "hydrography_YYYY_MM_DD.nc"

where (YYYY, MM, DD) is year, month and day-in-month number, respectively, with prepended zeroes as necessary, i.e. hydrography for February 15 2016 should be stored in file "hydrography_2016_02_15.nc". For convenience, the grid desciptor file may be merged with each hydrography file, but this requires a little extra storage, because the grid desciptor is duplicated many times. The templates for grid desciptor and hydrography frames are provided "grid.CDL" and "hydrography_YYYY_MM_DD.CDL" (see sections 3.2.1 and 3.2.2 respectively). CDL is the text translation of netCDF, so these files show exactly what IBMlib expects - just show the CDL file to your hydrography data provider. The period where you can conduct simulations correspond to the period covered by files hydrography_YYYY_MM_DD.nc. At runtime IBMlib tries to read the needed files hydrography_YYYY_MM_DD.nc and stops, if the file is not found (with the expected filename in the expected folder). You don't have to structure or declare the hydrographic database further, just place expected files in the path announced in the simulation input file with the proper names hydrography_YYYY_MM_DD.nc. In SRAAM the expected folder is the "POM" folder in the "IBMrun" directory located in your working directory.

If the format for one reason or another does not support your specific needs, it is recommended that you follow instructions within IBMlib for creating a specific physical interface for the data set and recompile IBMlib for your setup (see: https://github.com/IBMlib/IBMlib). IBMlib is free and open source, but if you are not familiar with fortran programming and code compilation, you may contact the IBMlib developers to explore possibilities and conditions for a collaboration. Below you will find the content of "grid.CDL" and "hydrography_YYYY_MM_DD.CDL" that can be copied and pasted into a plain text file, if needed.

3.2.1   Grid descriptor file format

```
// -----------------------------------------------------------------------------------------
// Grid is regular longitude-latitude (with arbitrary user provided longitude-latitude spacing),
// vertically sigma-type (with number of layers specified by user), dynamic sea-level elevation
// and arbitrary topography. This grid descriptor may be embedded in each hydrographic data
// frame hydrography_YYYY_MM_DD for simplicity.
// POM employs sigma coordinates, which are bottom-following coordinates that map the vertical
// coordinate from the vertical coordinate from -H < z < eta onto -1 < sigma_POM < 0, where z is
// -depth below ref level (not sea surface)
// H > 0 is the static variable h(x,y) (in grid file) loaded into wdepth0
// eta is dynamic variable elb(x,y) (in physics file) )
// fsm > 0.0 for wet points, fsm == 0.0 for dry points
// -----------------------------------------------------------------------------------------
netcdf grid {
dimensions:
            x = 182 ;   // longitude grid points
            y = 125 ;   // latitude grid points
            z = 35 ;    // vertical grid points
variables:
            double zz(z) ;
```

```
                                    zz:long_name = "sigma of cell centre" ;
                                    zz:units = "sigma_level" ;
                                    zz:standard_name = "ocean_sigma_coordinate" ;
                                    zz:formula_terms = "sigma: zz eta: elb depth: h" ;
                    double east_e(y, x) ;   // cell centers
                                    east_e:long_name = "easting of elevation points" ;
                                    east_e:units = "degree" ;
                                    east_e:coords = "east_e north_e" ;
                    double north_e(y, x) ;  // cell centers
                                    north_e:long_name = "northing of elevation points" ;
                                    north_e:units = "degree" ;
                                    north_e:coords = "east_e north_e" ;
                    double h(y, x) ;        // at cell centers
                                    h:long_name = "undisturbed water depth" ;
                                    h:units = "metre" ;
                                    h:coords = "east_e north_e" ;
                    double fsm(y, x) ;
                                    fsm:long_name = "free surface mask" ;
                                    fsm:units = "dimensionless" ;
                                    fsm:coords = "east_e north_e" ;


// global attributes:
                                    :title = "black_sea" ;
                                    :description = "POM grid file" ;
}
```

3.2.2 Hydrographic data format

```
// ---------------------------------------------------------------------------
//  POM employs sigma coordinates, which are bottom-following coordinates that map the
// vertical coordinate from the vertical coordinate from -H < z < eta onto -1 < sigma_POM < 0, /
// where z is -depth below ref level (not sea surface)
//  H > 0 is the static variable h(x,y) (in grid file) loaded into wdepth0  eta is dynamic variable
//  elb(x,y) (in physics file) )
//  nz is number of faces vertically so that the number of wet cells is nz-1 vertically.
//  Cell-centered arrays like t (temperature) are padded with an arbitrary value in last
//  element iz=35 (surface cell at iz=1)
//  netCDF variable w(x,y,z) refers to vertical faces (not cell centers), so w(x,y,1) ~ 0
//  at sea surface and w(x,y,nz=35) = 0 at the sea bed.
//  Currently load these fields (in native units/conventions, c-declaration index order):
//    float elb(y, x)   = "surface elevation in external mode at -dt"  units = "metre" ;
//    staggering  = (east_e, north_e)
//    float u(z, y, x)   = "x-velocity"                     units = "metre/sec" ;
//    staggering  = (east_u, north_u, zz)
//    float v(z, y, x)   = "y-velocity"                     units = "metre/sec" ;
//     staggering  = (east_v, north_v, zz)
//    float w(z, y, x)   = "sigma-velocity"                  units = "metre/sec" ;
```

```
//    staggering  = (east_e, north_e, z)
//    float t(z, y, x)   = "potential temperature" ;              units = "K" ;
//    staggering  = (east_e, north_e, zz)
//    float s(z, y, x)   = "salinity x rho / rhoref" ;           units = "PSS" ;
//    staggering  = (east_e, north_e, zz)
//    float rho(z, y, x) = "(density-1000)/rhoref" ;              units = "dimless"
//    staggering  = (east_e, north_e, zz)
//    float kh(z, y, x)  = "vertical diffusivity" ;              units = "m^2/sec";
//    staggering  = (east_e, north_e, zz)
//    float aam(z, y, x) = "horizontal kinematic viscosity" ;        units = "metre^2/sec";
//    staggering  = (east_e, north_e, zz)
// u(ix,iy,iz) in grid position (ix-0.5, iy    , iz)    (i.e. western  cell face)
// v(ix,iy,iz) in grid position (ix    , iy-0.5, iz)    (i.e. southern cell face)
// w(ix,iy,iz) in grid position (ix    , iy,    iz-0.5) (i.e. upper    cell face)
// The boundary condition:  w( ix, iy, nz+0.5 ) = 0   is implicit
// ----------------------------------------------------------------------
netcdf hydrography_YYYY_MM_DD {
dimensions:
                z = 35 ;
                y = 125 ;
                x = 182 ;
variables:
                float elb(y, x) ;
                            elb:long_name = "surface elevation in external mode at -dt" ;
                            elb:units = "metre" ;
                            elb:coordinates = "east_e north_e" ;
                float u(z, y, x) ;
                            u:long_name = "x-velocity" ;
                            u:units = "metre/sec" ;
                            u:coordinates = "east_u north_u zz" ;
                float v(z, y, x) ;
                            v:long_name = "y-velocity" ;
                            v:units = "metre/sec" ;
                            v:coordinates = "east_v north_v zz" ;
                float w(z, y, x) ;
                            w:long_name = "sigma-velocity" ;
                            w:units = "metre/sec" ;
                            w:coordinates = "east_e north_e zz" ;
                float t(z, y, x) ;
                            t:long_name = "potential temperature" ;
                            t:units = "K" ;
                            t:coordinates = "east_e north_e zz" ;
                float s(z, y, x) ;
                            s:long_name = "salinity x rho / rhoref" ;
                            s:units = "PSS" ;
                            s:coordinates = "east_e north_e zz" ;
                float rho(z, y, x) ;
```

```
                    rho:long_name = "(density-1000)/rhoref" ;
                    rho:units = "dimensionless" ;
                    rho:coordinates = "east_e north_e zz" ;
        float kh(z, y, x) ;
                    kh:long_name = "vertical diffusivity" ;
                    kh:units = "metre^2/sec" ;
                    kh:coordinates = "east_e north_e zz" ;
        float aam(z, y, x) ;
                    aam:long_name = "horizontal kinematic viscosity" ;
                    aam:units = "metre^2/sec" ;
                    aam:coordinates = "east_e north_e zz" ;


// global attributes:
                    :title = "black_sea" ;
                    :description = "restart file" ;
}
```

3.3 COARDS-compliant data formats

An often used data format for exchanging and storing hydrographic data is the COARDS format
(NOAA, 1995). The precompiled IBMlib version supporting this may run in single or multi file
mode. In single file mode, all physical variables at all times are collected in a single file; for a
long time series, this file can become pretty large, if the spatial resolution is high or the
simulation domain is extended. It is also possible to have each physical variable in separate
files, so all 3D temperature data is in one file, all 3D salinity data in another etc.; this also
reduce the file size a little by spreading data over several files, without increasing the net
volume of data. Because variable names are not fixed in the COARDS format, this information
must be passed to IBMlib, so it knows what to look for in the NetCDF files provided. In the
SRAAM setup, this is built into the GUI for NEMO and NCOM data; in this way you should be
able to run your simulation with free data from Copernicus or NOAA. If you apply another
COARDS compliant data set, you should make sure the simulation passed from the SRAAM
GUI to IBMlib contain these entries:
Single file mode:

```
!
hydroDBpath          = /home/data/NCOM_NOAA_Caribia
!
!  Either all data in one file (hydrography_file)
!  or split in three files (current_file, temperature_file, salinity_file)
!
hydrography_file    = NCOM_amseas_latest3d_bec1_fd79_ea18.nc
!
!  specify which variable names apply to each variable
!
longitude_name    = longitude
latitude_name     = latitude
```

50

```
                temperature_name  = water_temp
                salinity_name     = salinity
                u_name            = water_u
                v_name            = water_v
                !w_name           =   ! optional
```

Multi file mode:

```
                !
                hydroDBpath           = /home/data/NEMO_MedSea
                !
                !   Either all data in one file (hydrography_file)
                !   or split in three files (current_file, temperature_file, salinity_file)
                !
                current_file      = sv03-med-ingv-cur-rean-d_1528702309049.nc
                temperature_file  = sv03-med-ingv-tem-rean-d_1528702936527.nc
                salinity_file     = sv03-med-ingv-sal-rean-d_1528702809386.nc
                !
                ! specify which variable names apply to each variable
                !
                longitude_name    = lon
                latitude_name     = lat
                temperature_name  = votemper
                salinity_name     = vosaline
                u_name            = vozocrtx
                v_name            = vomecrty
                !w_name           =   ! optional
```

Notice that no grid descriptor is needed, IBMlib detects time points for data and the hydrographic grid and the topography directly from the netCFD data set.

When you download the SRAAM tool small examples of the NEMO and NCOM datasets are include for the Mediterranean and the Caribean respectively. Both data sets covers the period 01-01-2012 to 10-01-2012. The NEMO data set covers the spatial extent 9 – 11 degrees east, and 38 – 40 degree north. The NCOM data set covers the spatial extent of 275 – 276 degree east, and 23 – 24 degree north.

3.4 HBM data format

Many IBMlib studies have been conducted using data from the HBM model. The HBM (HIROMB-BOOS Model) in the operational setup by DMI (Danish Meteorological Institute) covers the Baltic-North Sea region (DMI, 2017). The model has been jointly developed by HBM consortium and used as an operational model in Denmark, Estonia, Finland and Germany. A biogeochemical module (ERGOM) is dynamically embedded in the HBM. With two-way dynamical nesting, HBM enables high resolution in regional seas and very high resolution in narrow straits and channels. With its support for both distributed and shared memory parallelization, HBM has matured as an efficient and portable, high quality ocean model code.

The HBM setup for the present hydrographic dataset has a horizontal grid spacing of 6 nautical miles (nm) in the North Sea and in the Baltic Sea, and 1 nm in the inner Danish waters. In the vertical the model has up to 50 levels in the North Sea and the Baltic Sea, and 52 levels in the inner Danish waters with a top layer thickness of 2 m. HBM is forced by DMI-HIRLAM with 10 m wind fields, sea level pressure, 2 m temperature and humidity and cloud cover. At open model boundaries between Scotland and Norway and in the English Channel, tides composed of the 8 major constituents and pre-calculated surges from a barotropic model of North Atlantic (Dick et al., 2001) are applied. Freshwater runoff from the 79 major rivers in the region is obtained from a mixture of observations, climatology (North Sea rivers) and hydrological models (Baltic Sea). At the surface the model is forced with atmospheric data from numerical weather prediction model HIRLAM (Petersen et al, 2005). The HBM setup performance has been validated on several occasions, e.g. Schmith and Borch 2013; Wan et al, 2012; Berg, 2012; Maar et al, 2011; She et al 2007a, She et al 2007b.

4.   Application examples

The two examples shown here cover the region including the North Sea, Skagerrak, Kattegat, The inner Danish straits and the western Baltic Sea. The first example is based on a static hydrographic dataset provided when the SRAAM software components and user data is installed and consists of hydrographic data set with a single time step that are continuously repeated during the simulation. The second example is based on a dynamic hydrographic dataset that corresponds to the HBM model for the regions setup and operated by Danish Meteorological Institute (DMI). This data set is not available as part of the installation, however output file is included in the SRAAM setup files (Arcuatula_senhousia_2005_2e+05.nc). For details on data and methodology, see Hansen et al. (2018).

4.1   Example using the Static hydrographic dataset

This is an example that can be run for demonstration purpose with the files that comes with the SRAAM installation. Because this example is based on a static hydrographic dataset with no temporal variability in current direction and magnitude, the results are not realistic but serve as an example on how the SRAAM functionality works. In the proceeding section 4.2 a more realistic example is shown.

4.1.1   SRAAM input

Flow directions and speed varies in space but are constant in time. The following SRAAM settings were used:

World view setup
Xgeo_min: 4
Xgeo_max: 14
Ygeo_min: 54
Ygeo_max: 60

Agent release settings
Agent release: Specified corner coordinates
Agent release period: 2009 03 02 – 2009 04 02
Agent release area: 4/54   14/60 (1 box)
Agent release depth interval:
Min depth 0 meters
Max depth 0 meters
No. of agents: 10 000

Dipsersal paramters

Pelagic larvae duation (PLD) 31 days

Include Active settling: disabled

Vertical distribution range: 0 – 20 meters

Dispersion, vertical: 0.001 m2/s

Dispersion, horizontal: 10 m2/s

Vertical sinking speed: 0

Simulation settings

Hyrdographic data format: Stationary_flow_field

Start time: 2009 03 02 0

End time: 2009 05 02 0

Time step: 1800 sec

Storing Frequency: 86400 sec

Result file: Results_SFF_10000.nc

Connectivity analysis parameters

Connectivity grid: 14 rows / 20 columns

Include only agents settled within habitat: Disabled

Temperature minimum tolerance: 0

Temperature maximum tolerance: 40

Salinity minimum tolerance: 0

Salinity maximum tolerance: 40

4.1.2   Results

A snapshot of agent distribution (red dots) on day 16 including agent trajectories (yellow tracks) is shown below together with the applied connectivity grid used in the connectivity analysis (red lines):
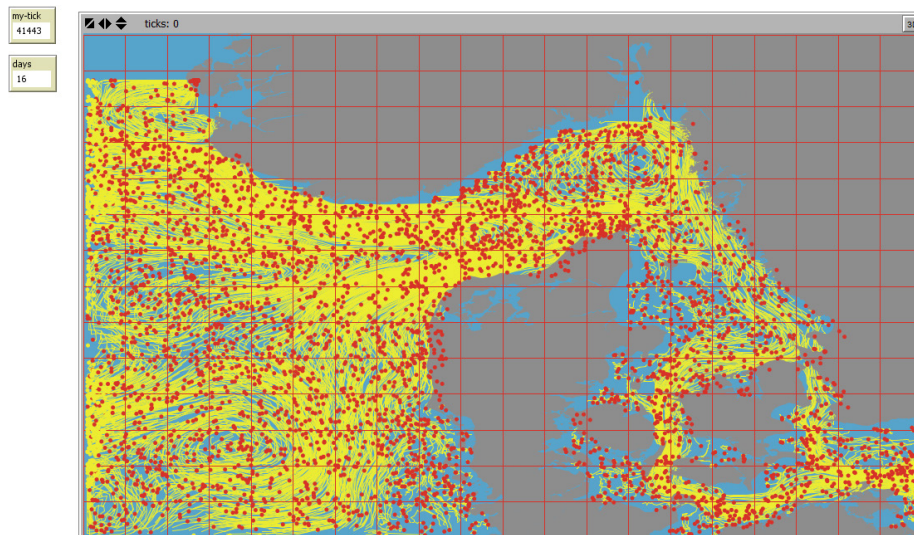
Figure 13. A snapshot of agent positions on day 16 (red dots) including agent trajectories (yellow tracks) and the connectivity grid (red lines) used for the connectivity analysis.

The output statistics of the connectivity analysis (below) shows that out of the 10 000 agents included in the IBMlib simulation, 10 000 agents have an initial position inside the user specified connectivity grid, 6042 have an end position inside the connectivity grid, 9988 agents lie within the salinity and temperature intervals, and 6030 agents in total were included in the connectivity analysis. If the option "Include only agents settled within habitat" had been enabled, the number of agents successfully settled within the habitat would have been included in the statistics.

```
CONNECTIVTY ANALYSIS
IBM Lib Result file:  C:/root_SRAAM_release/IBMrun/results_SFF_10000-all.nc
Calculating Connectivty matrices...
Creating R script file .....
Running R script (C:/root_SRAAM_release/conmat.r) ...

Connectivity analysis statistics:

10000    TOTAL NUMBER of agents in IBMlib result file
10000    Number of agents with START position inside connectivity grid
6042    Number of agents with END position inside connectivity grid
9988    Number of agents within SALINITY and TEMP tolerance
6030    Number of agents in CONNECTIVTY ANALYSIS
Updating world view
Setting up world...
Done
```

The densitiy of the initial positions of agents of each connectivity grid cell and which are included in the connectivity analysis is shown in figure Figure 14. The somewhat uneven distribution with low (or no) densities in some areas can be explained by the fact that agents with an initial position in these areas are exported out of the area covered by the connectivity grid as a result of ocean currents, and thus are not included in the connectivity analysis.
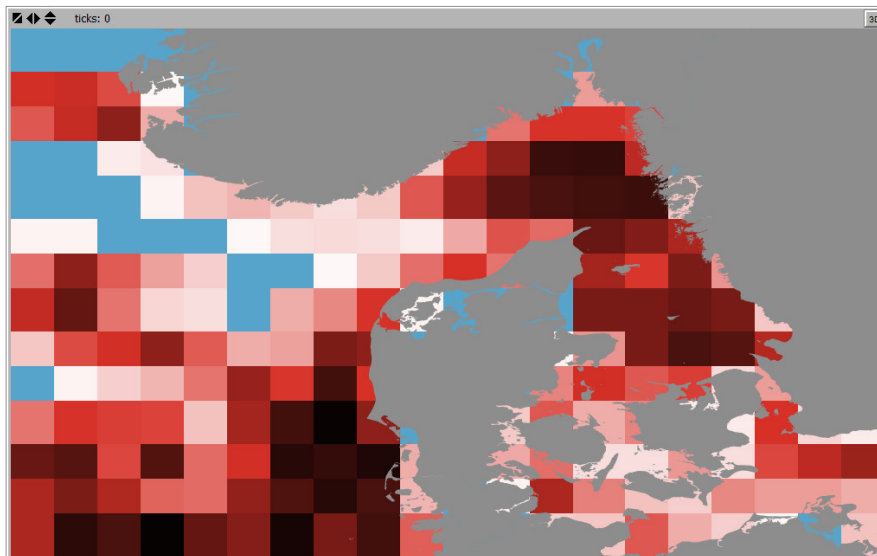

Figure 14. Density of initial positions of agents per grid in the connectivity grid included in the connectivity analysis. Minimum value 1 (~white) , maximum value 81 (dark red). Blue color refers to "0".

```
Plot: Number of agents per grid in connectivity analysis (~Start positions):
Minimum value - 1
Maximum value - 81
```

The delineation of hydrographic regions using the cluster analysis methodology "Infomap", results in 16 well define regions, see Figure 15.
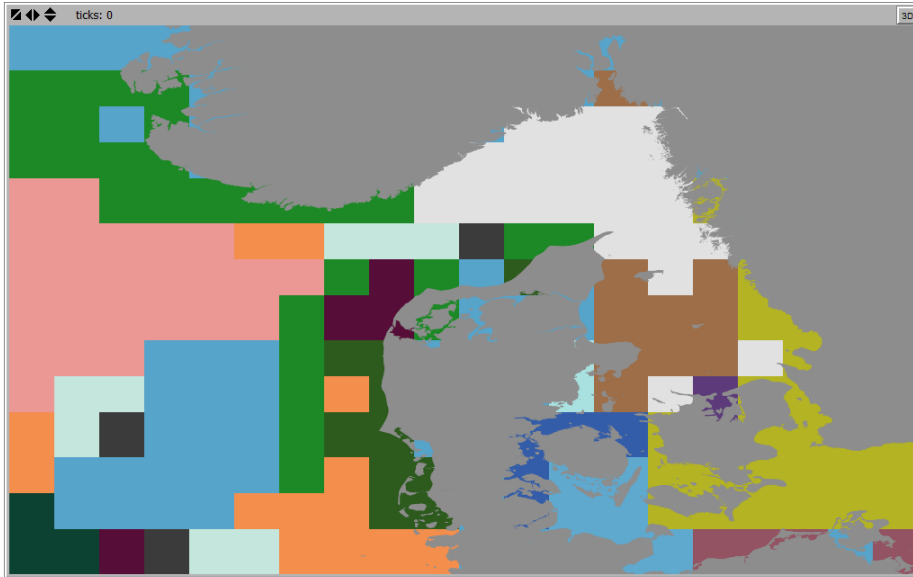

Figure 15. Example of delineated hydrographic regions using the cluster analysis methology "Infomap".

```
Number of regions  : 16
Max value of color legend: 16
Min value of color legend: 1
Done
```

Regions plotted as a graph representation are shown in Figure 16. Each Node represents the geometrical centroid of the individual region. Node numbers refer to the coherence (or self-recruitement) of each region as probabilities (in pct) refering to the probabiilty that an agent with an initial position inside the region settle within the same region. Edges (~arrows) direction and thichness refer to the probabilities (in pct) that an agent with an initial position inside a region will settle in one of the other regions. Regions and region centroids/nodes have the same color. Notice that sometimes connectivity grid cells far apart may belong to the same region, and thus region nodes here defined as geomtrical centroid may be placed "outside" the regions outline.
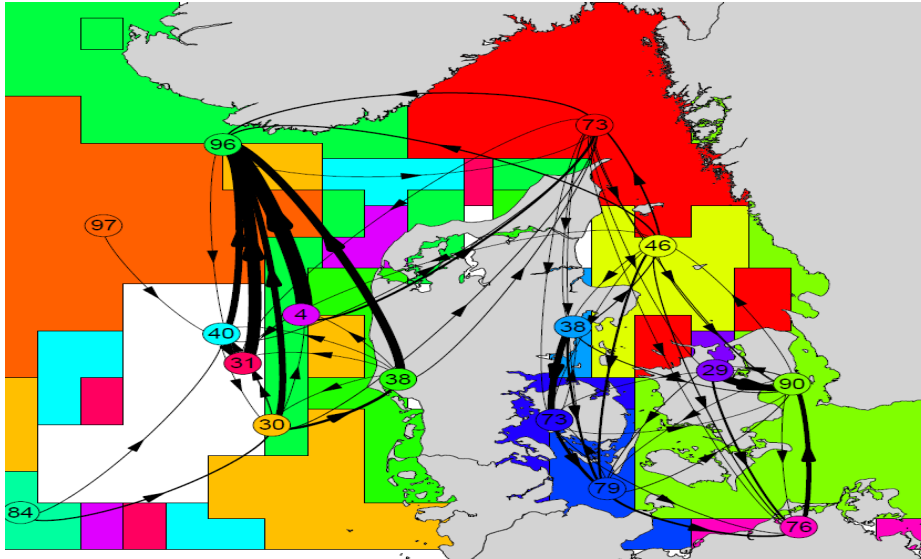
Figure 16. Graph representation of the within and between region connectivity probability.

To access the exact values representing the between regions connectivity probability, please refer to the clconprob_collist.csv or edges.shp files.

I Figures 17 and 18 are shown examples on how to extract downstream and upstream connectivity probabilites for a single location using the "Display connectivity probability" tool as described in section 2.2.4.
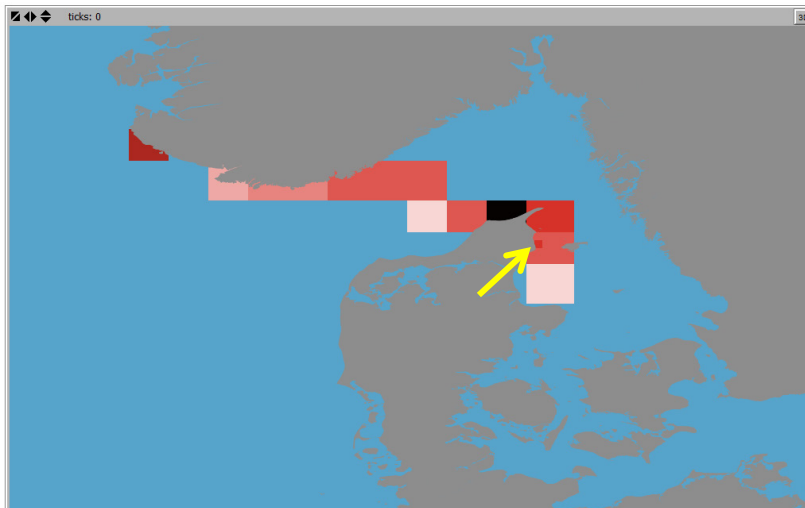

Figure 17. Downstream connectivity probability of a specified location indicated by yellow arrow. The color legend range from 0 (blue) to 0.196 (darkest red). Values represent the probability that an agent released in the specific location (grid cell indicated by a yellow arrow) will end up in any other grid cell.

Figure 18. Upstream connectivity probability of a specified location indicated by yellow arrow. The color legend range from 0 (blue) to 0.356 (darkest red). Values represent the probability that an agent with an end position in the specified location (grid cell indicated by a yellow arrow) will originate from (~have their start position in) any other grid cell.

4.2 Example using a dynamic hydrographic dataset

This example uses the hydrographic dataset generated by the HBM model for the North Sea, Skagerrak, Kattegat, Inner Danish Straits and the Baltic Sea (for details: Berg and Poulsen 2012). The model uses a nested horizontal grid with a grid resolution of 3 nautical miles (~ 5.6 km's) in the North Sea and Skagerrak and 0.5 nautical miles (~0.9 km's) in the Kattegat, Inner Danish Straits and the Western Baltic sea, The vertical resolution is 50 layers in the North Sea and 52 layers in transition zone between the North Sea and the Baltic Sea including the Kattegat, the Inner Danish Straits and the Western Baltic Sea. The dataset used for the SRAAM setup include current speed and direction, water temperature and salinity. All values are stored as daily means.
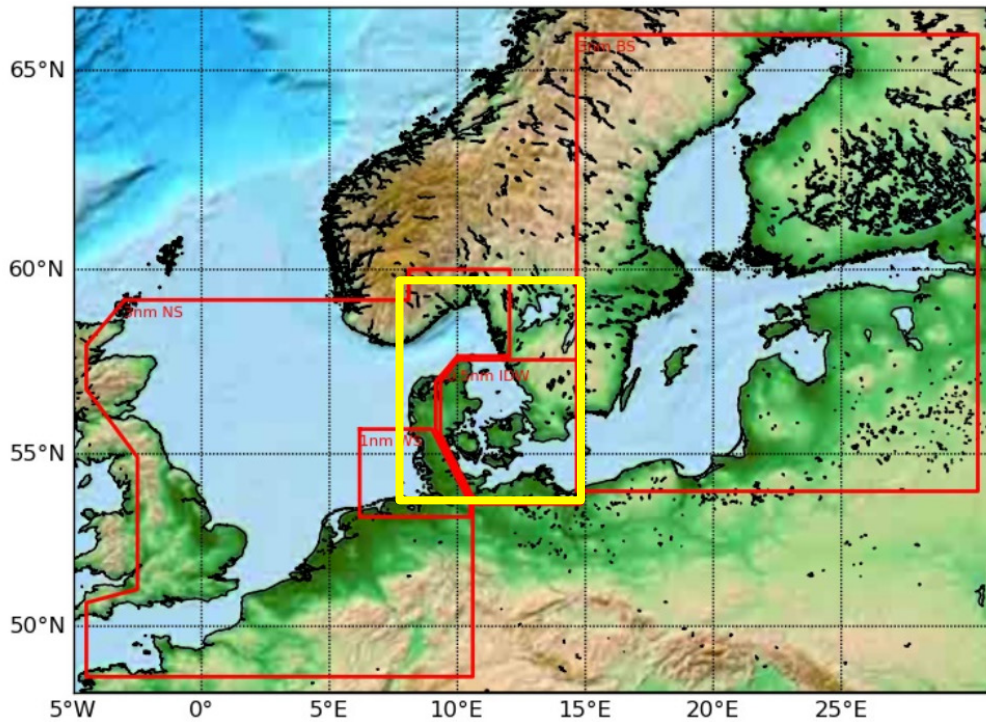
Figure 19. The map shows the extent of the HBM model setup for the North Sea, Skagerrak, Kattegat, the Inner Danish Straits and the Baltic Sea (Berg and Poulsen 2012). Red color outline indicate nested sub-areas of the model domain with different horizontal grid resolutions. Yellow outline indicate the sub-area of the example of a SRAAM application covered in this section.

The study area including Skagerrak, Kattegat, Inner Danish Straits and the Wester Baltic Sea represent a transition area between the highly saline North Sea and the brackish Baltic Sea. Thus, the study area is subject to highly variable salinity conditions due to wind stowing processes and tides. Figure 20 gives an indication of the salinity gradient of annual mean bottom salinities along the salinity gradient from the saline North Sea to the brackish Baltic Sea.
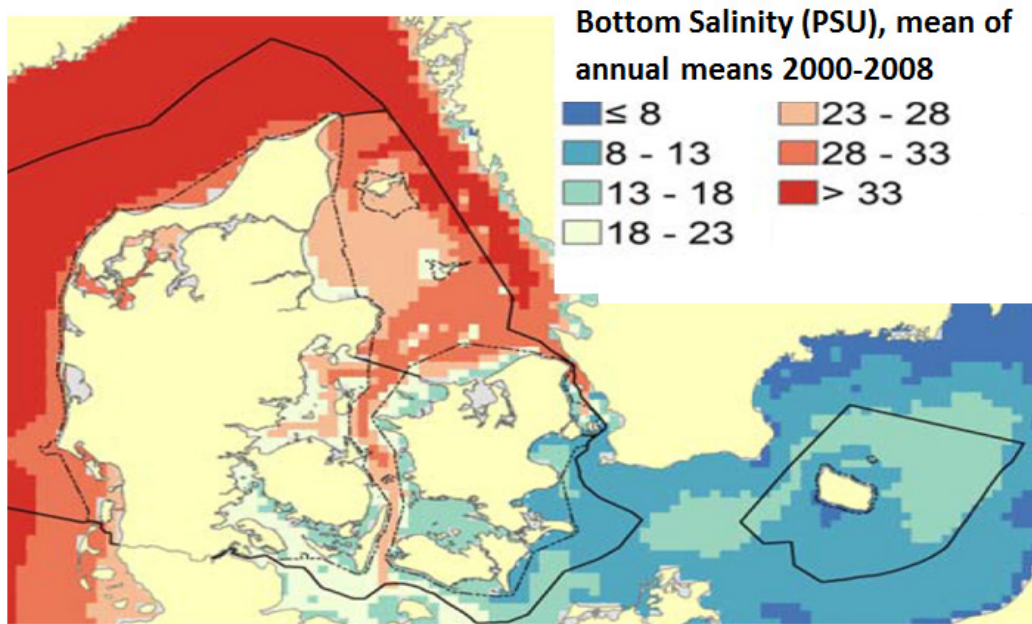
Figure 20. Mean of annual means of bottom salinity (PSU) 2000-2008. Data extracted from a hydrodynamic model (see: Hansen et al. 2012).

In this SRAAM example we use the marine invasive species Asian Date Mussel (*Arcuatula senhousia)*, Figure 21.

Figure 21. Picture of the Asian Date Mussel (*Arcuatula senhousia*). Source: www.cabi.org.

Dispersal parameters and habitat preferences are shown in Tables 1 and 2. A habitat distribution map is shown in Figure 22. The habitat map is derived based on habitat preferences (Table 2) including preferred bottom substrate for sessile stages, salinity preferences/tolerances and preferred water depths. The suitable habitat is divided into two types indicating the optimal(green) and sub-optimal yellow) distribution of preferred habitat within the study area that comply with the known salinity tolerance. For details see Hansen et al. (2018). In short, to classify the suitable habitat into two areas according to the salinity tolerance, minimum and maximum salinities where extracted from the hydrographic dataset for 3 selected hydrographic years. Then the mean of the 3 years were calculated, and areas where the mean of annual minimum values were above the minimum salinity threshold were colored "green". Areas where the mean of the annual maximum values were above minimum threshold were colored "yellow".

This way, "green" areas represent habitats where salinity conditions are expected to be favorable at all times (or most of the time), while "yellow" areas represent habitats where salinity conditions are expected to be favorable only within shorter or longer periods. Both green and yellow areas are used as spawning areas in the IBMlib simulation, however the discrimination between primary (green) and secondary (yellow) habitat may be used as part of the result interpretation and in particular in case where results are to be used in risk assessment context.

Table 1. Dispersal paramters for Asian Date Mussel (*Arcuatula senhousia*).

PLD (days)	14
No. of generations per year	1
Start month for spawning	7
End month for spawning	8

Table 2. Habitat preferences for Asian Date Mussel (*Arcuatula senhousia*)

Depth (m)	0 – 20
Substrate	All types
Sallinity min (psu)	17 psu
Salinity max (psu)	-
Temp. min (deg.C)	-
Temp. max (deg.C)	-
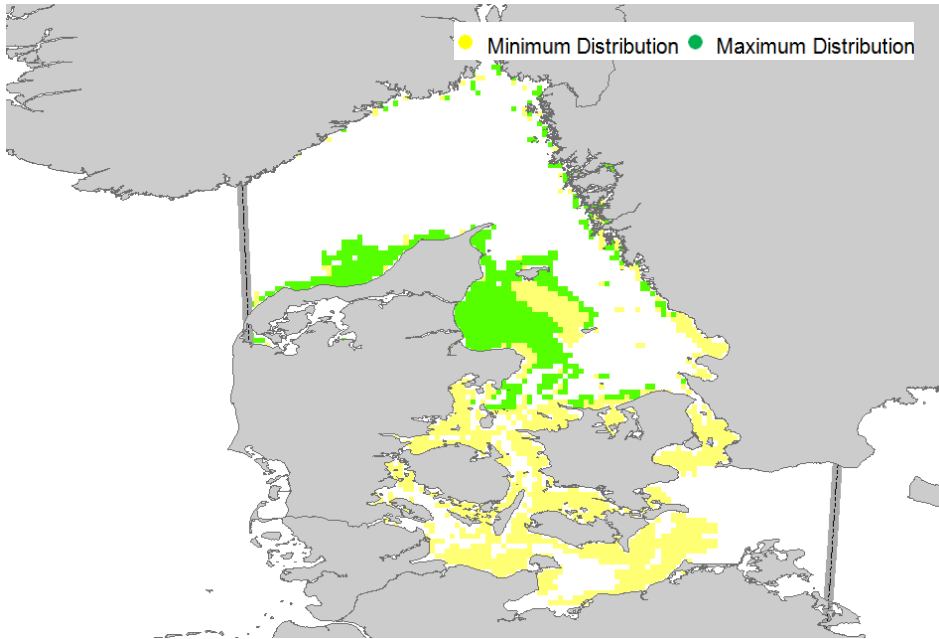
Figure 22. The map show the distribution of preferred habitats for Asian Date Mussel (*Arcuatula senhousia*) in the study area. Habitat selected based on habitat preferences (Table 2) including preferred bottom substrate for sessile stages, salinity preferences/tolerances and preferred water depths. Green areas represent areas where salinity conditions are expected to be favorable all (or most) of the time, while yellow areas represent habitats where salinity conditions are expected to be favorable in shorter or longer periods. The grey border lines indicate the western and eastern boundaries of the study area respectively.

4.2.1   SRAAM input

The SRAAM input are desdcribed below. The result file from the IBMlib simulation is available in the SRAAM setup files (Arcuatula_senhousia_2005_2e+05.nc) in order to be able to reproduce the maps and outputs presented in the following. The file include only the last time step, however initial positions are stored as part of the result file (see section 2.5.5). The HBM hydrographic dataset is not included.

World view setup

Xgeo_min: 8
Xgeo_max: 14
Ygeo_min: 54
Ygeo_max: 60
Landshp: land_small.shp
Scaling factor: 10

Agent release settings

Agent release: Habitat map

Agent release period: 2005 07 01 – 2005 09 01

Agent release area: Habitat map (see Figure 22)

Agent release depth interval

        Min depth: 0 meters

        Max depth: 0 meters

No. of agents: 200 000

Dipsersal parameters

Pelagic larvae duation (PLD) 14 days

Include Active settling: disabled
Habitat input file: "hab_arcuatula_119x200_all_0-20m_stt-maxrange.asc"

Vertical distribution range: 0 – 40 meters

Dispersion, vertical: 0.001 m2/s

Dispersion, horizontal: 10 m2/s

Vertical sinking speed: 0

Simulation settings

Hyrdographic data format: HBM (nested)

Start time: 2005 07 01 0

End time: 2005 09 15 0

Time step: 1800 sec

Connectivity analysis parameters

Connectivity grid: 20 rows / 20 columns

Include only agents settled within habitat: Enabled

Temperature minimum tolerance: 0

Temperature maximum tolerance: 40

Salinity minimum tolerance: 17

Salinity maximum tolerance: 40

4.2.2 Results

The initial and end positions of all simulated agents are shown in Figure 23. The initial and end positions are stored in the files sourcelist_hab.csv and sinklist_hab.csv respectively. To plot the same figures as shown in Figure 23 load the csv files into a GIS system and make XY plots.
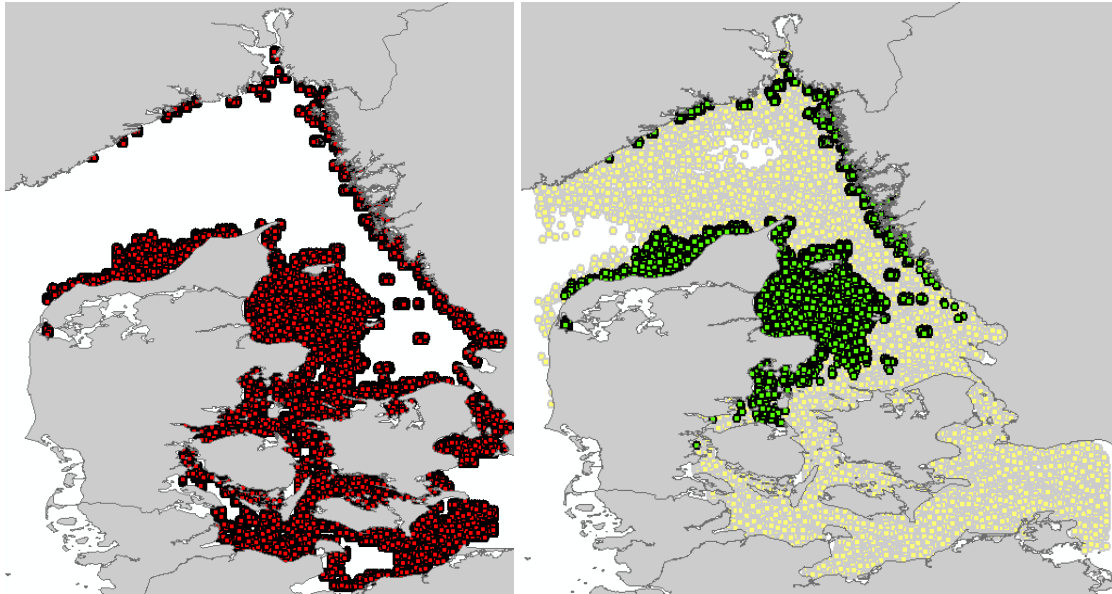
Figure 23. Left: Initial positions of all simulated agents. Right: end position of all simulated agents. Green color indicates agents that successfully settle within suitable habitat. Yellow indicates agents that settle outside suitable habitat.

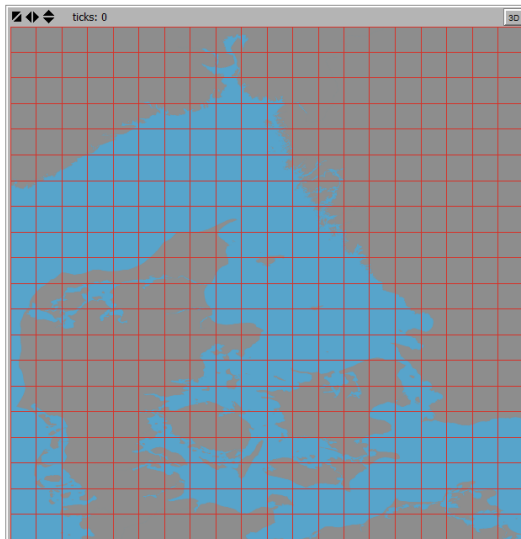The connectivity grid used for the connectivity analysis include 20 rows and 20 columns, see Figure 24.

Figure 24. The 20x20 connectivity grid used for the connectivity analysis.

The results presented below, are based on a connectivity analysis using agent filters, i.e. including only agents that successfully settle within suitable habitat (Figure 22), AND, excluding all agents experiencing salinities below the minimum tolerance threshold of 17 psu. As shown below, out of a total of 186 162 agents successfully simulated in the IBMlib simulation, only 12

955 agents are included in the connectivity analysis. A large proportion of the agents are settled outside the suitable habitat, and similarly a large proportion of the agents are excluded because of unfavorable salinity conditions.

```
CONNECTIVTY ANALYSIS
IBM Lib Result file:  C:/data_work/2018/SRA_casestudy/Results/Arcuatula_senhousia_2005_2e+05.nc
Calculating Connectivty matrices...
Creating R script file .....
Running R script (C:/root_SRAAM_release/conmat.r) ...

Connectivity analysis statistics:

186162   TOTAL NUMBER of agents in IBMlib result file
186162   Number of agents with START position inside connectivity grid
183818   Number of agents with END position inside connectivity grid
48814   Number of agents within SALINITY and TEMP tolerance
79507   Nubmer of agents settled successfully within HABITAT
12955   Number of agents in CONNECTIVTY ANALYSIS
Updating world view
Setting up world...
Done
```

Figure 25 shows the densities of 12 955 agents with initial positions within suitable habitat that eventually also settle successfully within suitable habitat, AND, that do not experience exceedance of the salinity tolerance interval during the simulated dispersal. Values vary considerably between 0 and 1597 number of agents per grid cell, with the largest numbers in the core area of the preferred habitat (in the central part of the study area) and smaller values towards the edge of the habitat extent and towards the southern distribution. This pattern is partly due to agents being more likely to be exported to areas with unfavorable physical habitat conditions by ocean currents if the initial position is located at the edge of the habitat extent, and partly because the experienced salinity during dispersal exceeds the species salinity tolerance interval. The latter is the primary reason for the absence of agents included in the connectivity analysis with an initial position located in the southern part of the study area where salinities decreases towards the Baltic sea.
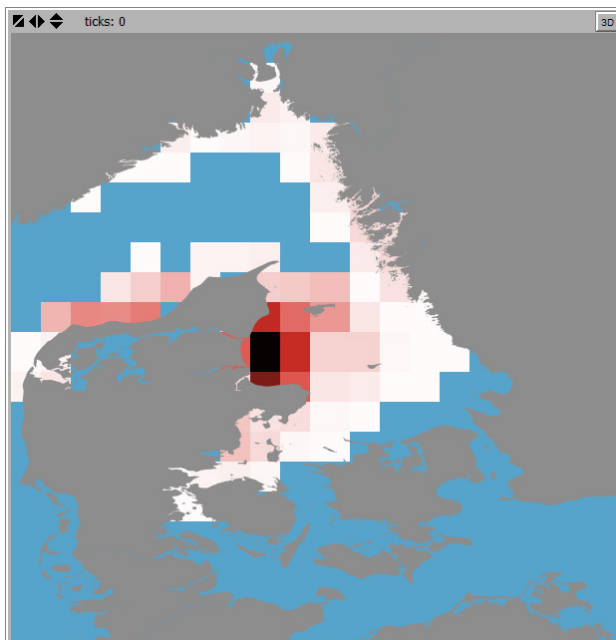

Figure 25. Densities of agents with initial positions withing suiable habitats that eventually settle successfully within suitable habitat, AND, that do not experience exceedance of the salinity tolerance interval during the simulated dispersal. Color legend – blue = "0", dark red = 1597.

```
Plot: Number of agents per grid in connectivity analysis (~Start positions):
Minimum value - 1
Maximum value - 1597
```

The output of the cluster analysis for *Arcuatula senhousia* including 6 hydrographic regions are shown in Figures 26 and 27 as a simple region map and as a graph representation of the within and between regions connectivity respectively. The graph representation in Figure 27 shows individual regions with unique colors. Graph nodes (= circles) represent individual regions with numbers representing the coherence (~self-recruitment) in pct, i.e. the proportion of agents that have an initial position within the regions, which eventually settle within the same region. Graph edges between nodes (arrows) indicate the direction of the connectivity between individual regions, and the thickness of the edges indicates the relative magnitude of the connectivity probabilities.
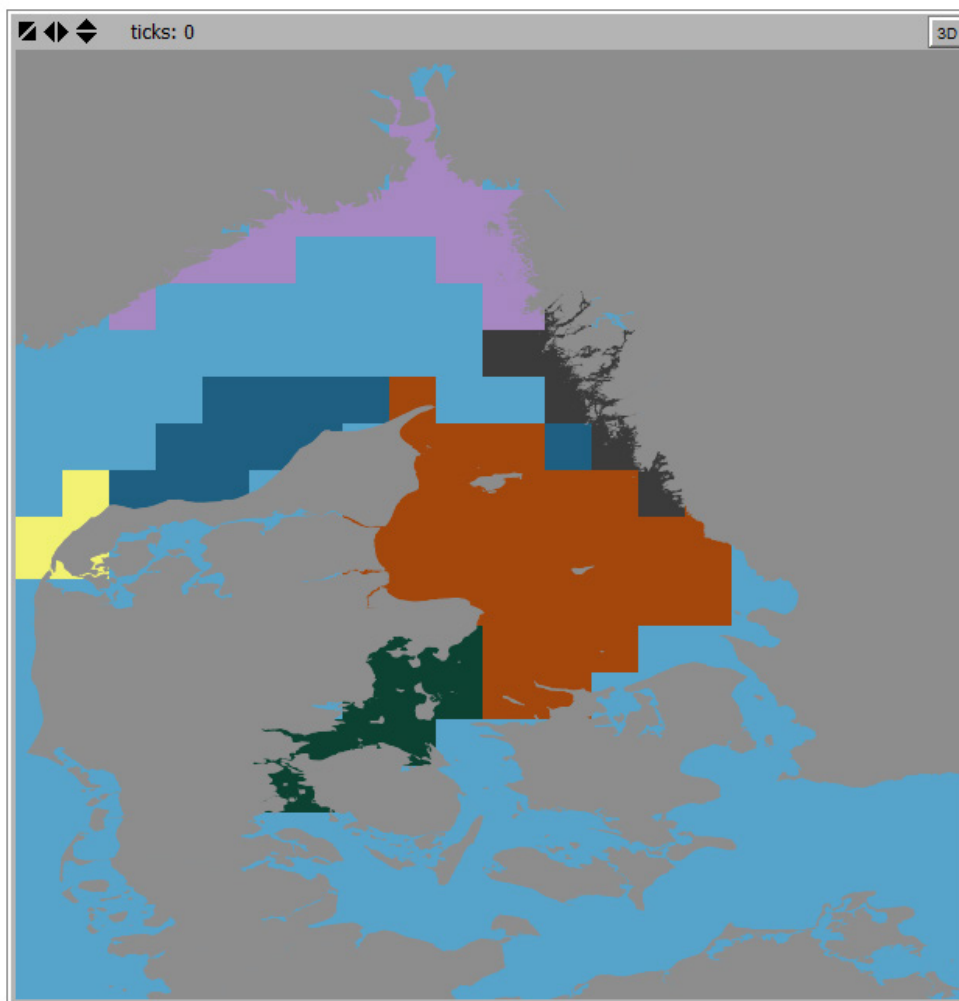
Figure 26. The output of the cluster analysis for *Arcuatula senhousia* shows 6 well defined Hydrographic regions, here represented with unique coloring in the Netlogo World View.
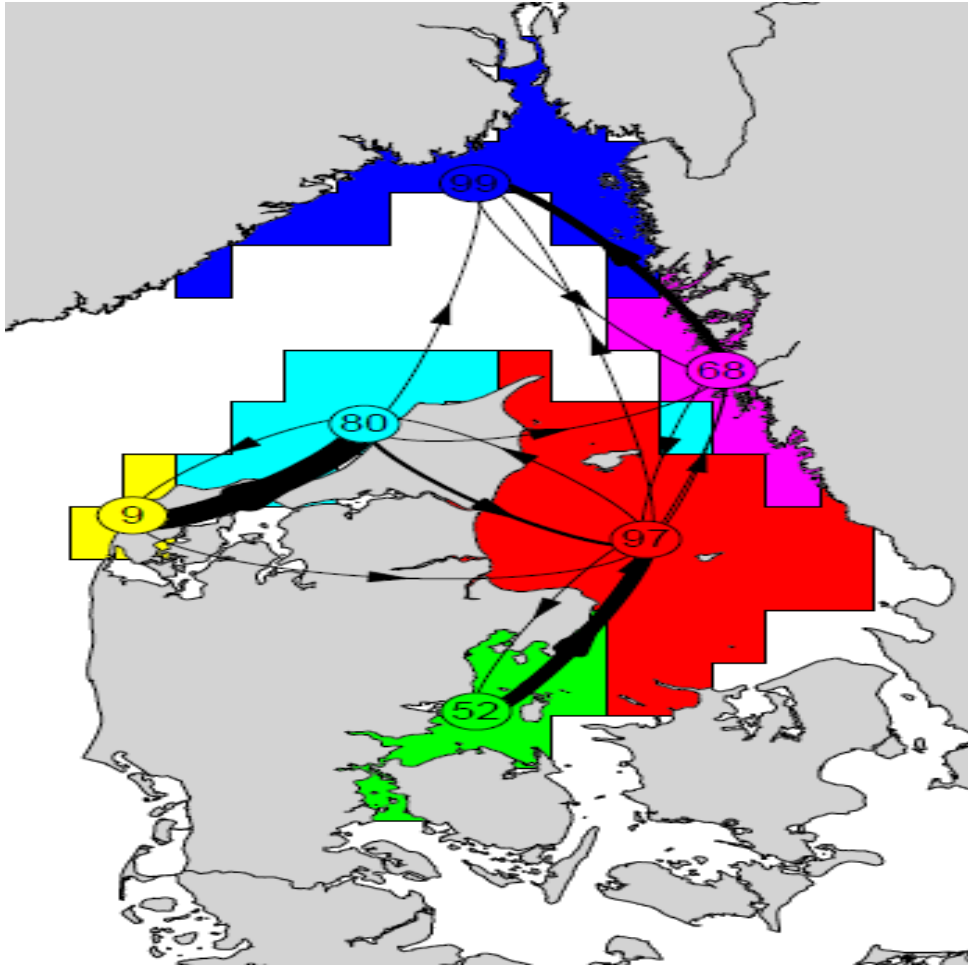
Figure 27. The output of the cluster analysis for *Arcuatula senhousia* with 6 hydrographic regions shown as a graph representation (pdf) with unique colors for individual regions. Graph nodes (= circles) represent individual regions with numbers representing the coherence (~self recruitement) in pct. Graph edges between nodes (arrows) indicate the direction of the connectivity and the thickniess of the edges indicate the relative magnitude of the connectivity probabilities.

The exact values used for the graph representation of the within and between regions connectivities are strored in 2 comma separated files: "clconnos.csv" and "clconprob.csv". See Table 3 and Table 4 respectively.

Table 3. The table represent between regions connectivity adjacency matrix, with absolute number of agents connecting the 6 regions. Species: *Arcuatula senhousia. File: clconnos.csv.*

	1	2	3	4	5	6
1	8004	0	6	5	63	149
2	4	28	0	285	0	0
3	460	0	498	0	0	5
4	322	1	0	1667	39	57
5	0	0	0	0	521	7
6	12	0	0	0	215	491

Table 4. The table represents between regions connectivity probability matrix, with probabilities (values between 0 and 1) representing the chances of agents with an initial position in one region, will end up in one of the other 5 regions. Species: *Arcuatula senhousia. File: clconprob.csv*.

	1	2	3	4	5	6
1	0.972894	0	0.000729	0.000608	0.007658	0.018111
2	0.012618	0.088328	0	0.899054	0	0
3	0.477674	0	0.517134	0	0	0.005192
4	0.154362	0.000479	0	0.799137	0.018696	0.027325
5	0	0	0	0	0.986742	0.013258
6	0.016713	0	0	0	0.299443	0.683844

An example of extracting the downstream (left) and upstream (right) connectivity probabilities for a specific location from the connectivity probability matrix is shown in Figure 28. In this case a location corresponding to one of the main harbors in Kattegat, Frederikshavn. The downstream connectivity probability map (Figure 28 left)) shows values that represent the probability (or likelihood) that an agent released close to Frederikshavn harbor (~grid cell indicated by a yellow arrow) will end up in any other grid cell. In a similar way, the upstream connectivity probability map (Figure 28 right) shows values that represent the probability (or likelihood) that an agent that ends in at location near Frederikshavn has come from any of the other grids cell in the study area.
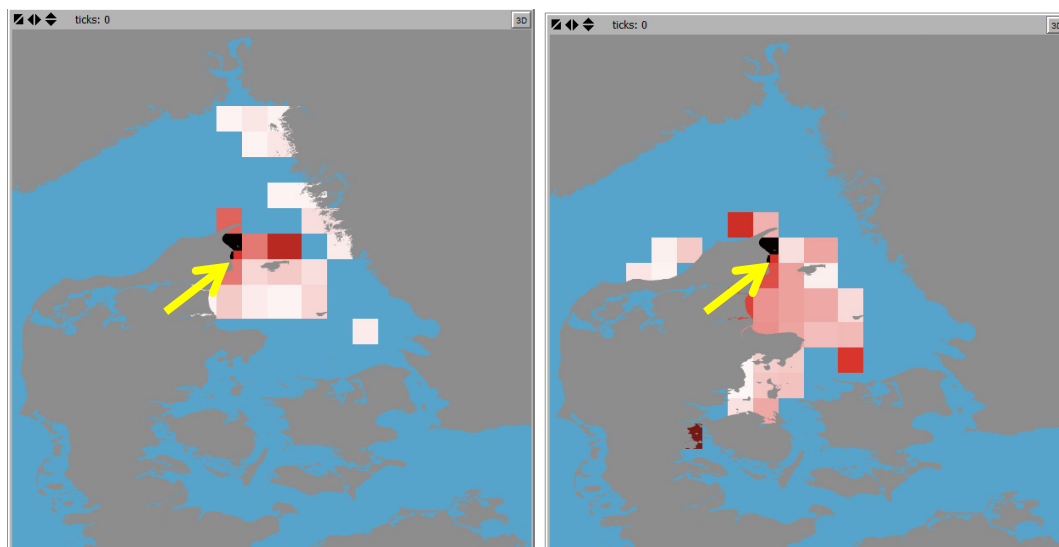

Figure 28. Example of displaying the downstream (left) and upstream (right) connectivity probabilities for a specific location, in this case a location corresponding to one of the main harbors in Kattegat, Frederikshavn (indicated by yellow arrows). Blue color = "0". Darkest red = "0.273".

For a more comprehensive insight into various considerations regarding the setup, simulation and result interpretation and presentation, please see Hansen et al. (2018 in prep) and Stuer-Lauritzen et al. (2018).

5. Installation guide

The installation of the SRAAM tool require as a minimum 3 software components:

- R 3.2.3 for Windows
- Netlogo 5.3.1
- IBMLib

Since Netlogo requires JAVA, make sure you have the latest JAVA version installed on your pc. The tool comprising the individual software components has been tested on Windows 7 and Windows 10 64-bit operation systems.

5.1 R installation

5.1.1 Install R 3.2.3 for Windows

The R software can be downloaded here:
https://cran.r-project.org/bin/windows/base/old/3.2.3/

R-3.2.3 for Windows (32/64 bit)

Download R 3.2.3 for Windows (64 megabytes, 32/64 bit)
Installation and other instructions
New features in this version

If you want to double-check that the package you have downloaded exactly matches the package distributed by R, you can compare the md5sum of the .exe to the true fingerprint. You will need a version of md5sum for windows: both graphical and command line versions are available.

Frequently asked questions

Please see the R FAQ for general information about R and the R Windows FAQ for Windows-specific information.

Last change: 2015-12-10, by Duncan Murdoch

5.1.2 Install R extensions

To run the SRAAM tool, you need the following R-extension packages:

- diagram
- igraph
- maps
- maptools
- Matrix
- magrittr
- ncdf4
- raster
- Rcpp
- rgeos
- rJava
- shape
- shapefiles
- sp

The packages have been included in the SRAAM download in the "r-packages" – folder. You can copy all the sub-folders included in the "r-packages"-folder into the R installation folder depending on which installation folder you chose when installing, e.g. : "C:\Program Files\R\R-3.2.3\library\". Alternative the "r-packages" folders can be copied to the user C:\Users\"..username.."\Documents\R\win-library\3.2.

To check if these R extensions are already installed, open the R Console (default window when opening RGui from the Windows Start menu). Type e.g. "library(raster)". If no error occurs then this extension is installed and has been loaded. If an error occurs in the R-GUI, you need to install the packages as described above. Alternatively install the packaged by opening the R program and select the menu "Packages > Install package(s)". To select a CRAN Mirror to install from a "HTTPS CRAN Mirror" selection box will be shown. Select the country and the server from where you want to install the extension. Next, from a selection box "Packages", all available extensions are listed in alphabetical order:
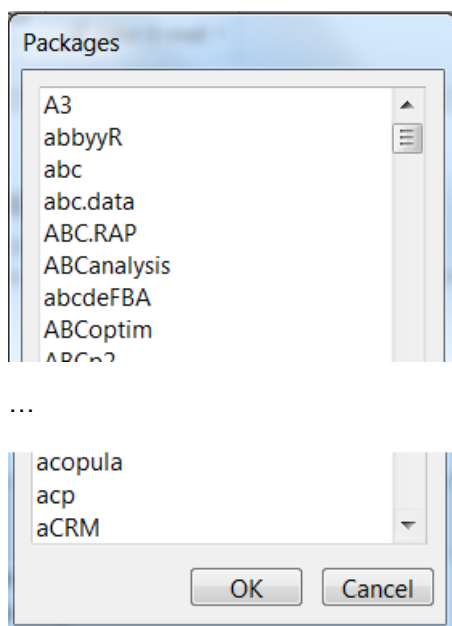
Scroll down and select the extension "raster" to install the "raster" extension for R. Repeat for each of the required R-extensions.

If packages are correctly installed, but loading packages from within R GUI fails, you will need to check and update the system paths, see 5.4, and reboot the pc.

5.2   Netlogo installation

5.2.1   Install Netlogo 5.3.1 for Windows

The Netlogo 5.3.1 installation file can be found here:
https://ccl.northwestern.edu/netlogo/5.3.1/

Select either 32-bit or 64-bit version for Windows.

Note that this version has been developed and tested only on a 64-bit version for Windows 7 and Windows 10.

5.2.2   Install Netlogo extensions

Six extensions need to be installed for your Netlogo installation.

- gis
- r
- shell
- matrix
- csv
- xw

The extensions are included in the SRAAM download in the subfolder "Netlogo_extension".

All extension have to be saved to the "extensions" sub-folder located in the directory where Netlogo is installed, e.g.:
C:\Program Files\NetLogo 5.3.1\app\extensions\

Each extension consist of a folder with the extension name and with extension files (*.jar) inside the folder.

You can also find the extension here:
https://github.com/NetLogo/NetLogo/wiki/Extensions/

Download/copy the extensions, and place the extension folders in " ….\NetLogo 5.3.1\app\extensions\". For details on the R extension for Netlogo, see: Thiele and Grimm (2010).

5.3 Download SRAAM tool setup files

Download and un-zip the SRAAM tool and setup files available at:
https://github.com/IBMlib/SRAAM
into a working directory of your choice. E.g. C:\SRAAM\setup\.

5.3.1 The SRAAM setup folder
The SRAAM setup folder is where input files for the SRAAM tool is located. Hydrographic input and outpout files for the IBMlib simulation are stored in the IBMrun-sub-folder, see next section.

The files included in the SRAAM setup folder include:
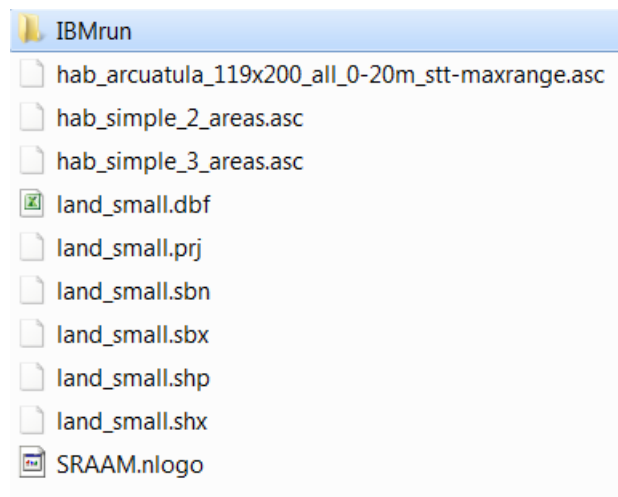
The SRAAM.nlogo file is the Netlogo file that opens the SRAAM user interface. From within the SRAAM userinterface any changes to the setup may be saved to this file or another filename.

The 3 ascii files (file extentions: *.asc) are example of habitat maps used in the examples presented in section 4.2.

The files named "land_small.*" are shapefiles used to represent land areas in the examples presented in section 4.2. The default SRAAM.nlogo file include a World View extension that covers the North Sea and The Wester Baltic Sea and the land areas of the shape file. This default settings support the Hydrographic data format "Stationary_flow_field" for tool demonstration purposes.

5.3.2   The IBMrun sub-folder

The subfolder "IBMrun" is where the IBMlib simulation input (and output) files are stored:

Name	Date modified	Type	Size
NCOM	30/08/2018 14:55	File folder	
NEMO	30/08/2018 14:55	File folder	
HBM	30/08/2018 15:02	File folder	
POM	30/08/2018 15:02	File folder	
ECOSMO_tl5_physics_testframe.dat	09/09/2016 11:52	DAT File	3,662 KB
grid_desc_ecosmo	09/09/2016 11:52	File	1 KB
postinfo.for	09/09/2016 11:52	FOR File	253 KB
Arcuatula_senhousia_2005_2e+05.nc	27/06/2018 21:24	NC File	11,150 KB
ibmrun_connect_bootHD.exe	30/08/2018 11:11	Application	3,434 KB
ibmrun_connect_COARDS.exe	30/08/2018 11:11	Application	3,416 KB
ibmrun_connect_genericHD.exe	30/08/2018 11:11	Application	3,421 KB
ibmrun_connect_HBM.exe	30/08/2018 11:11	Application	3,512 KB

The 4 subfolders are where the applied hydrographic dataset needs to be stored. The subfolders are named referring to the model the hydrographic data has been generated by, i.e. HBM, POM, NEMO and NCOM.

For each compatible hydrographic data format an IBMlib executable exists, i.e. ibmrun_connect_HBM.exe, ibmrun_connect_COARDS.exe, ibmrun_connect_genericHD.exe and ibmrun_connect_bootHD.

In addition 3 files are included supporting the statistic hydrographic flow field for demonstration purpose:

- ECOSMO_tl5_physics_testframe.dat
- Grid_desc_ecosmo
- Postinfo.for

Finally, a result file based on the HBM hydrographic data set and used for simulating the dispersal and connectivity of the Asian Date Mussel (*Arcuatula senhousia*) as presented in section 4.2 is included:

- Arcuatula_senhousia_2005_2e+05.nc

To open the SRAAM user interface, open the "Setup" folder, and click on the "SRAAM.nlogo" file to open the SRAAM project file:
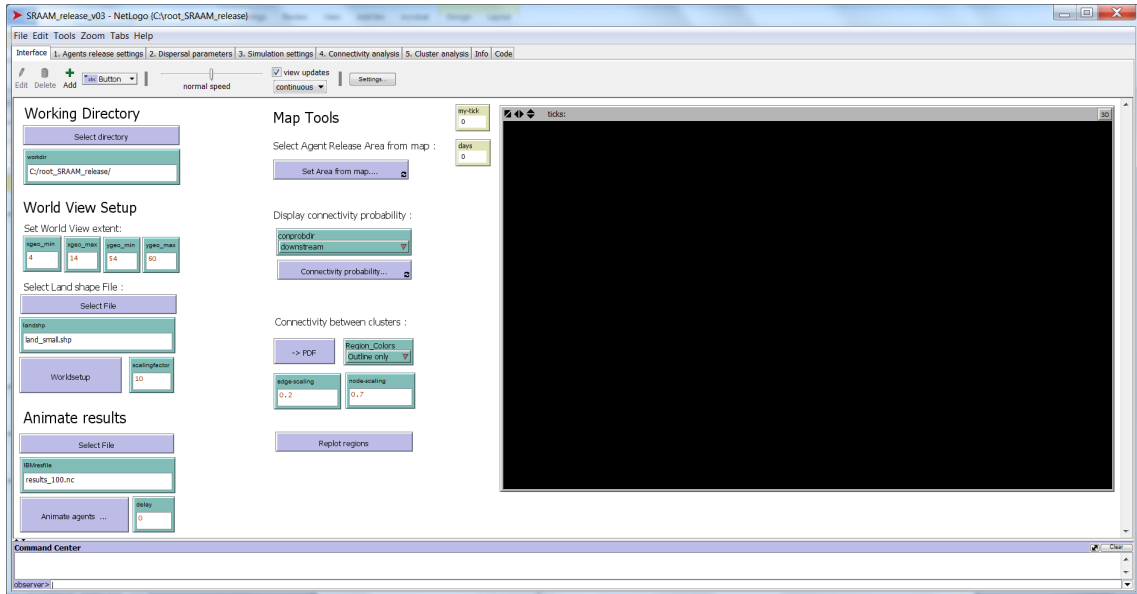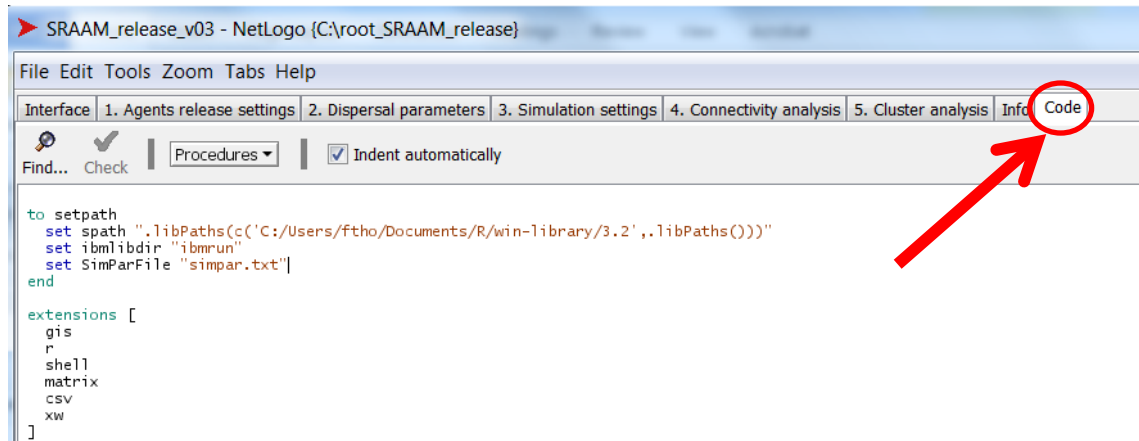

5.4 Setting the paths

5.4.1   Setting the path to R-extensions in Netlogo

Depending on where you have installed the R-extensions (see 5.1.2), you need to set the path in Netlogo before the SRAAM tool will function correctly. Otherwise you will get an error like this:
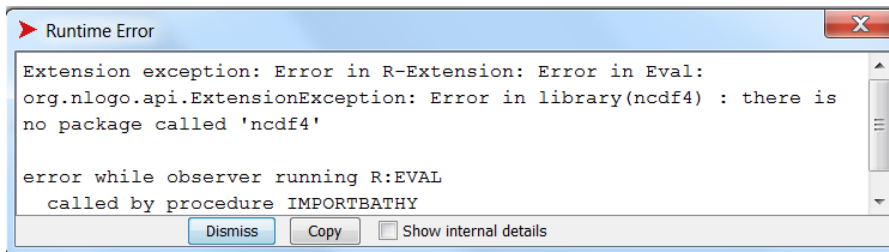
In the Netlogo user interface, click on the "code" tab:

In the top section you have to set the path:
to setpath
set spath ".libPaths(c('C:/Users/StartUser/Documents/R/win-library/3.2',.libPaths()))"
…
….
end

Replace the yellow highlighted path-string with the path that points to the folder where R-extensions are installed on your PC. Save the project and proceed applying the SRAAM tools.

5.4.2 Setting system paths for R-extension

When you are running 64-bit Netlogo version you need manually to set the system paths for three system variables:

- R_HOME (required)
- JRI_HOME (required)
- JAVA_HOME (if rJava extentions cannot be loaded from R)

If variables are not correctly set, this error may occur when you open the nlogo-file "SRAAM.nlogo":

"Error in R-extension: Error in runOnce: java.lang.NullPointerException".

Make sure you have installed 64-bit versions of R, and Java.

Then follow the procedure for installation 64-bit version of R-extension for Netlogo. The document is located in the Netlogo installation folder:
C:\Program Files\NetLogo 5.3.1\app\extensions\r\doc\Install_R-xtension_on_Win_with64bit.pdf

Follow the procedures including the testing of individual steps. Remember to reboot the computer when the paths have been updated.

If you are already familiar with the path settings of system variables, see below. :

In short, you need to set the paths to the 2 (possibly 3) system variables as specified below, adjusted to the folder structures of your installations. After pc reboot, if errors still occur re-opening SRAAM.nlogo, please go through the procedures in detail as described in "Install_R-xtension_on_Win_with64bit.pdf".

R_HOME

3. **Set environment variables for R**: an R.dll and R.exe should be found in C:\Program Files\R\R-3.2.3\bin\x64 (depends on the path in step 1),

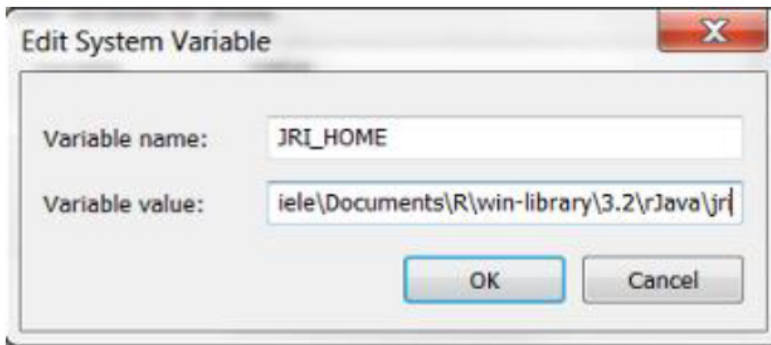Set at first the R_HOME variable to C:\Program Files\R\R-3.2.3.

Edit System Variable	X
Variable name:	R_HOME
Variable value:	C:\Program Files\R\R-3.2.3
	OK Cancel
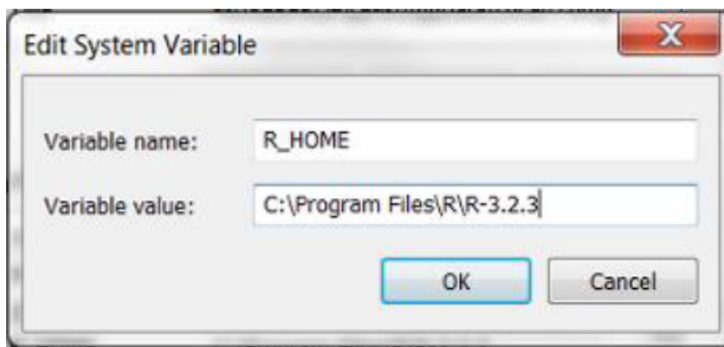
Now, append the PATH variable by %R_HOME%/bin/x64 (or directly by C:\Program Files\R\R-3.2.3\bin\x64).

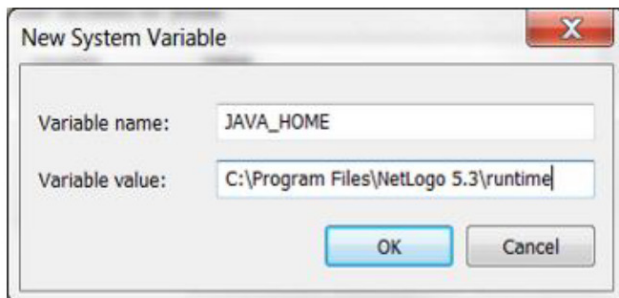| Edit System Variable	X
Variable name:	Path
Variable value:	·1.9.2\BIN;%R_HOME%\BIN\X64;%JAVA_H
	OK Cancel
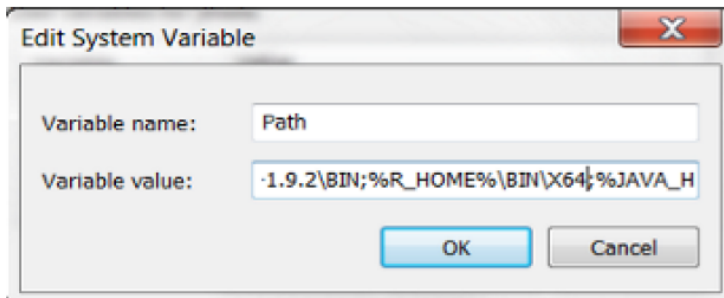
JRI_HOME

C:\Users\jthiele\Documents\R\win-library\3.2\rJava\jri.

JAVA_HOME

8. Add/Change the *JAVA_HOME* environment variable with the path to the 64-bit Java (e.g. bundled with NetLogo).

Remember to restart you pc for the changes you have made to be registered properly.

6. References

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