

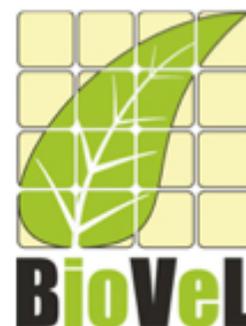
BioVeL training

Matthias Obst, Francisco Quevedo, Elisabeth Paymal

The background image is a composite of several elements: a white swan in flight on the left, a butterfly with yellow and black wings on the right, a green forest landscape in the center, and a laboratory setting with a test tube and a rack of multi-colored microcentrifuge tubes on the right. A semi-transparent grey horizontal band is overlaid across the middle of the image, containing the title text.

BioVeL workflows for taxonomic data processing and ecological niche modelling

TRAINING WORKSHOP
Paris, FR, March 25, 2014



25 mars 2014 - 9h00- 17h00, [MNHN](#), Salle des logs, bâtiment de géologie, 43 rue Buffon 75005 Paris

[Confirmed programme : BioVeL workflows for cleaning an refining data and for studying ecological niche modelling](#)

Note: [this training will be offered in English; interprétation possible](#)

[Trainers :](#)

[Matthias Obst](#), [University of Gothenburg](#), [Sweden](#)

[Francisco Quevedo](#), [Cardiff University](#), [UK](#)

[Elisabeth Paymal](#), [Fondation pour la Recherche sur la Biodiversité \(FRB\)](#)

09:00 - [About DRW and ENM and scientific examples](#)

[Intro to BioVeL and the Taxonomic Data Refinement Workflow \(DRW\), with examples of scientific applications](#)

9:20 [Demo of DRW](#)

9:30 - 10:00 - [Sign on the portal and start of hands-on session](#)

10:00 - [Download data from GBIF, clean and refine them.](#)

11:30 - [Integrate my own data w/ GBIF's, and upload again. Clean the merged set.](#)



12:00 - Lunch

13:00- Introduction to ecological niche modeling, (ENM), and presentation of scientific applications

Showcase and demonstration of the Ecological Niche Modelling workflow

14:00 - Hands-on session of the Ecological Niche Modelling workflow

Use your data set that we prepared for you and run ENM

15:00 - Demonstration and hands-on session of the statistical analysis

- Use your data set that we prepared for you and statistical analysis

15:30 - Demonstration and hands-on session of with the climatic envelop workflow

- Use your data set that we prepared for you with the climatic envelop workflow

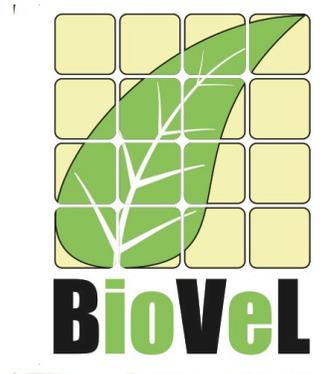
16:00 - 16:20 - Pause café/thé

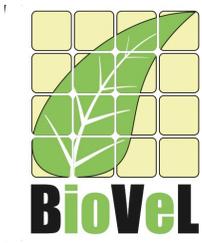
16h:20 - Wrap up discussion (both GBIF and BioVeL): feedback and suggestions for research projects and improvements

17:00 - Clôture de la session

Tour de table

Introduction to the BioVeL infrastructure





Aims of the Biodiversity Virtual e-laboratory (BioVeL)

BioVeL provides functions to:

- Access data from cross-disciplinary resources (Data mining)
- Access analytical methods a range of disciplines (Interoperability)
- Digest large data (Scalability)
- Repeat complex analytical processes (Reproducibility)
- Access to virtual communities (Sociability)

Provide (web)services for the interdisciplinary analysis of biodiversity

Provide analytical pipelines (workflows) based on these services

Taxonomy

Phylogenetics

Genomics

Population modelling

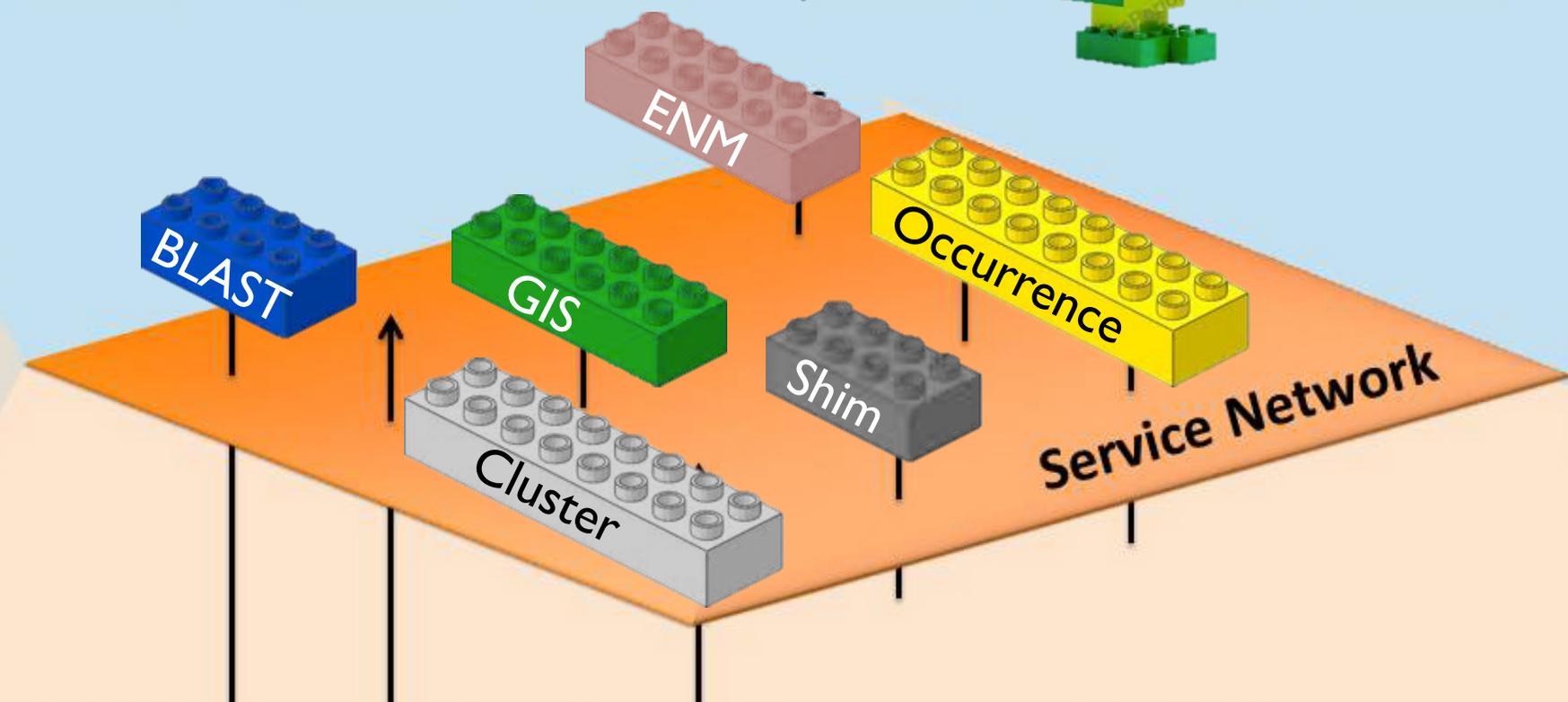
Ecological niche modelling

Ecosystem functioning/
valuation

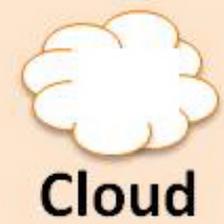
...

Biodiversity research

Workflow uses Web Services



Web Services deployed on different computing infrastructures



Access web-services at *biodiversitycatalogue.org*

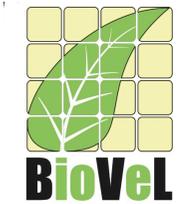
The screenshot displays the BiodiversityCatalogue website interface. At the top, the logo reads "BiodiversityCatalogue" with the tagline "The Biodiversity Sciences Web Services Registry". Navigation links include "Getting Started", "About Us", "Contact Us", and "API Docs". A search bar and a "Go!" button are present, along with menu items for "Home", "Services", "Register a Service", and "Providers".

The main content area features a "Top 20 tags on BiodiversityCatalogue" section with a list of tags: aphaid, catalogue of life, computation, darwincore, data upload, ecology, gbif, interpolation, marine, modelling, MrBayes, MultiCPU, occurrence, raster, registry, shim, taverna, taxa, taxon, and visualization. A "See All Tags" link is also available.

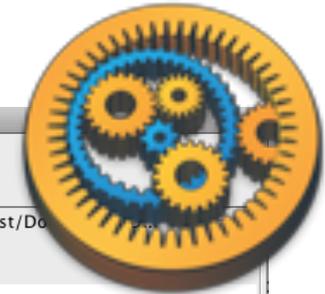
Below this, a "Filtering" sidebar on the left shows "Current Filters Applied" as "none" and offers an "Enable tag filters" button. It lists "Service Types" (REST: 12, SOAP: 5) and "Service Categories" (Taxonomy: 7, Analysis: 3, Modelling: 4, Geospatial: 1, Data: 3).

The central area displays "all 17 services" with options to "Include archived services?" and "Sort by: Newest" and "View: Grid". Six service cards are visible, each with a green checkmark icon and a 3D LEGO brick graphic:

- PESINameService** (SOAP): Taxonomy. Description: "As a user or developer you can use the PESI webservice to feed your own application with standard PESI taxonomy." Provider: www-eu-nomen-eu.
- European Nuc ... ENA) Browser** (REST): Data Retrieval. Description: "The European Nucleotide Archive (ENA) Browser provides functionality to view and retrieve data and meta-data archived..." Provider: [European Bioinformatics Institute \(EBI\)](http://European Bioinformatics Institute (EBI)).
- AphiaNameService** (SOAP): Taxonomy, Taxonomic Name Resolution, Taxonomic Synonym Resolution. Description: "The data is licensed under a Creative Commons 'BY' 3.0 License, see <http://creativecommons.org/licenses/by/3.0/deed.e...>" Provider: www-marinespecies-org.
- openModeller** (SOAP): Niche Modelling (Species Distribution). Description: "Functionally equivalent to the openModeller service provided by modeller-cria-org-br, this endpoint is located in Eur..." Provider: omws-i3m-upv-es.
- BGBM CDM Cat ... ife REST** (REST): Taxonomy, Taxonomic Synonym Resolution, Taxonomic Diversity, Checklist and Classification. Description: "This web service namespace is an add-on to the already existing CDM REST API and provides information relating to sci..." Provider: BGBM EDIT.
- MrBayes 16 CPUs** (REST): Description: "The service launch a bayesian phylogenetic inference with MrBayes 3.2 (<http://mrbayes.sourceforge.net/>) asking as inp..." Provider: alicegrid17-ba-infr.



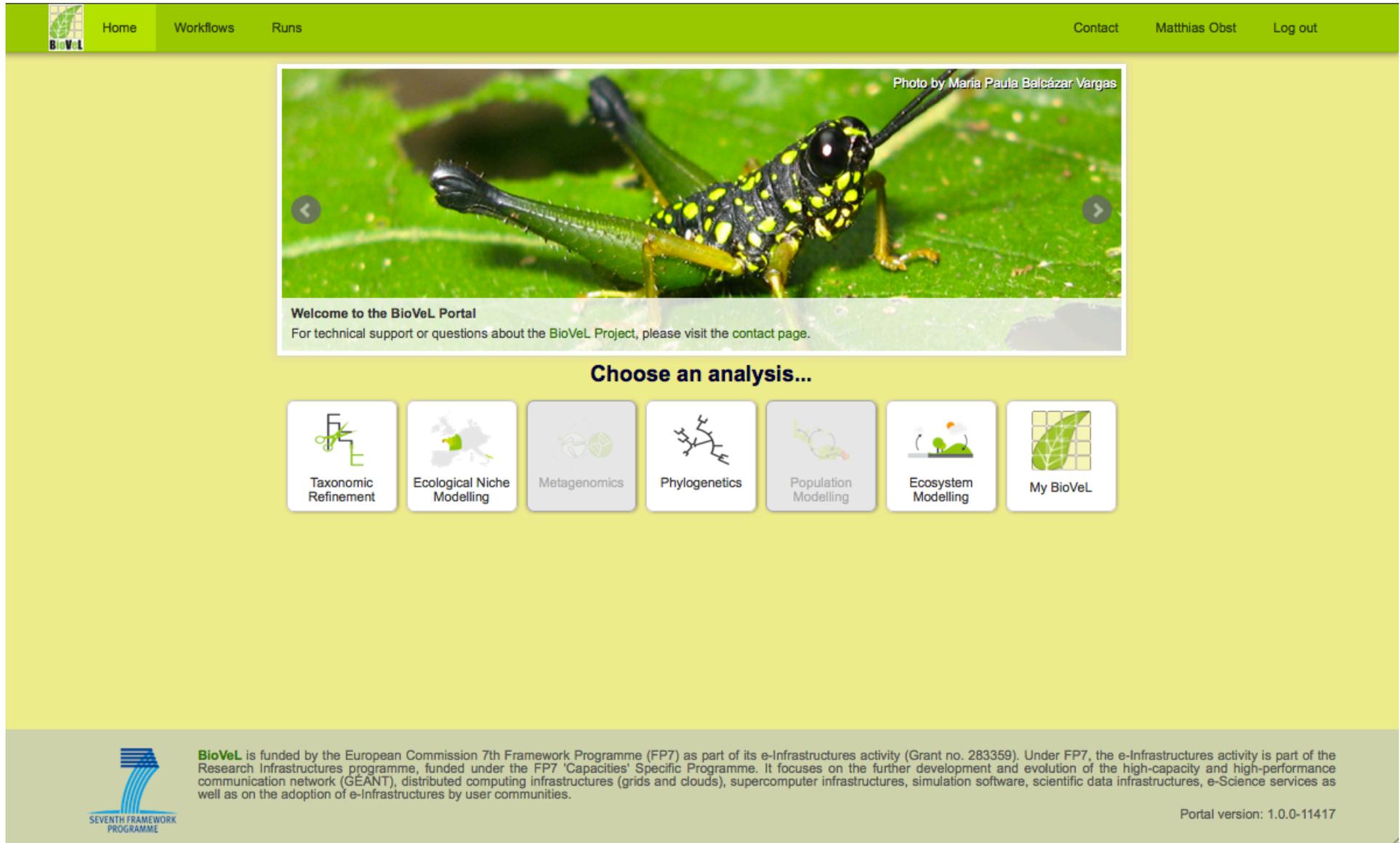
Build your own workflow on the Taverna workbench



The screenshot displays the Taverna Workbench 2.4.0 interface. On the left, the "Service panel" is visible, showing a list of available services under categories like "Service templates", "Local services", and "Biomart". Below this, the "Workflow explorer" shows a tree view of the current workflow, "Data_Refinement_Work", with sub-elements like "Workflow input ports", "Workflow output ports", and "Services". The main workspace on the right shows a complex workflow diagram with various nodes and connections. A 3D model of a green dinosaur is visible in the bottom right corner of the workspace.

Ecological niche modelling workflow

Running workflows from the portal



The screenshot shows the BioVeL Portal homepage. At the top, there is a green navigation bar with the BioVeL logo on the left and links for Home, Workflows, Runs, Contact, Matthias Obst, and Log out on the right. Below the navigation bar is a large banner image of a grasshopper on a green leaf, credited to Maria Paula Balcázar Vargas. Underneath the banner is a welcome message: "Welcome to the BioVeL Portal" and a link to the contact page for technical support. The main content area is titled "Choose an analysis..." and features seven interactive buttons: Taxonomic Refinement, Ecological Niche Modelling, Metagenomics, Phylogenetics, Population Modelling, Ecosystem Modelling, and My BioVeL. The footer contains the logo for the Seventh Framework Programme and a paragraph of text explaining that BioVeL is funded by the European Commission 7th Framework Programme (FP7) as part of its e-Infrastructures activity. The footer also includes the portal version number: 1.0.0-11417.

Home Workflows Runs Contact Matthias Obst Log out

Photo by Maria Paula Balcázar Vargas

Welcome to the BioVeL Portal
For technical support or questions about the BioVeL Project, please visit the [contact page](#).

Choose an analysis...

- Taxonomic Refinement
- Ecological Niche Modelling
- Metagenomics
- Phylogenetics
- Population Modelling
- Ecosystem Modelling
- My BioVeL

 **BioVeL** is funded by the European Commission 7th Framework Programme (FP7) as part of its e-Infrastructures activity (Grant no. 283359). Under FP7, the e-Infrastructures activity is part of the Research Infrastructures programme, funded under the FP7 'Capacities' Specific Programme. It focuses on the further development and evolution of the high-capacity and high-performance communication network (GÉANT), distributed computing infrastructures (grids and clouds), supercomputer infrastructures, simulation software, scientific data infrastructures, e-Science services as well as on the adoption of e-Infrastructures by user communities.

Portal version: 1.0.0-11417

The objective of this course

Introduce you to *scalable analytical methods that integrate data access with analysis* for species distribution modeling

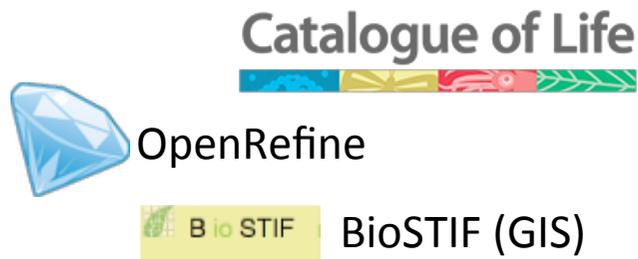
Please note, these are *not new bioinformatics tools*, but rather existing ones that are seamless connected



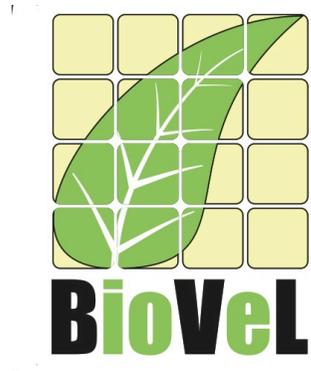
Taxonomy

Species distribution modeling

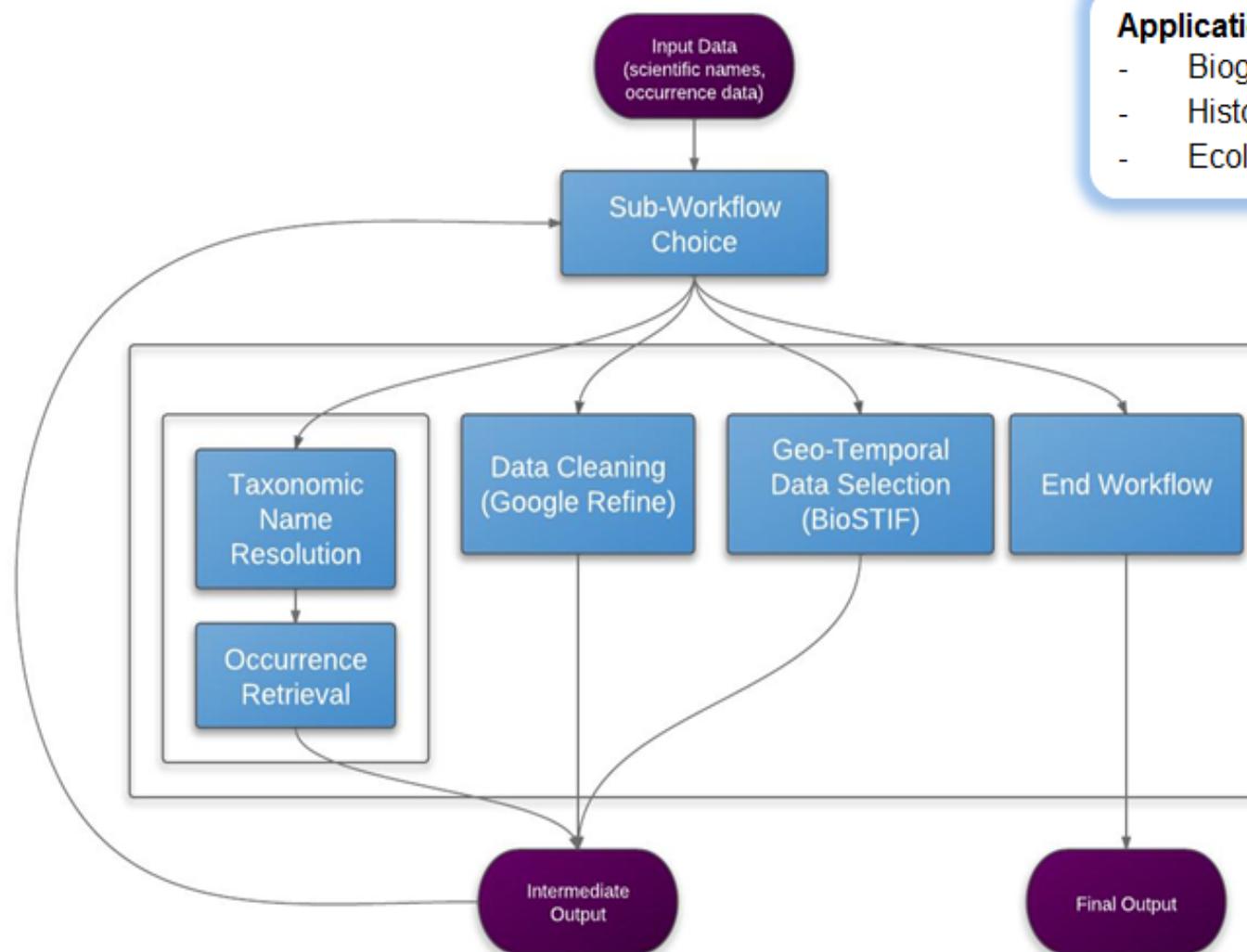
Statistics



Introduction to the Data Refinement Workflow and scientific applications



Data Refinement Workflow



Application examples

- Biogeographic analysis
- Historical analysis
- Ecological niche modeling

Taxonomic Data Refinement workflow (DRW)

tavlite1.biovel.eu/runs/969

BioVeL

Home Workflows Runs

Running: BioVeL [BETA] Data Refinement Workflow

Action Required

Choose Sub-Workflow

- Synonym expansion
- Taxonomic name resolution
- Occurrence retrieval
- Spell checking
- Geographic and taxonomic cleaning
- Temporal refinement
- Data processing log

www.biovel.eu

The screenshot displays the BioVeL Data Refinement Workflow interface. The top section, titled "Resolve Taxonomic Concept", shows the input name "Crassostrea gigas" and a list of resolved taxonomic concepts. The "Accepted Name" is "Crassostrea gigas (Thunberg, 1793)". The "Synonym" list includes "Crassostrea angulata (Lamarck, 1819)", "Crassostrea talienwhanensis Crosse, 1862", "Dioeclostrea hispaniola Orton, 1928", "Gryphaea angulata Lamarck, 1819", and "Lopha posjetica (Razin, 1934)".

The middle section, titled "Google refine 1386277919951", shows a table of 4412 rows of taxonomic data. The table has columns for "sample effort", "nameComplete", "nameAccepted", "authorship", "rank", "Family", and "Class". The table lists various species such as "Owenia fusiformis", "Echinocardium flavescens", "Leptorhinus squamatus", "Alentia gelatinosa", "Suberites ficus", "Halidoria oculata", "Leptochiton asellus", "Pecten maximus", "Ornus lacteus", and "Marthasterias glacialis".

The bottom section shows a map of Europe with a selection layer and a time series plot. The map selector tools include a dropdown menu, a map selector tool, an aggregation type, and a "Hide coordinates" checkbox. The time series plot shows 34 results with time information from 2006 to 2010.

Historical analyses of biodiversity

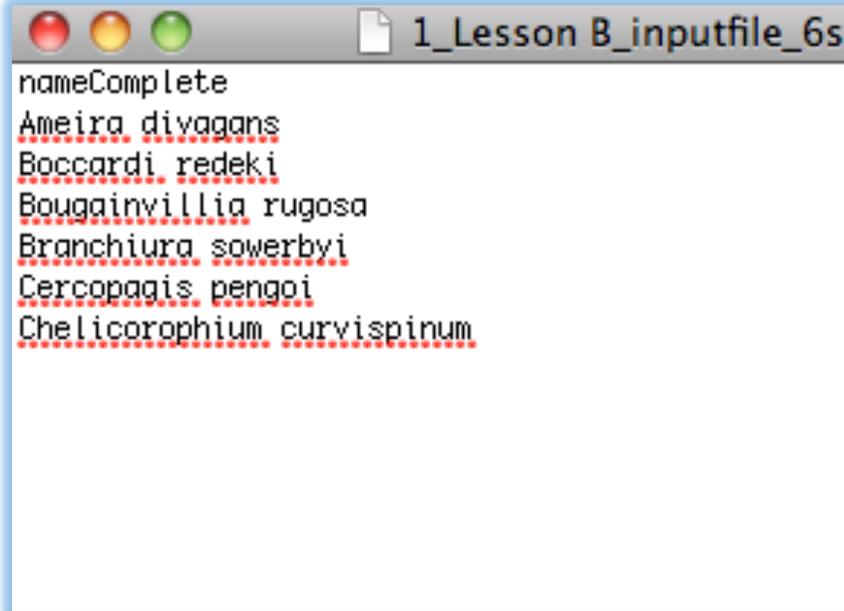


Register on the portal
<http://portal.biovel.eu/>

Demo - Taxonomic Name Resolution and Occurrence Retrieval

LESSON B (9.20-9.30)

1. Load input file with 6 species names
2. Expand names
3. Retrieve records
4. Taxonomic refinement
 - data quality
 - re-name
 - Clustering (NJ, PPM, 5, 8)
 - delete recs
 - data process log
 - Export
5. Geo-temporal refinement



```
nameComplete  
Ameira divagans  
Boccardi redeki  
Bougainvillia rugosa  
Branchiura sowerbyi  
Cercopagis pengoi  
Chelicorophium curvispinum
```

Input file

Practical – taxonomic data refinement

LESSON A (9.30-11.00, incl. coffee?)

1. Divide in groups of 2
 - 6 groups: <http://portal.biovel.eu/>
 - 6 groups: <https://workshop.at.biovel.eu>
3. Start DRW
 - Load input file LessonA_Inputfile_105recs_v3.csv
 - Choose 'Data Quality'
 - Run tutorial p. 16-38
 - Answer exercises 1-7
4. Short discussion of results

Assignment (11.00-12.00)

You want to study the potential distribution of the invasive oyster (*Crassostrea gigas*) using species distribution modeling approaches.

You have collected occurrence records of the species in your region (Scandinavia) and want to enrich your records with public data from GBIF, and thereafter create, test, and project an ecological niche model for the species under various climate scenarios.

1. Generate an input file to download GBIF data with the DRWorkflow
2. Retrieve, clean, and refine occurrence data for this species from GBIF
3. Integrate your data with the GBIF records

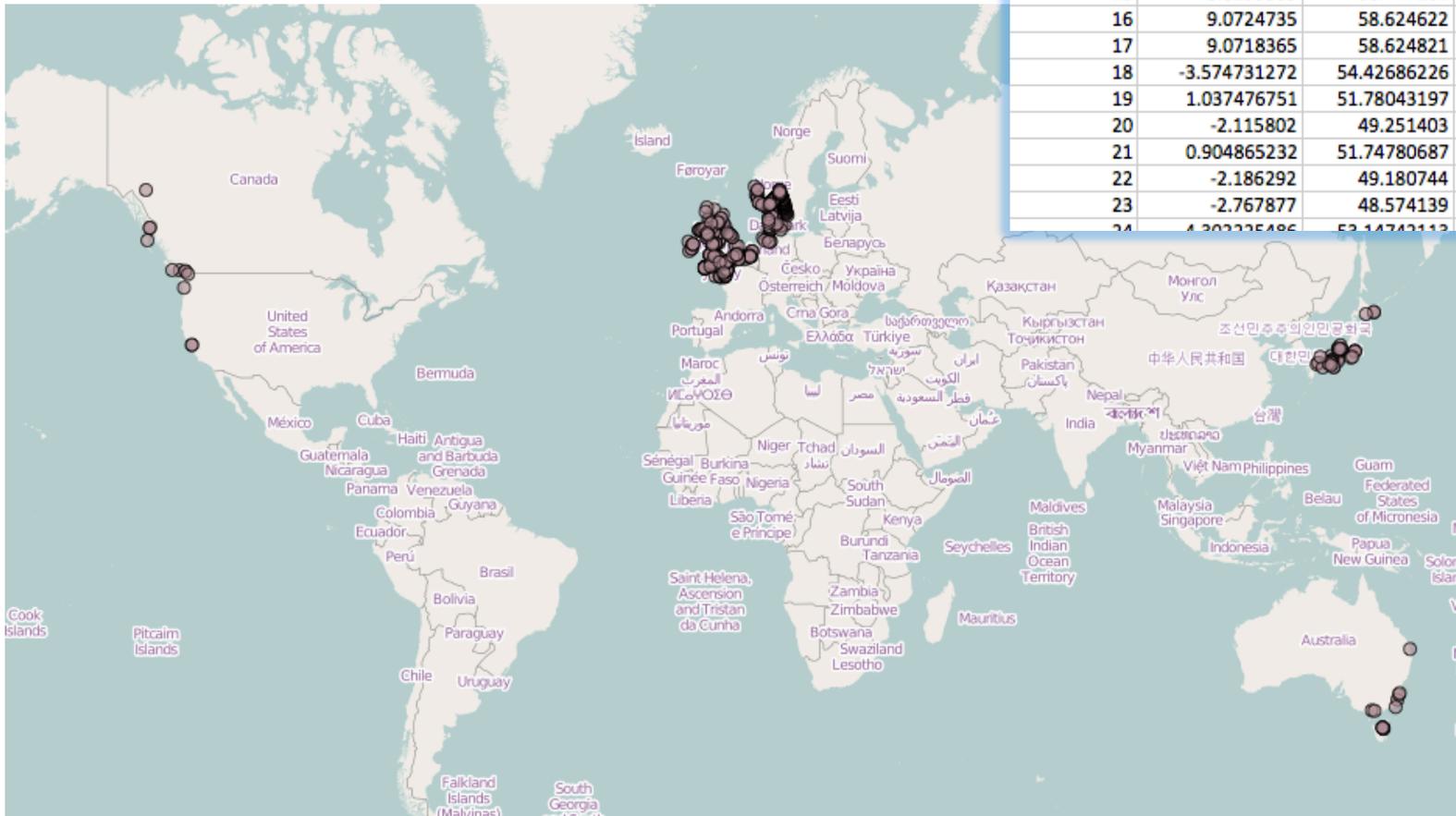
Lunch

4. Create model
5. Test model
6. Project model
7. Statistical analysis of projections

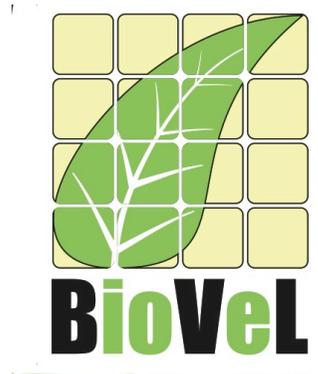
ENM input files with 4 columns

- ID
- Lat
- Long
- Species name

occurrenceID	decimalLongitude	decimalLatitude	nameComplete
1	8.428	55.0315	Crassostrea gigas
2	8.4339	55.0304	Crassostrea gigas
3	8.4314	55.0312	Crassostrea gigas
4	8.4314	55.0312	Crassostrea gigas
5	8.428	55.0315	Crassostrea gigas
6	8.4339	55.0304	Crassostrea gigas
7	8.4172	55.0368	Crassostrea gigas
8	8.428	55.0315	Crassostrea gigas
9	8.4314	55.0312	Crassostrea gigas
10	8.4339	55.0304	Crassostrea gigas
11	8.4314	55.0312	Crassostrea gigas
12	8.4339	55.0304	Crassostrea gigas
13	8.428	55.0315	Crassostrea gigas
14	8.4172	55.0368	Crassostrea gigas
15	8.8255959	58.447262	Crassostrea gigas
16	9.0724735	58.624622	Crassostrea gigas
17	9.0718365	58.624821	Crassostrea gigas
18	-3.574731272	54.42686226	Crassostrea gigas
19	1.037476751	51.78043197	Crassostrea gigas
20	-2.115802	49.251403	Crassostrea gigas
21	0.904865232	51.74780687	Crassostrea gigas
22	-2.186292	49.180744	Crassostrea gigas
23	-2.767877	48.574139	Crassostrea gigas
24	4.202235485	52.14743112	Crassostrea gigas



Introduction to Species Distribution Modeling



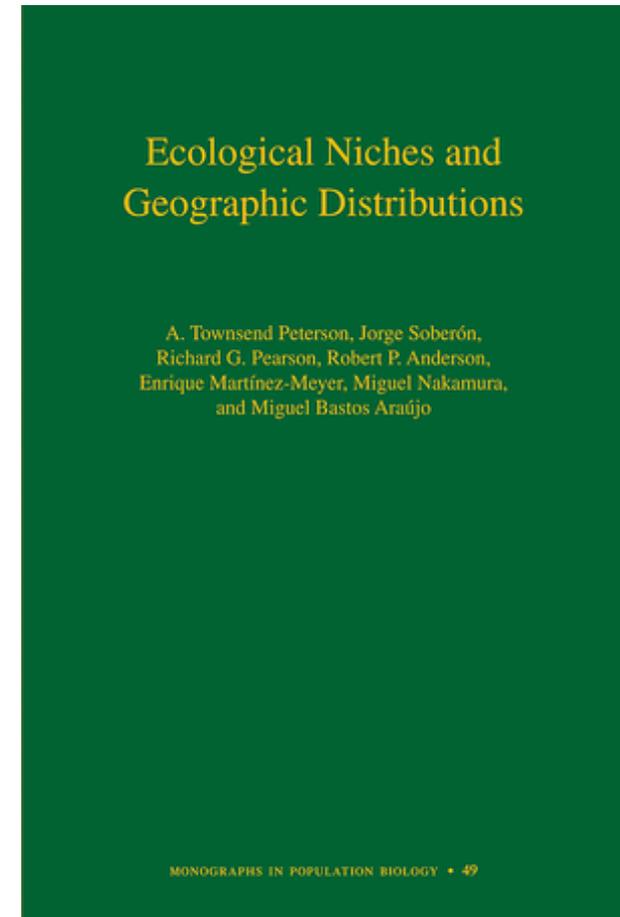
Literature

Townsend Peterson, A., Soberón, J., Pearson, R.G., Anderson, R.P., Martínez-Meyer, E., Nakamura, M. & Araújo, M.B. (2011). Ecological Niches and Geographic Distributions (Monographs in population biology; no. 49). Princeton University Press. 328 pp. ISBN: 9780691136882 (hard cover), 9780691136868 (Paperback) and 9781400840670 (eBook).

Pearson, R.G. (2007) Species' Distribution Modeling for Conservation Educators and Practitioners. Synthesis. American Museum of Natural History. Available at <http://ncep.amnh.org>

Elith, J., et al. Novel methods improve prediction of species' distributions from occurrence data. *Ecography*, 2006. 29(2): p. 129-151.

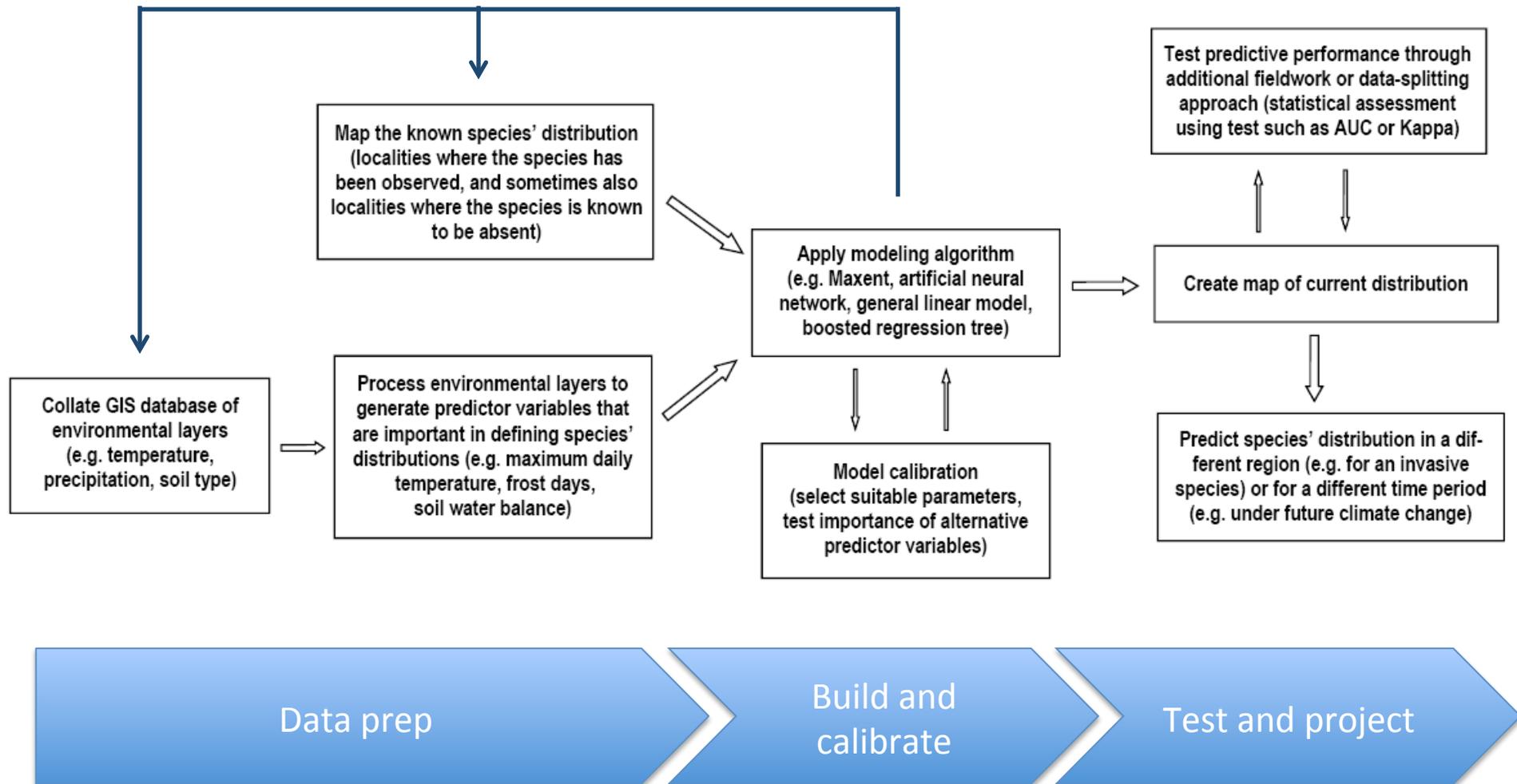
Soberón, J. and A.T. Peterson. Interpretation of models of fundamental ecological niches and species' distributional areas. *Biodiversity Informatics*, 2005. 2: p. 1-10.



Model types

Model type	Principle	Advantages	Disadvantages
Correlative (statistical extrapolation)	Model distribution by Correlating environmental conditions with a species' occurrence	Only two data types (species occurrence, environmental) Computational modest	Shows only correlations Can not predict beyond the observational boundaries
Mechanistic (process-based models)	Model distributions from estimates of responses to environmental conditions	Incl. physiological responses to environment Projection beyond observed conditions	Resource intense Require detailed knowledge of physiological responses Little data available

Principal steps required for building and validating a correlative Species distribution model



The basic approach of ENM

1. a study area is modeled as a raster map composed of grid cells at a specified resolution
2. the dependent variable is the known species' distribution
3. a suite of environmental variables are collated to characterize each cell
4. a function of the environmental variables is generated so as to classify the degree to which each cell is suitable for the species

Important factors influencing the quality of the outputs

Data

A model is only as good as the data it contains. The data preparation and choice of layers is just as important as the modeling.

Model extrapolation

'Extrapolation' is when you make predictions outside the observational boundaries.

For example, if a distribution model was calibrated within temp. range of 10–20 C, and the model is projected into a temp. range of 10-25 C, then the model is extrapolating and the prediction may be very uncertain.

The niche concept

Hutchinson defined **the *fundamental niche*** of a species as the set of environmental conditions within which a species can survive and persist.

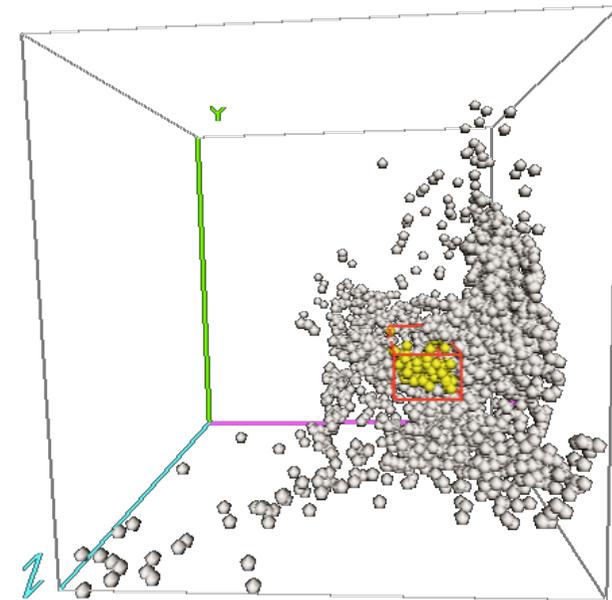
The fundamental niche may be thought of as an '*n*-dimensional hypervolume', every point in which corresponds to a state of the environment that would permit the species to exist indefinitely (Hutchinson, 1957)

Fundamental niche (environmental-space) =
Potential distribution (geographical-space)

Occupied niche (environmental-space) =
Actual distribution (geographical-space)

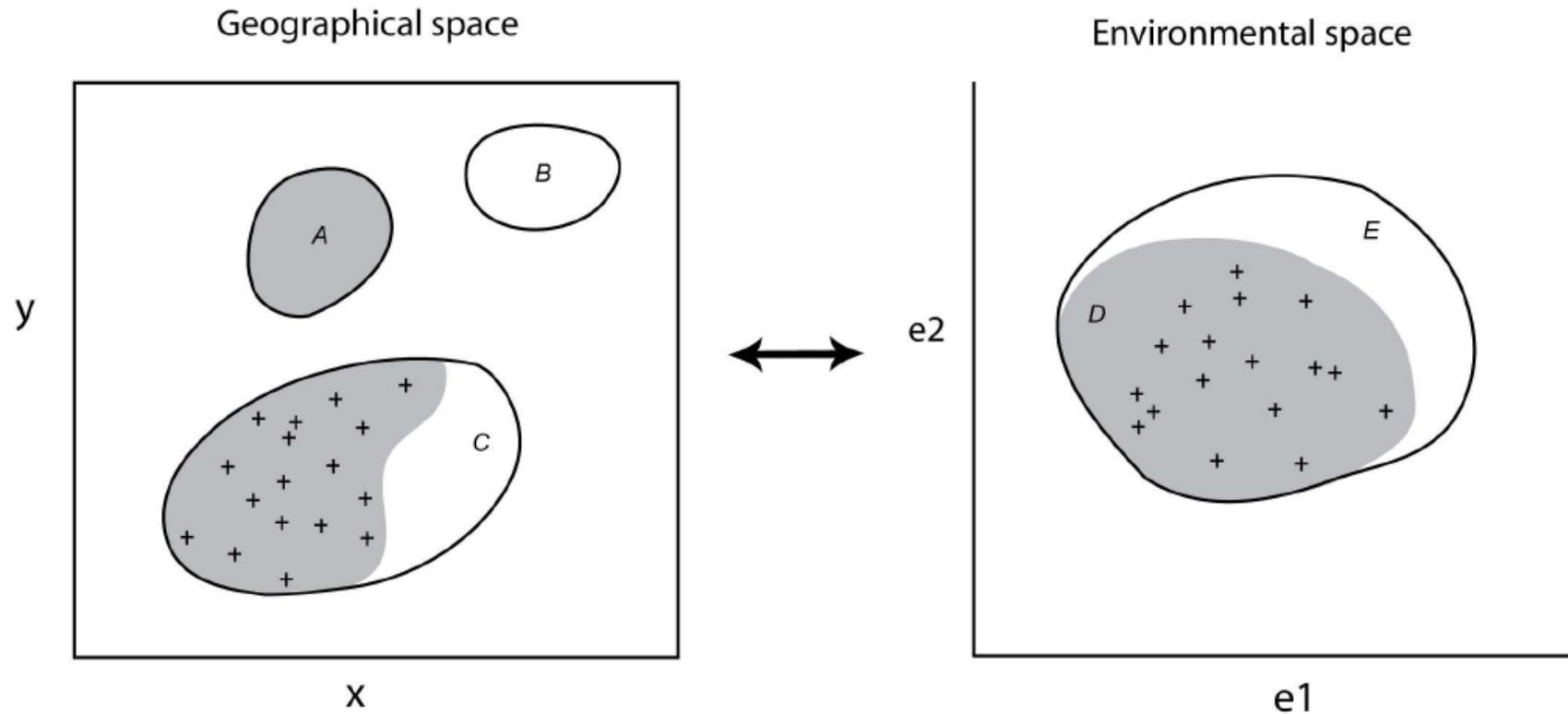
Constraints that influence the potential from
actual distribution

- Ecological interactions (predators, competition, parasites)
- Dispersal barriers
- Historical



*Fundamental niche depicted in
environmental-space*

Geographical versus environmental space



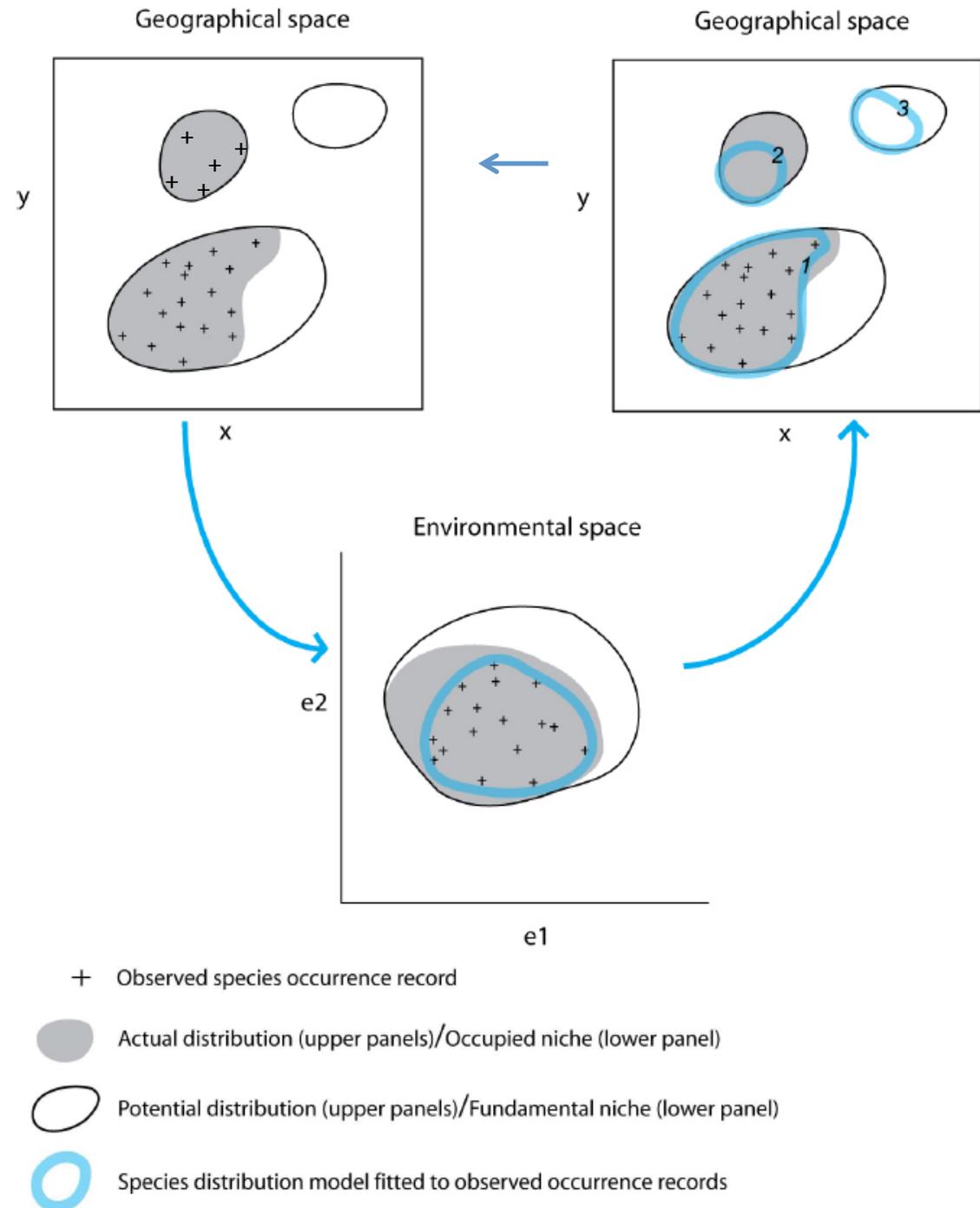
+ Observed species occurrence record

● Actual distribution (left panel)/Occupied niche (right panel)

○ Potential distribution (left panel)/Fundamental niche (right panel)

Species' distribution models may identify

- 1) Protection areas**, the area around the observed occurrence records that is expected to be occupied (area 1)
- 2) Unobserved populations**, currently unknown distributions (area 2).
- 3) Invasive or re-introduction areas**, potential distribution that is not occupied (area 3)



Species data

Data types

- Presence only
- Presence/absence
 - only for well studied species
 - False absence lead to serious bias

Quality criteria

- Should be well distributed in g-space (for projecting the model, enclosed sea problem) and e-space (for building the model)
- Resolution: what resolutions makes sense for the organism and question you investigate
- Species data typically need thorough cleaning/refinement



Enclosed sea problem (Ready et al., 2010)

Species data sources

- Personal
- inventories and museums
- Colleagues and networks
- Online resources
- Literature

Sources of errors

- Are the species records sustained observations (sink vs source)
- Incorrect identification
- Inaccurate spatial reference
- Sampling bias (along roads/rivers)

Environmental data

Types

- Categorical (habitat maps)
- Continuous (salinity, temperature)

Formats

- Point vector data (typically converted to Grid/raster data)
- Polygon vector data (typically converted to Grid/raster data)
- Grid/raster data

Resolution

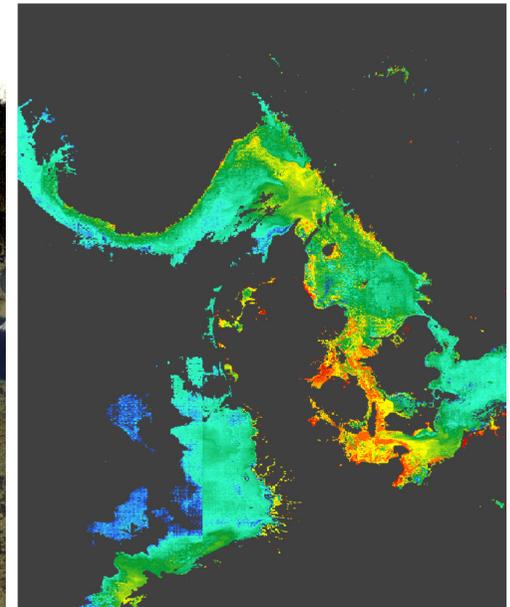
- Should be conform with species data resolution

Variables

- Climatic (temperature)
- Geographic (altitude)
- Habitat (soil type)
- Ecological (habitat builders)

Number of layers

- Empirical evidence shows that 4-8 layers are sufficient to generate good models
- Quality before quantity



Algorithms

The algorithm identifies environmental conditions that are associated with species occurrence

The choice of algorithm depends on your question and what the model should produce, e.g. if you want to protect a species you should identify ***actual distributions***, but if you want to re-introduce a species you should identify ***potential distributions***.

The choice of algorithms also depends on

- the quality/quantity of your species data
- use presence-only, presence-background, presence-absence
- categorical vs. continuous environmental data
- give binary vs. continuous predictions
- causality vs. predictability

Good algorithms are those that minimize predictions of areas that are neither the actual nor the potential distribution

Algorithms

MaxEnt is very good for predictions inside the observational boundaries, but can generate faulty extrapolations

Algorithms that can incorporate interactions among variables are preferable (Elith et al. 2006), e.g. a more accurate description of a plant's requirements may be that it can occur at localities with mean monthly precipitation between 60mm and 70mm if soil clay content is above 60%, and in wetter areas (>70mm) if clay content is as low as 40%.

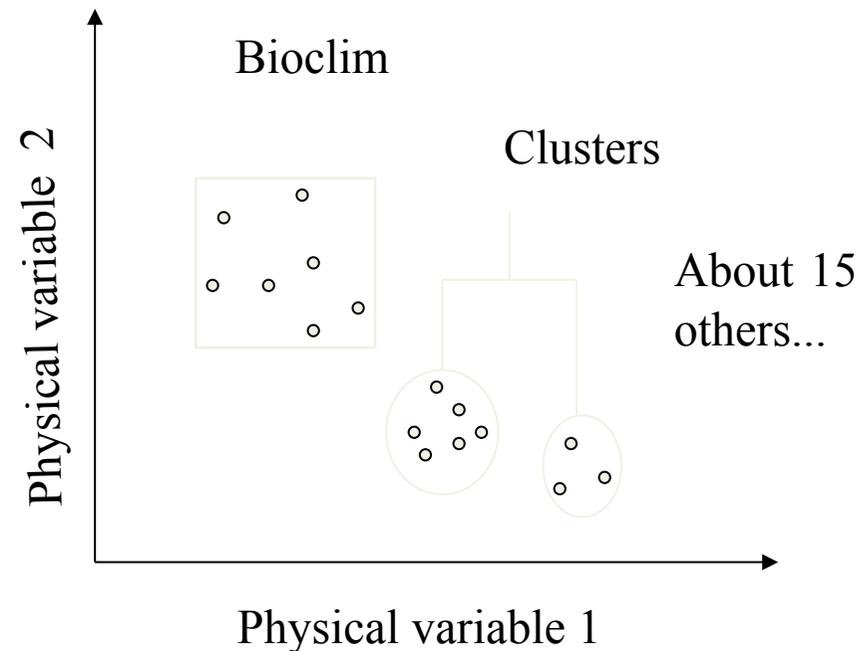


Table 4. Modelling methods implemented.

Method	Class of model, and explanation	Data ¹	Software	Std errors? ²	Contact person
BIOCLIM	envelope model	p	DIVA-GIS	no	CG, RH
BRT	boosted decision trees	pa	R, gbm package	no	JE
BRUTO	regression, a fast implementation of a gam	pa	R and Splus, mda package	yes	JE
DK-GARP	rule sets from genetic algorithms; desktop version	pa	DesktopGarp	no	ATP
DOMAIN	multivariate distance	p	DIVA-GIS	no	CG, RH
GAM	regression: generalised additive model	pa	S-Plus, GRASP add-on	yes	AG,AL,JE
GDM	generalised dissimilarity modelling; uses community data	pacomm	Specialized program not general released; uses Arcview and Splus	no	SF
GDM-SS	generalised dissimilarity modelling; implementation for single species	pa	as for GDM	no	SF
GLM	regression; generalised linear model	pa	S-Plus, GRASP add-on	yes	AG,AL,JE
LIVES	multivariate distance	p	Specialized program not general released	no	JLi
MARS	regression; multivariate adaptive regression splines	pa	R, mda package plus new code to handle binomial responses	yes	JE, FH
MARS-COMM	as for MARS, but implemented with community data	pacomm	as for MARS	yes	JE
MARS-INT	as or MARS; interactions allowed	pa	as for MARS	yes	JE
MAXENT	maximum entropy	pa	Maxent	no	SP
MAXENT-T	maximum entropy with threshold features	pa	Maxent	no	SP
OM-GARP	rule sets derived with genetic algorithms; open modeller version	pa	new version of GARP not yet available	no	ATP

3 types of presence-only methods

1. Methods that rely *solely based on presence records* (e.g. BIOCLIM), e.g. the prediction is made without any reference to other samples from the study area
2. Methods that use '*background*' environmental data for the entire study area (e.g. Maxent, ENFA), e.g. focus on how the environment where the species is known to occur relates to the environment across the rest of the study area. Occurrence localities are also included as part of the background.
3. Methods that sample '*pseudo-absences*' from the study area. In The aim here is to assess differences between the occurrence localities and a set of localities chosen from the study area that are used in place of real absence data. Pseudo-absence models do not include occurrence localities within the set of pseudo-absences.

Assessing predictive performance

Strategies for obtaining test data

Typically split the data into: 30% test data and 70% calibration data

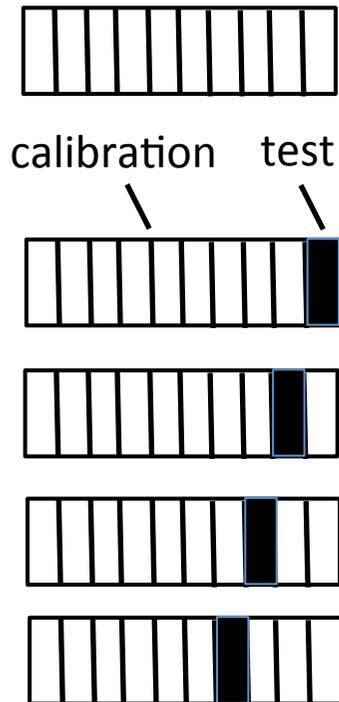
Bootstrapping

- sample the original set of data randomly with replacement
- same occurrence record could be included in the test data more than once
- predictive performance is assessed from multiple re-samplings

k-fold partitioning

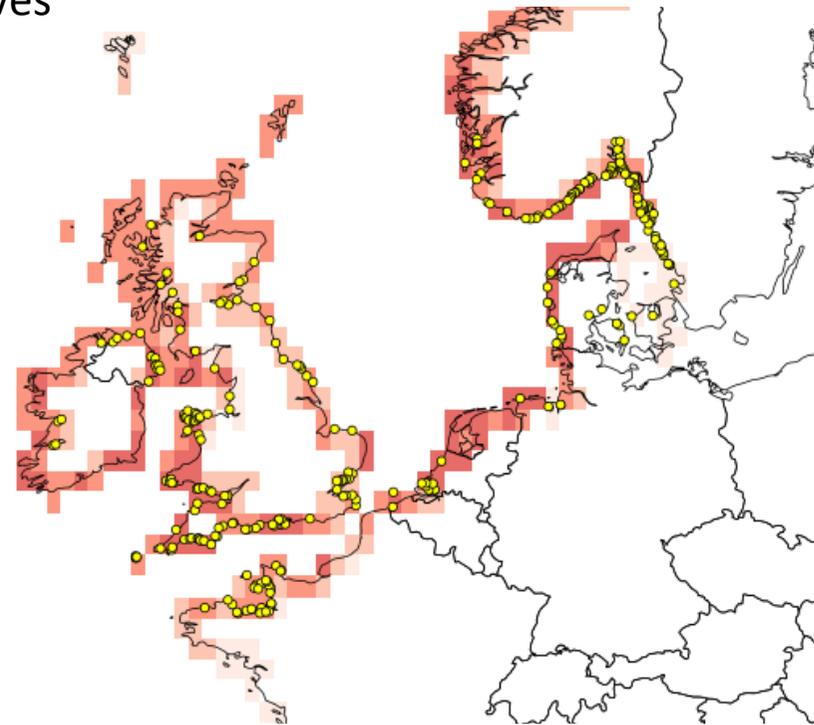
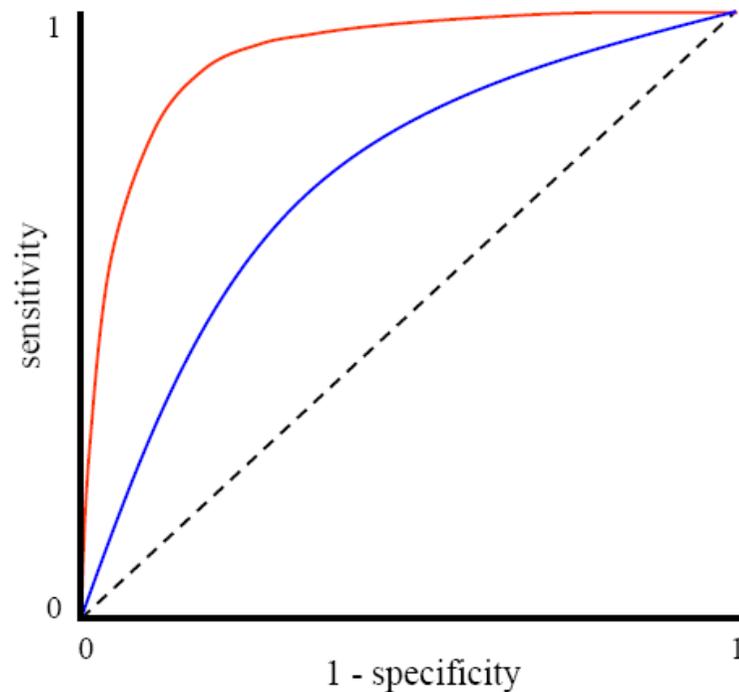
- data are split into *k* parts of roughly equal size and each part is used as a test set with the remaining (*k*-1) sets used for model calibration.

10-fold partitioning



Assessing predictive performance - validation statistics

Receiver Operating Characteristic (ROC) Curves



AUC (area under the ROC curve)

- summarizes the predictive performance across the full range of thresholds
- ranges from 0.5 for models that are no better than random to 1.0 for models with perfect predictive ability

Examples of species' distribution models in conservation biology

Type of use	Example reference(s)
Guiding field surveys to find populations of known species	Bourg et al. 2005, Guisan et al. 2006
Guiding field surveys to accelerate the discovery of unknown species	Raxworthy et al. 2003
Projecting potential impacts of climate change	Iverson and Prasad 1998, Berry et al. 2002, Hannah et al. 2005; for review see Pearson and Dawson 2003
Predicting species' invasion	Higgins et al. 1999, Thuiller et al. 2005; for review see Peterson 2003
Exploring speciation mechanisms	Kozak and Wiens 2006, Graham et al. 2004b
Supporting conservation prioritization and reserve selection	Araújo and Williams 2000, Ferrier et al. 2002, Leathwick et al. 2005
Species delimitation	Raxworthy et al. 2007
Assessing the impacts of land cover change on species' distributions	Pearson et al. 2004
Testing ecological theory	Graham et al. 2006, Anderson et al. 2002b
Comparing paleodistributions and phylogeography	Hugall et al. 2002
Guiding reintroduction of endangered species	Pearce and Lindenmayer 1998
Assessing disease risk	Peterson et al. 2006, 2007

Guisan and Thuiller (2005) Ecology Letters

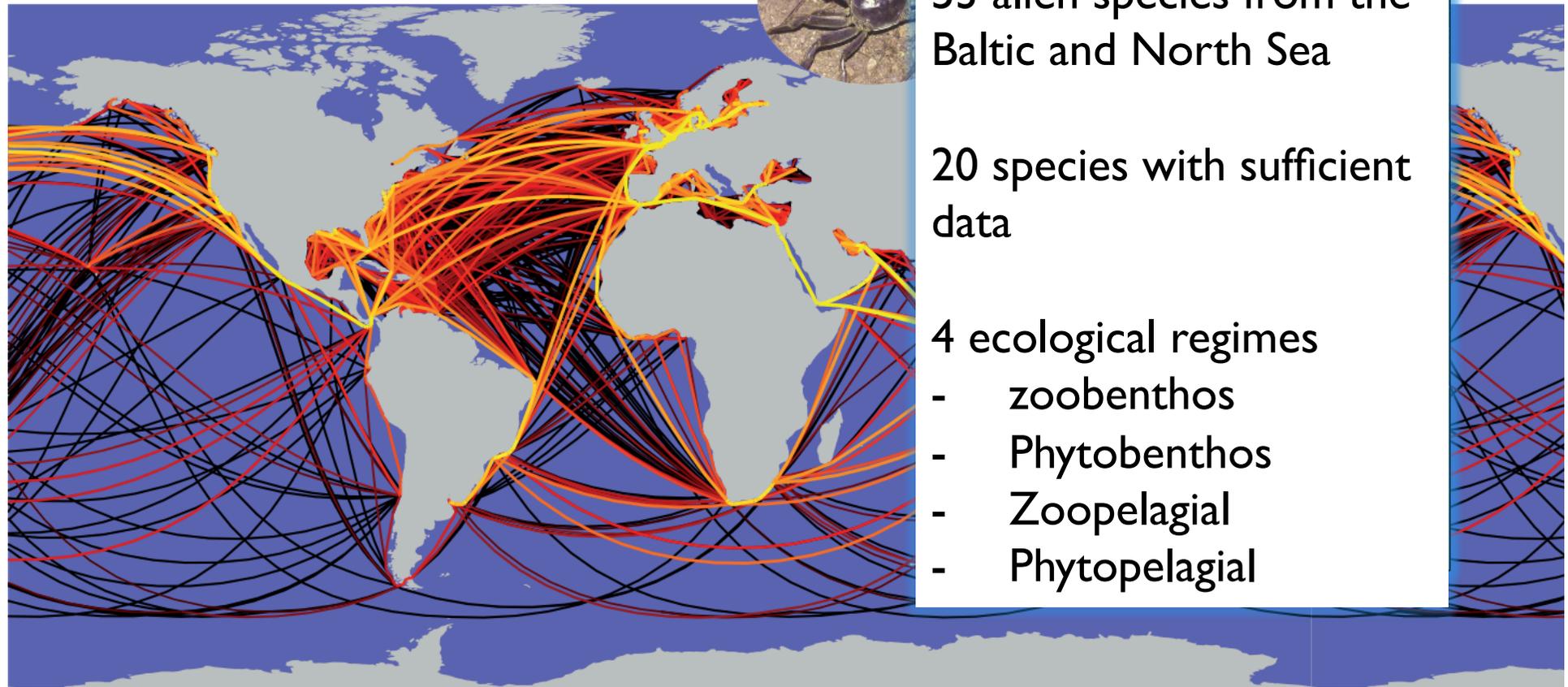


53 alien species from the
Baltic and North Sea

20 species with sufficient
data

4 ecological regimes

- zoobenthos
- Phytobenthos
- Zoopelagial
- Phytipelagial



<10 20 50 100 200 500 1000 2000 >5000 journeys

Kaluza et al (2013)

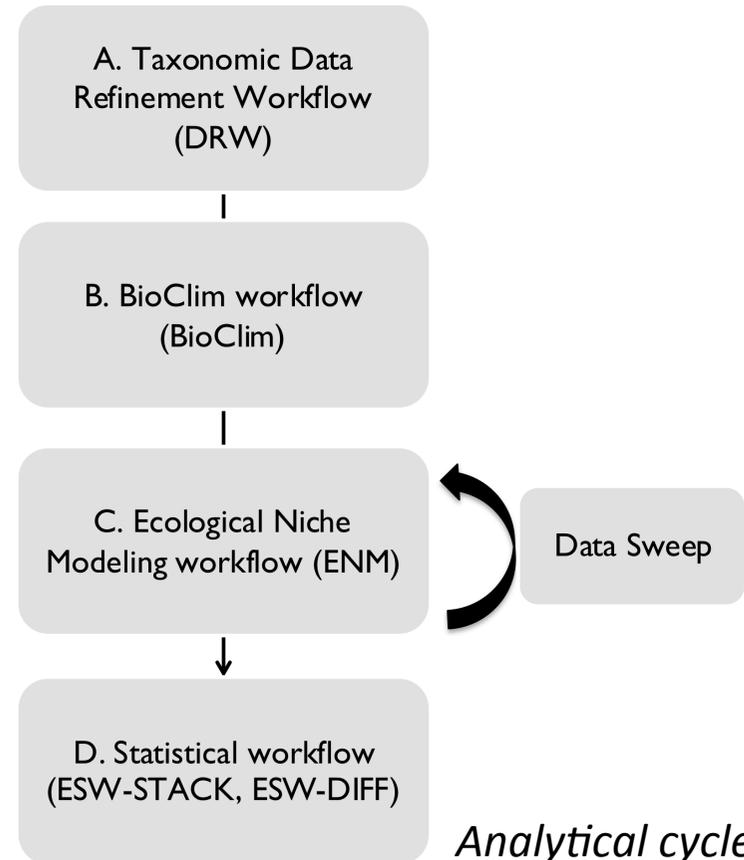
Data discovery



Occurrence records for 31 species

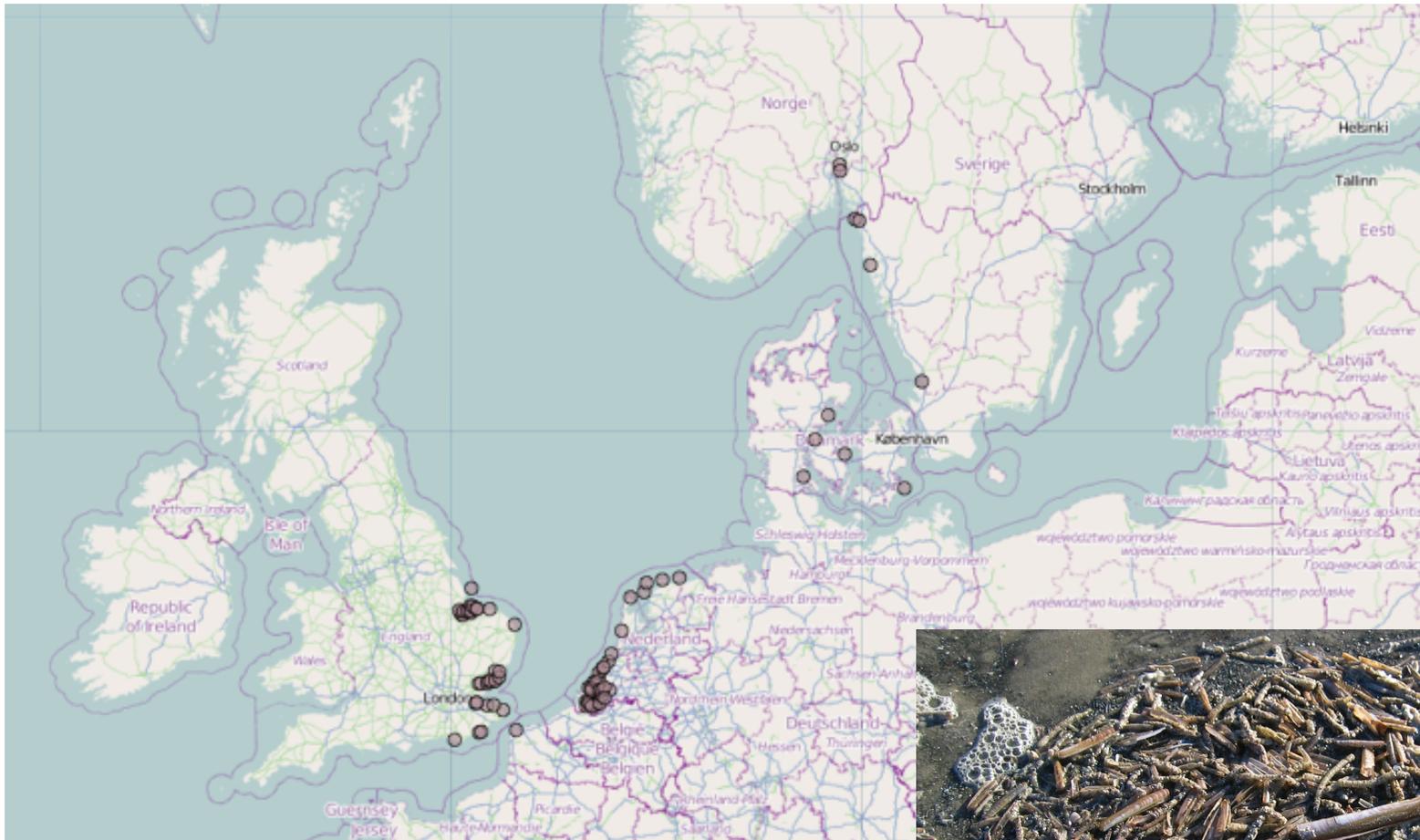
Sources

- Personal data
- Digital repositories (ICES, GBIF, national environmental agencies)
- Scientific networks
- Literature digitization



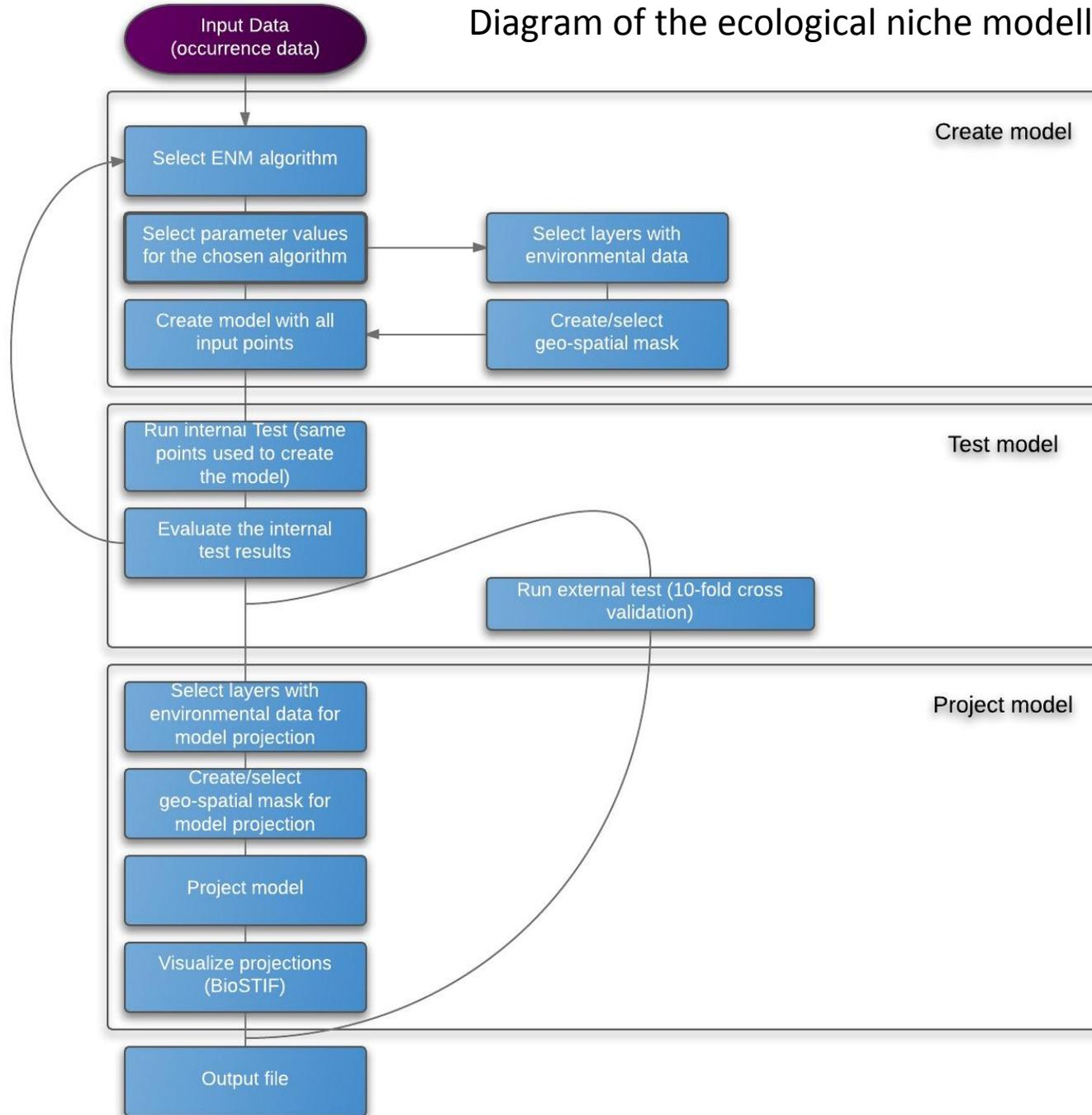
Analytical cycle

Species, Authors	Eco-group	Origin	Invasion Path	Introduction/		Total # of records	References of Occurrence data
				First observation			
				North Sea	Baltic Sea		
<i>Austrominius modestus</i> (Darwin, 1854)	ZB	S Pacific	S	1953	-	709	GBIF (709)
<i>Crassostrea gigas</i> (Thunberg, 1793)	ZB	NW Pacific	A, ST	1991	1980s	967	GBIF (967)
<i>Ensis directus</i> (Conrad, 1843)	ZB	NW Atlantic	S	1978/79	1981/1993	817	GBIF (807), Thomsen et al. 2009 (5), www.frammandearter.se (1), own observations (4)
<i>Eriocheir sinensis</i> H. Milne Edwards, 1853	ZB	NW Pacific	S	1915	1926/1932	740	GBIF (613), Drotz et al. 2010 (46), Normant et al. 2000 (8), Ojaveer et al. 2011 (1), Ojaveer et al. 2007 (68), Otto and Brandis 2011 (4)
<i>Gammarus tigrinus</i> Sexton, 1939	ZB	NW Atlantic	ST	1965	1975/1985	1648	GBIF (1566), Berezina 2007 (2), Guszka 1999 (44), Jazdzowski et al. 2004 (6), Kotta et al. 2013 (26), Strode et al. 2013 (4)
<i>Marenzelleria viridis</i> (Verrill, 1873)	ZB	NW Atlantic	S	1983	2004	789	GBIF (718), Andrulewicz 1997 (4), Bastrop and Blank 2006 (3), Gruszka 1999 (43), Thomsen et al. 2009 (18), Zettler 1996 (3)
<i>Mytilopsis leucophaeata</i> (Conrad, 1831)	ZB	NW Atlantic	S	1835/ <1994	1930s/ <1994/2000	268	GBIF (258), Dziubinska 2011 (1), Laine et al. 2006 (5), Verween et al. 2005 (1), Darr and Zettler 2000 (2), www.frammandearter.se (1)
<i>Pilumnus hirtellus</i> (Linnaeus, 1761)	ZB	NW Atlantic	S	-	2004	1270	GBIF (1258), Berggren 2012 (10), www.frammandearter.se (2)
<i>Potamopyrgus antipodarum</i>	ZB	S Pacific	S	1927	1887/1908	990	GBIF (990)



Distribution of the invasive Atlantic jackknife clam (*Ensis directus*) in Europe. Data aggregated from GBIF and scientific networks.

Diagram of the ecological niche modelling workflow



Create Model:

- model algorithm
- parameter values
- environmental layer selection
- geospatial mask
- Model created
- background or pseudo-absence points are sampled from the masked region

Test model:

- statistical evaluation of the model prediction

Project Model:

- select the layers and masks for model projection
- projections and associated occurrence points are visualized



Ecological Niche Modeling Workflow (ENM)



Home

Workflows

Run of Gene
myExperiment

User: Sarah Bou

Current State: ru

The run was sta

This is the first tim

Cancel Run

INTERACTIO

Available algorithm

- AquaMaps (beta)
- Bioclim
- Climate Space Model
- GARP (single run) - DesktopGARP implementation
- GARP with best subsets - DesktopGARP implementation
- ENFA (Ecological-Niche Factor Analysis)
- Envelope Score
- Environmental Distance
- GARP (single run) - new openModeller implementation
- GARP with Best Subsets - new openModeller implementation
- Maximum Entropy
- Niche Mosaic
- Artificial Neural Network

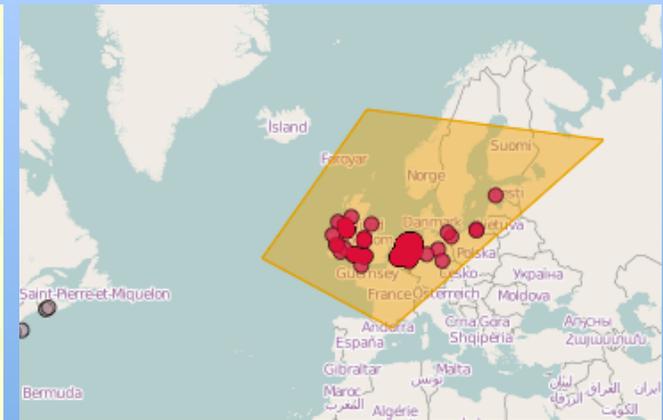
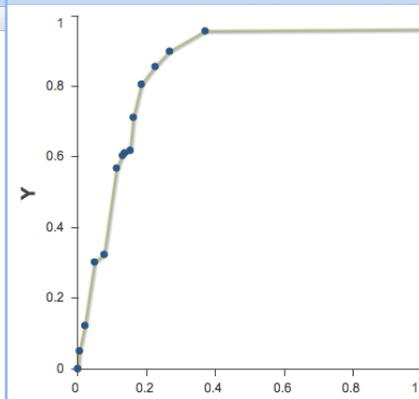
Select layers to create the model

- HCAFv4
 - geography
 - 30arc-minutes
 - Mean depth in meters
 - Mean annual distance to land in Kilometers
 - Minimum depth in meters
 - Maximum depth in meters
 - present
 - 30arc-minutes
 - Mean annual bottom salinity in psu
 - Mean annual surface salinity in psu
 - Mean annual bottom temperature in Celsius
 - Mean annual surface temperature in Celsius
 - Mean annual sea ice concentration
 - Mean annual primary production (chlorophyll A) in mgC/m2/day
 - terrestrial
 - plants
- Submit selected layers

Confusion matrix

Name	Value
Accuracy	84.32%
CommissionError	-
FalsePositives	422
OmissionError	15.68%
Threshold	0.5
TruePositives	2269

ROC Curve (AUC=0.96)



when used with the Gower metric and maximum distance 1, this algorithm should produce the same result of the algorithm known as DOMAIN.

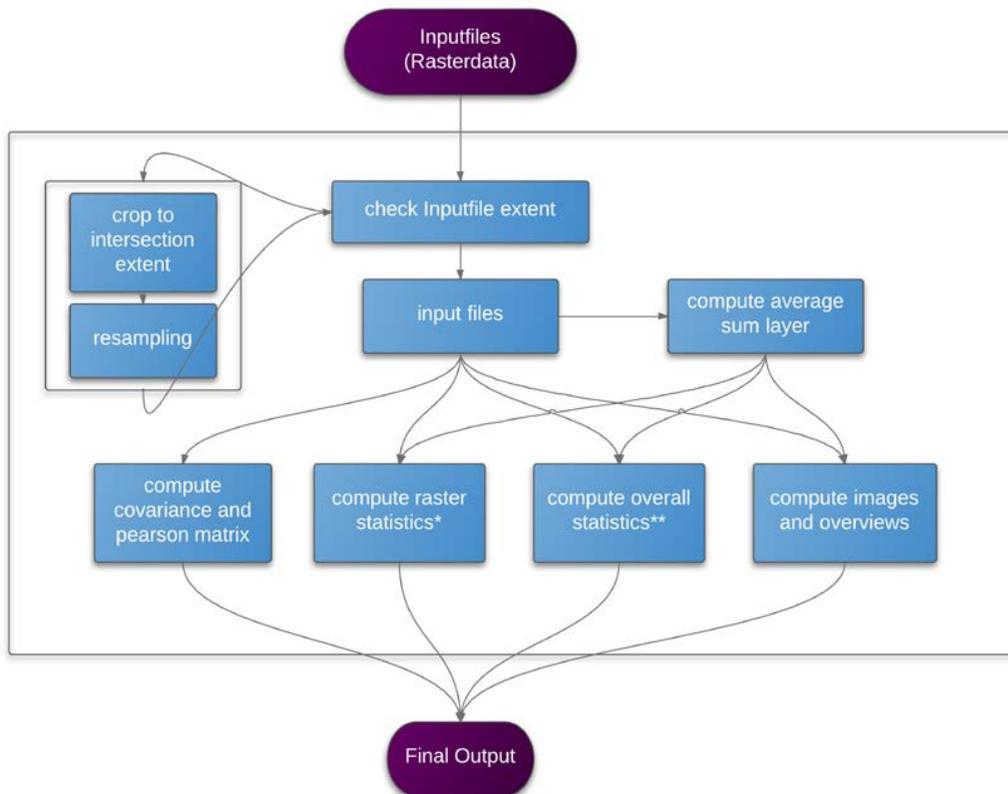
Author(s) Mauro E. S. Munoz, Renato De Giovanni, Danilo J. S. Bellini

Bibliography Carpenter G, Gillison AN, Winter J (1993) DOMAIN: A flexible modeling procedure for mapping potential distributions of animals and plants. *Biodiversity and Conservation* 2: 667-680. Farber O & Kadmon R 2003. Assessment of alternative approaches for bioclimatic modeling with special emphasis on the Mahalanobis distance. *Ecological Modelling* 160: 115&1130.

Developer(s) Danilo J. S. Bellini, Renato De Giovanni

ENM Statistical Workflows

ESW STACK workflow using R



*computed raster statistics: number of cells, mean, median, coefficient of variation (cv), standard deviation (sd), min, max

**computed overall statistics:

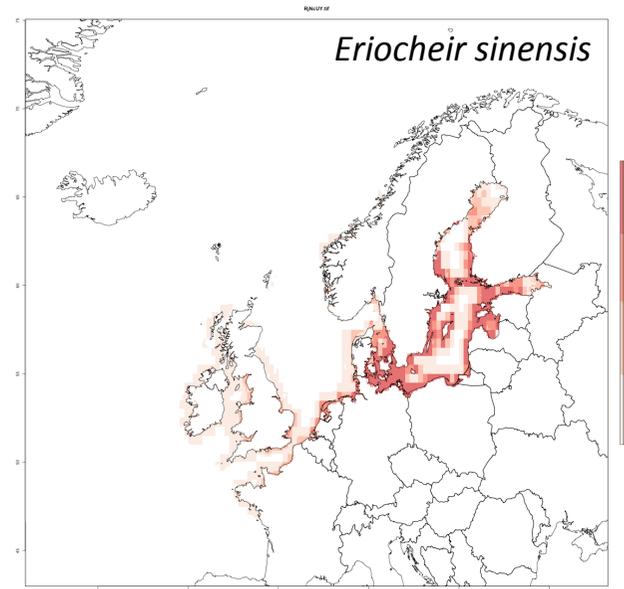
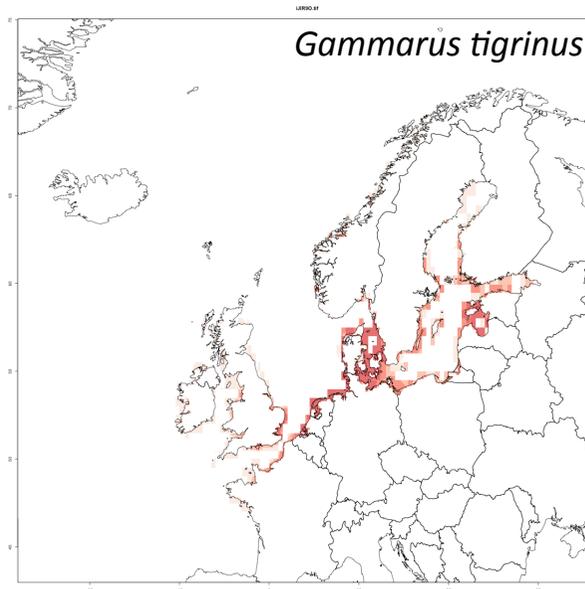
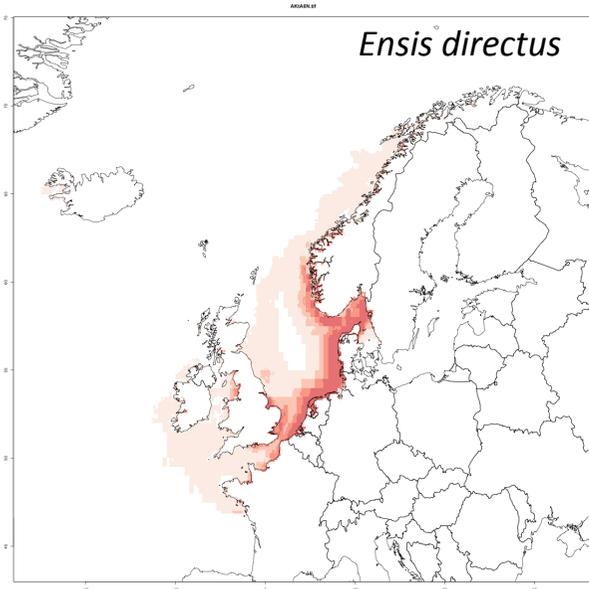
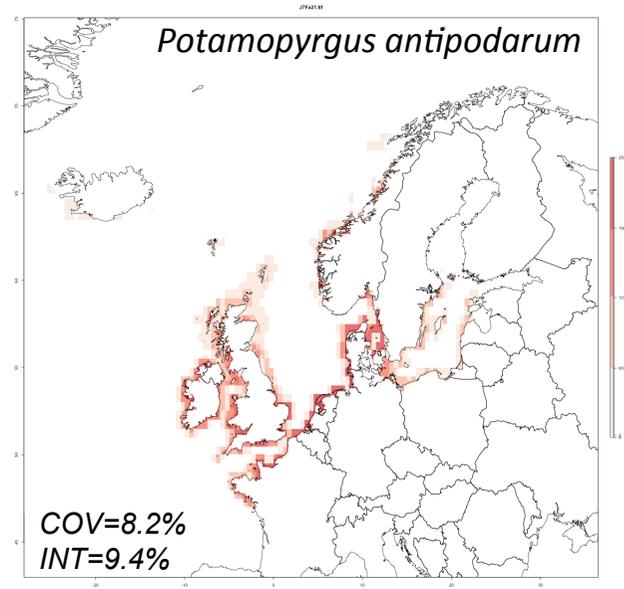
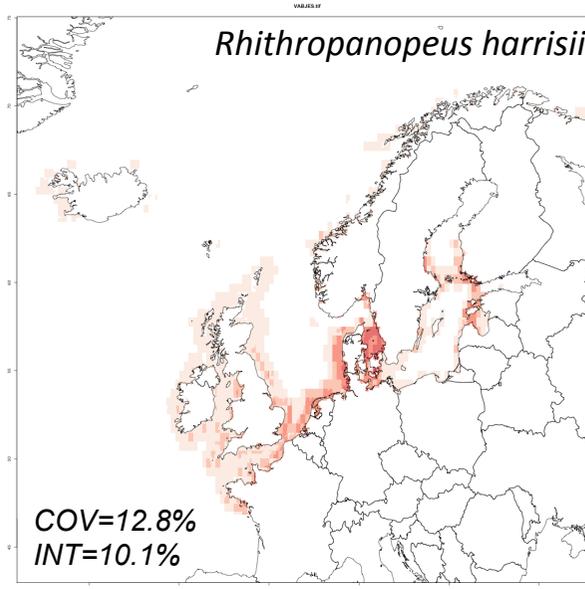
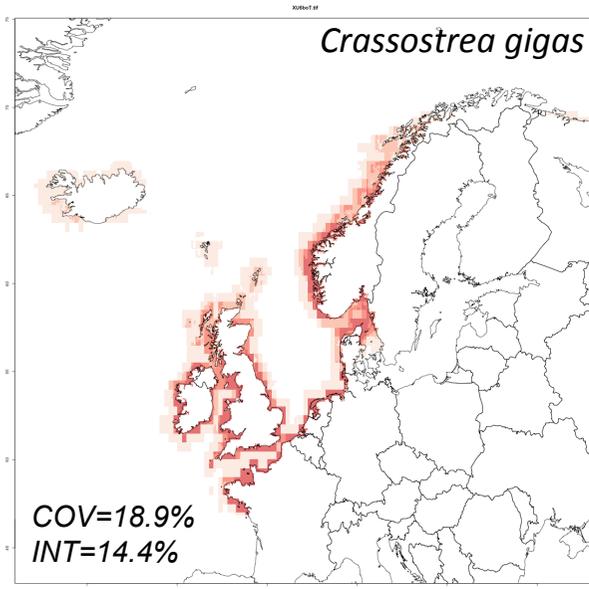
- overall coverage as the percentage of raster cells with values >0,
- overall intensity as the sum of all valued cells divided by the number of raster cells,
- differences between the coverage and intensity between the input files

- 1) ESW DIFF
- 2) ESW STACK
- 3) ESW SHIFT

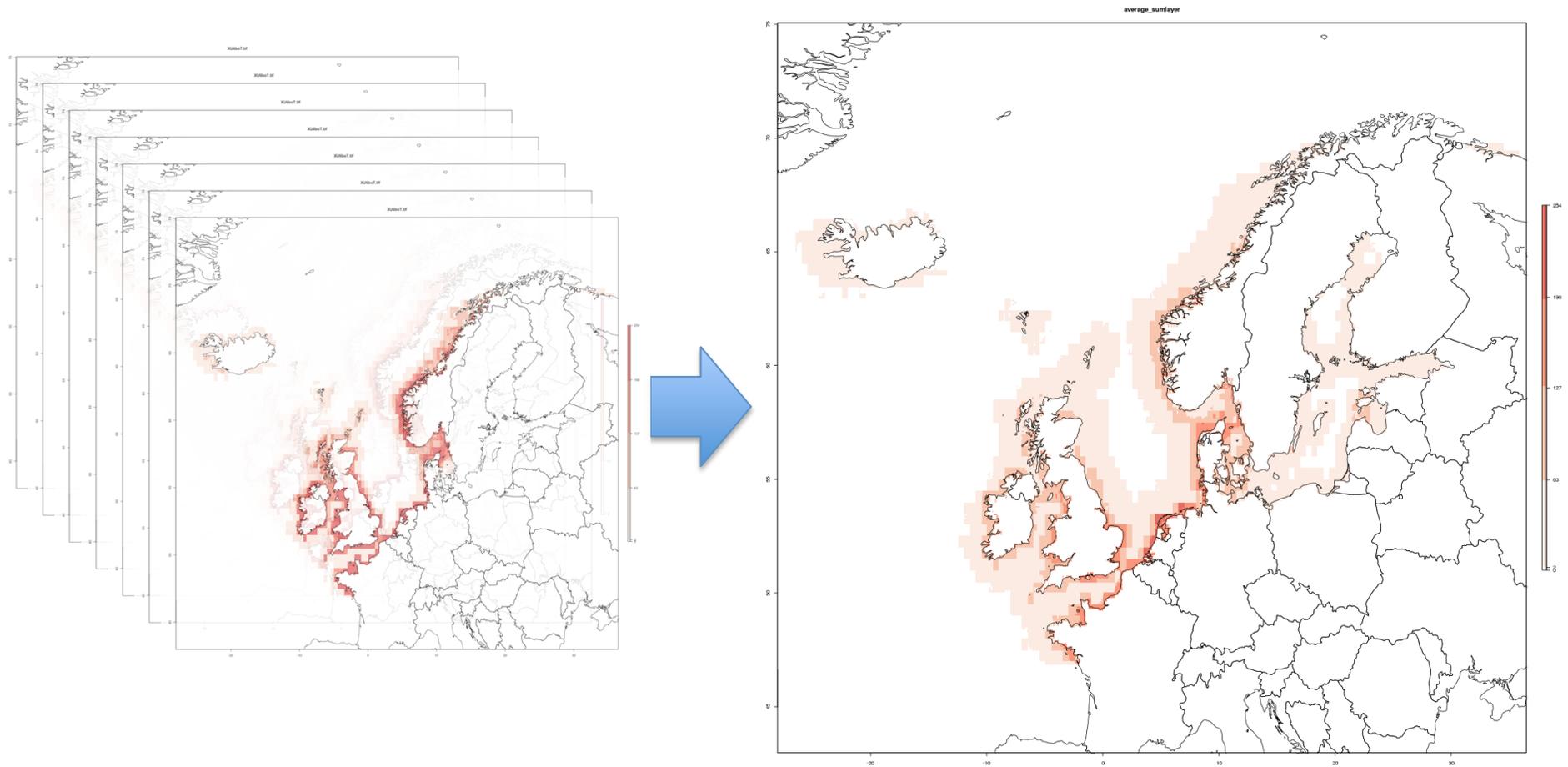


XX	Number of raster cells	Mean of all raster cell values	Median of all raster cell values	Coefficient of Variation
currentLayer	643104	2.889023	0	472.7624667
predictionLayer	643104	2.8119792	0	462.6982272
diff.Layer	643104	-0.077043835	0	-11966.1249

Invasive heatmaps



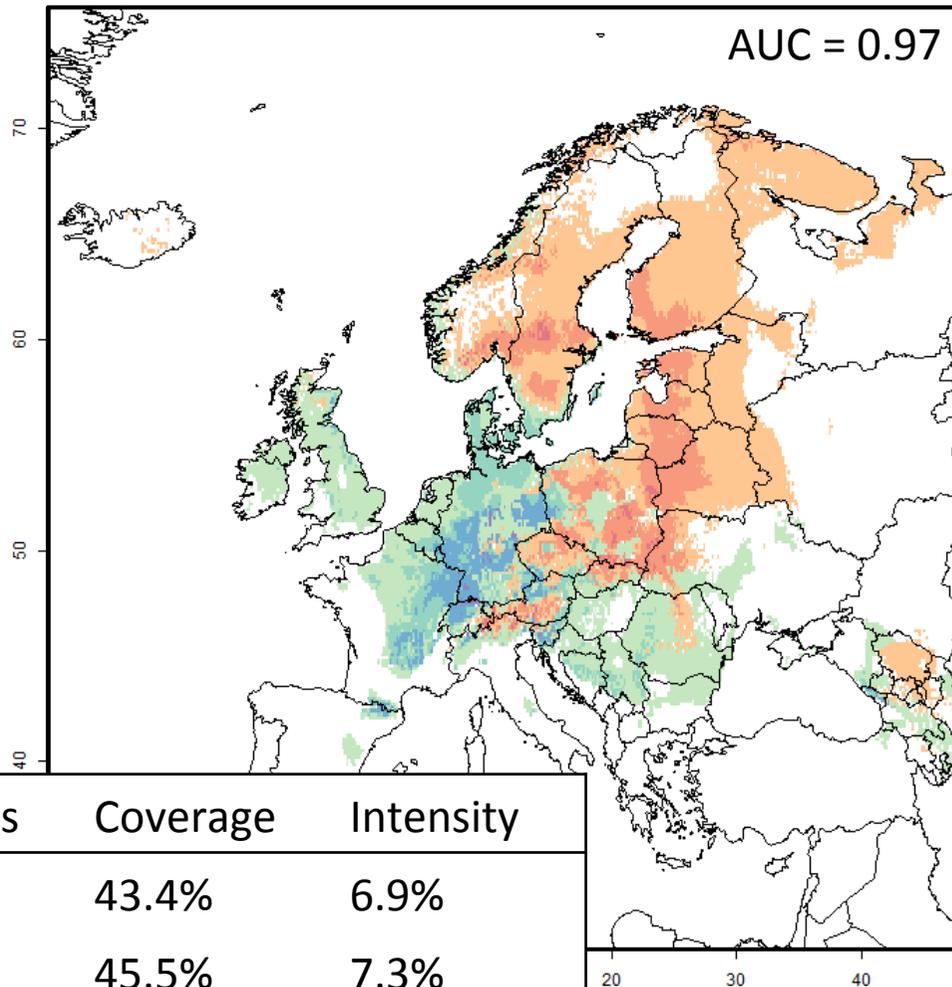
Accumulated invasive potential for ecological groups



Stack of macrozoobenthic invasion heatmaps



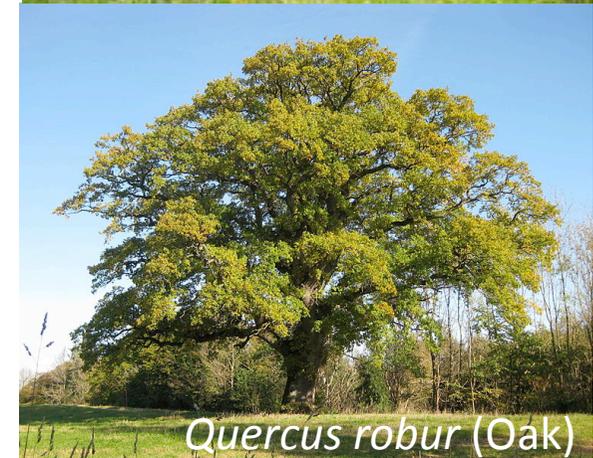
Dynamic projection of forest pest species based on distribution of host trees



Erannis defoliaria
(mottled Umber)



Betula pendula (silver birch)



Quercus robur (Oak)

Assignment (14.00-16.20)

You want to study the potential distribution of the invasive oyster (*Crassostrea gigas*) using species distribution modeling approaches.

You have collected occurrence records of the species in your region (Scandinavia) and want to enrich your records with public data from GBIF, and thereafter create, test, and project an ecological niche model for the species under various climate scenarios.

1. Generate an input file to download GBIF data
2. Retrieve, clean, and refine occurrence data
3. Integrate your data with the GBIF records

Lunch

4. Create model
5. Test model
6. Project model for 2013 and 2050
7. Statistical analysis of difference between projections

occurrenceID	decimalLongitude	decimalLatitude	nameComplete
1	8.428	55.0315	Crassostrea gigas
2	8.4339	55.0304	Crassostrea gigas
3	8.4314	55.0312	Crassostrea gigas
4	8.4314	55.0312	Crassostrea gigas
5	8.428	55.0315	Crassostrea gigas
6	8.4339	55.0304	Crassostrea gigas
7	8.4172	55.0368	Crassostrea gigas
8	8.428	55.0315	Crassostrea gigas
9	8.4314	55.0312	Crassostrea gigas
10	8.4339	55.0304	Crassostrea gigas
11	8.4314	55.0312	Crassostrea gigas
12	8.4339	55.0304	Crassostrea gigas
13	8.428	55.0315	Crassostrea gigas
14	8.4172	55.0368	Crassostrea gigas
15	8.8255959	58.447262	Crassostrea gigas
16	9.0724735	58.624622	Crassostrea gigas
17	9.0718365	58.624821	Crassostrea gigas
18	-3.574731272	54.42686226	Crassostrea gigas
19	1.037476751	51.78043197	Crassostrea gigas
20	-2.115802	49.251403	Crassostrea gigas
21	0.904865232	51.74780687	Crassostrea gigas
22	-2.186292	49.180744	Crassostrea gigas
23	-2.767877	48.574139	Crassostrea gigas
24	4.20332486	53.14743113	Crassostrea gigas

Create model

Algorithm: Environmental distance

Parameter values: 2, 0, 1

Environmental layers:

- Mean Depth
- Mean Distance to Land
- Mean Surface Salinity
- Mean Surface Temperature
- Mean Sea Ice concentration

Geographic mask:

- GBIF_training_mask_1800arcs
ecs_25MAR2014

Test and project model

Test model

- Inspect AUC
- Cross validation (replicates: 10, measure AUC, threshold LPT)

Projection model

- Native projection (same layers, same mask)
- Another projection: Press yes
- 2050 projection (2050 layers of same environmental variables, same mask)
- Another projection: Press no
- Finish workflow and download all results

Homework assignment

Use your own and GBIF data to project habitat suitability for the invasive oyster *C. gigas* into Swedish and Norwegian Exclusive Economic zone. How many percent increase of suitable habitat can we expect until 2050?

1. Mobilize and integrate occurrence data (DRW)
2. Filter environmentally unique points (BioClim)
3. Build and test global model; make local projections into Swedish/Norwegian Exclusive Economic Zones for 2013 and 2050 (ENM)
4. Analyze difference in rather projections between 2050 and 2013 in Norway and Sweden