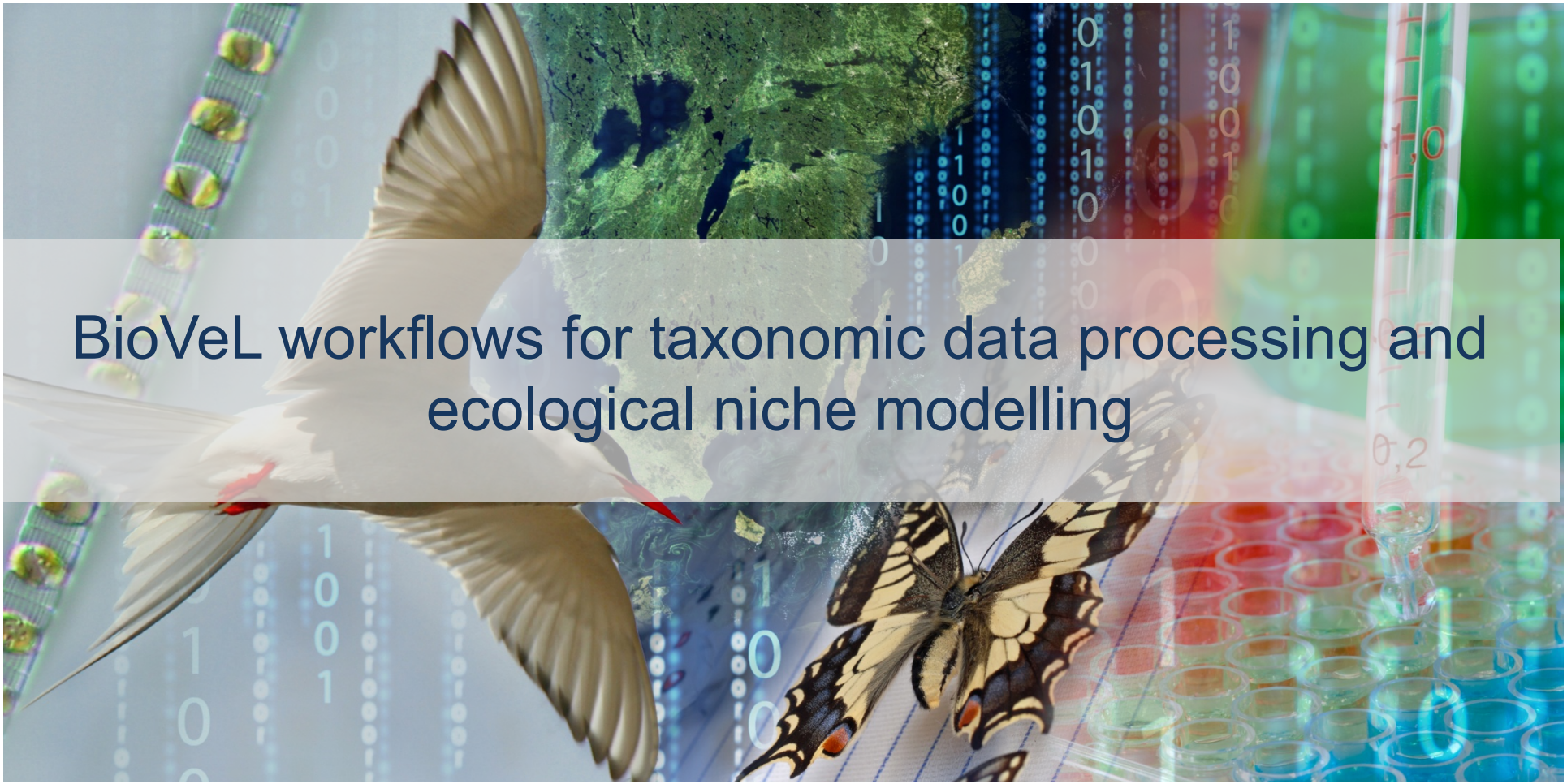
BioVeL training

Matthias Obst, Francisco Quevedo, Elisabeth Paymal



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

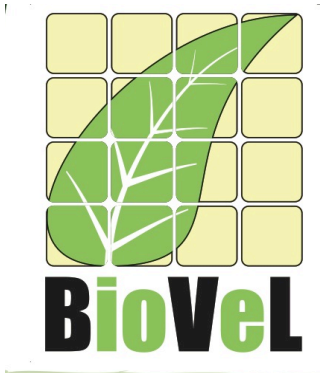
16:00 - 16:20 - Pause café/thé

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



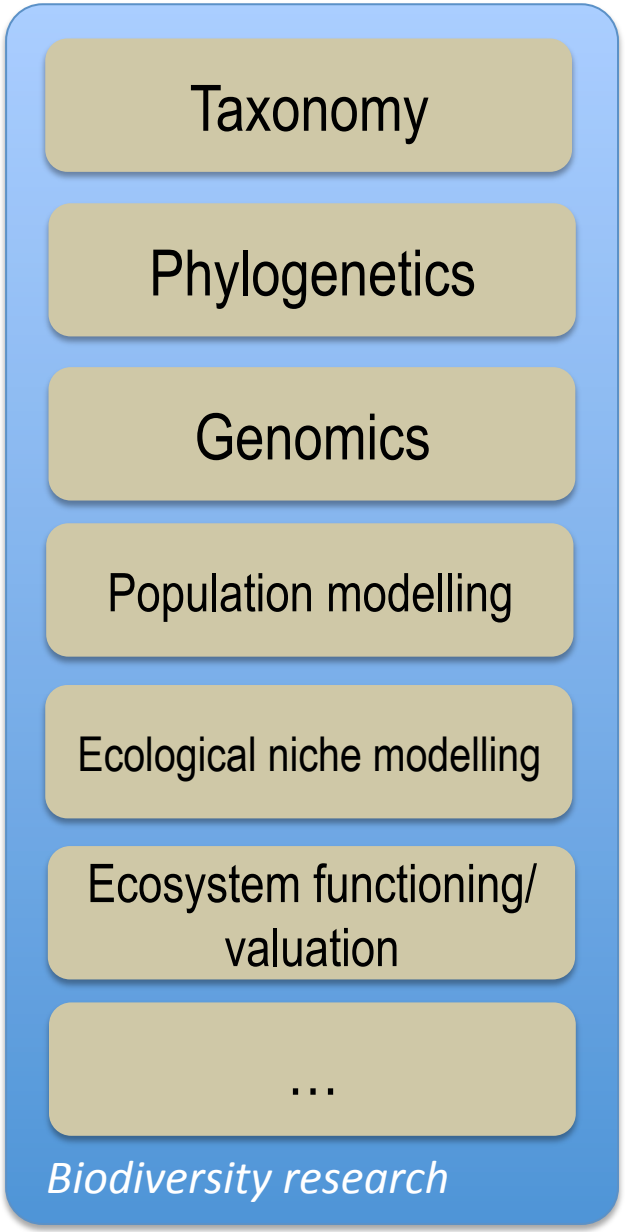
Aims of the Biodiversity Virtual e-laboratory (BioVeL)

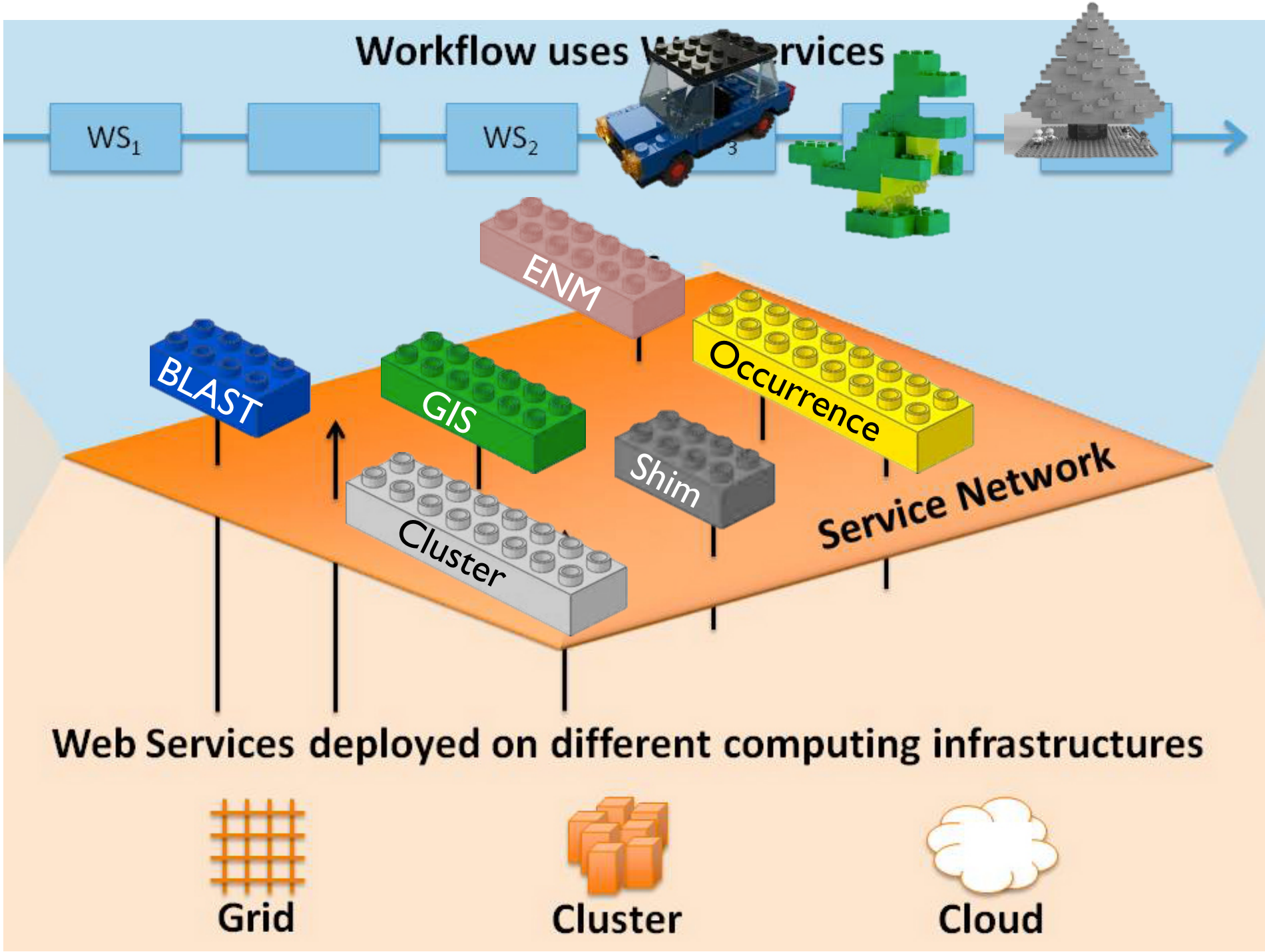
BioVeL provides functions to:

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

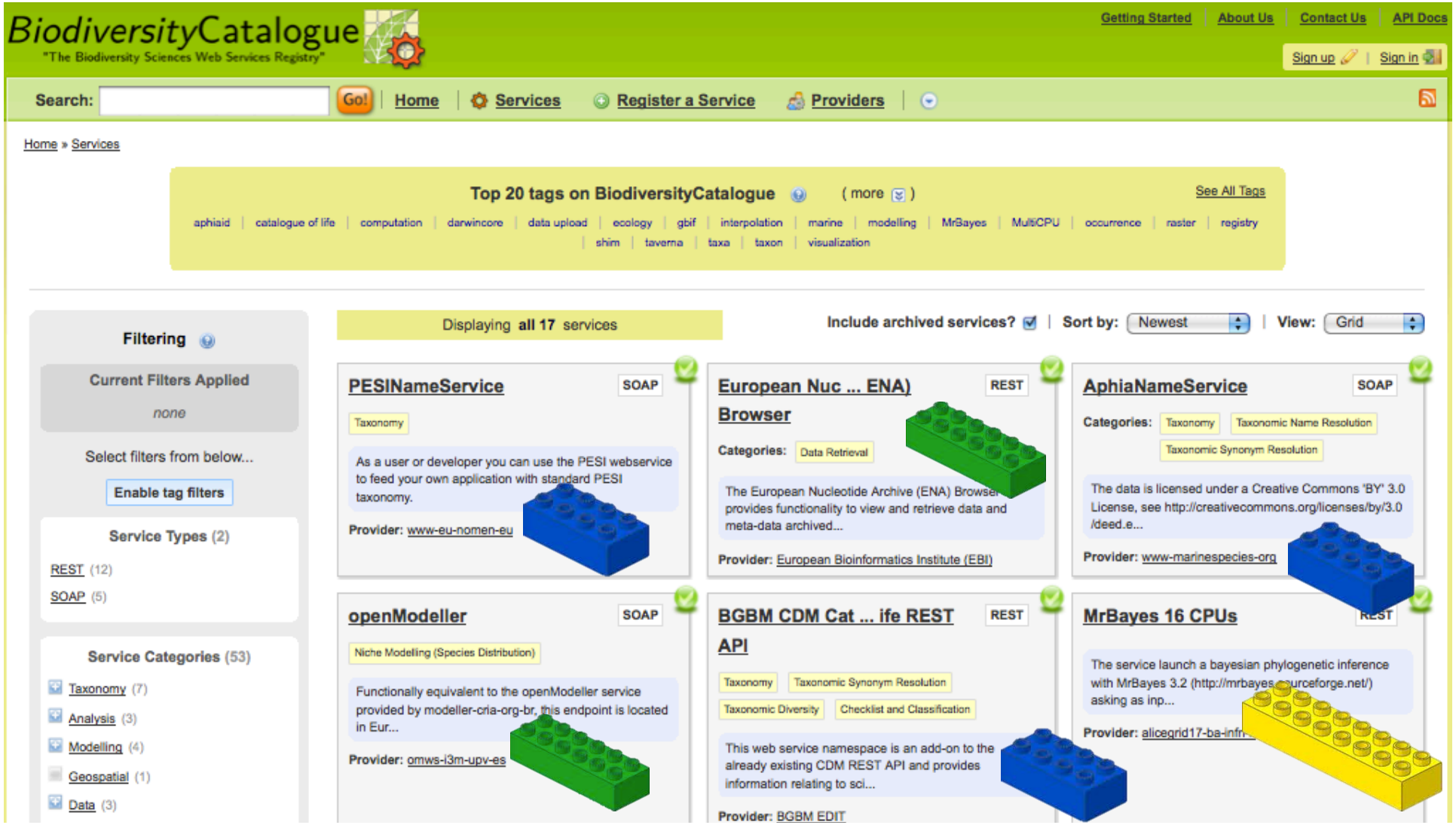
Provide (web)services for the interdisciplinary analysis of biodiversity

Provide analytical pipelines (workflows) based on these services

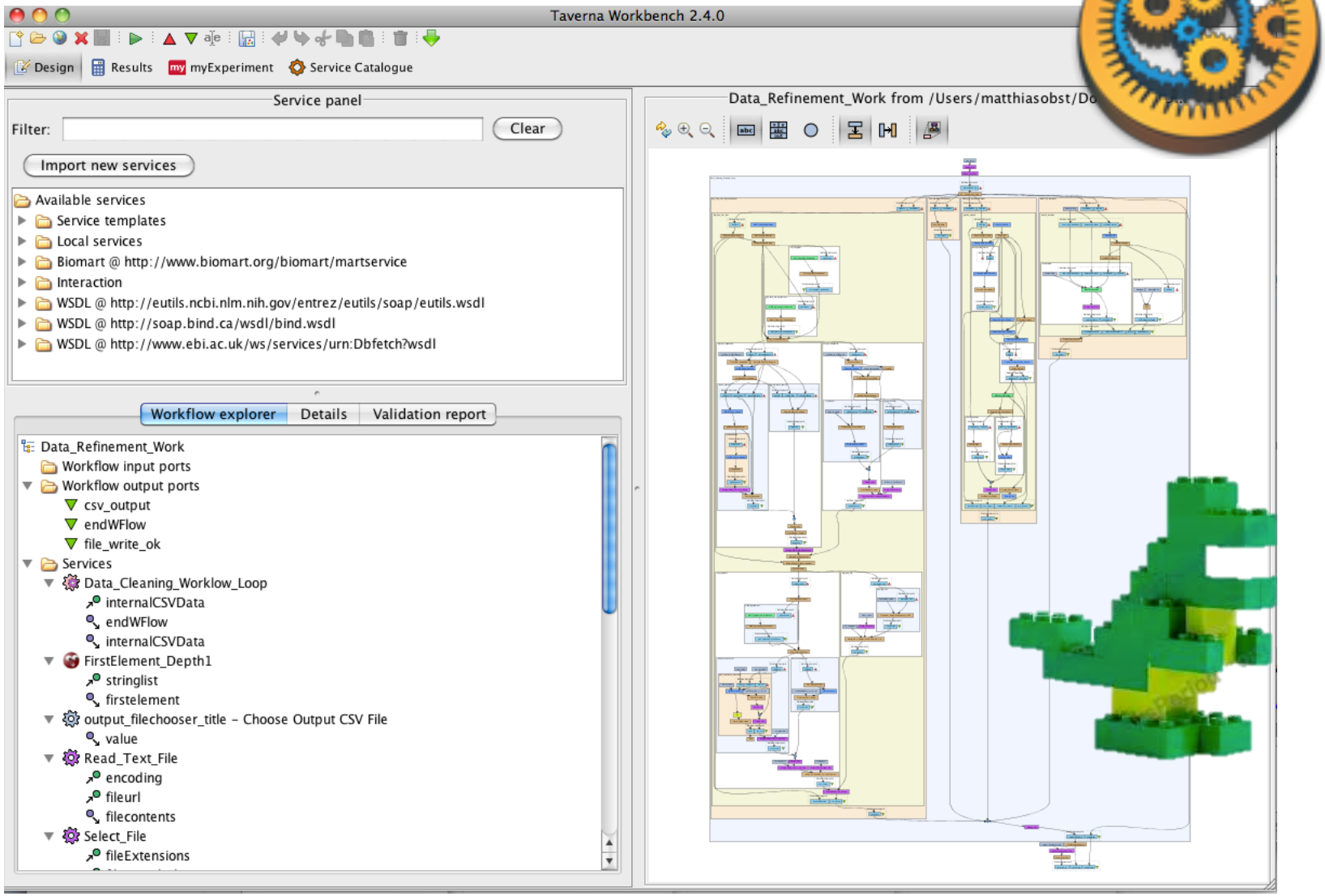



Workflow uses Web Services
WS1
WS2
ENM
BLAST
GIS
Occurrence
Shim
Cluster
Service Network
Web Services deployed on different computing infrastructures
Grid
Cluster
Cloud

Access web-services at *biodiversitycatalogue.org*

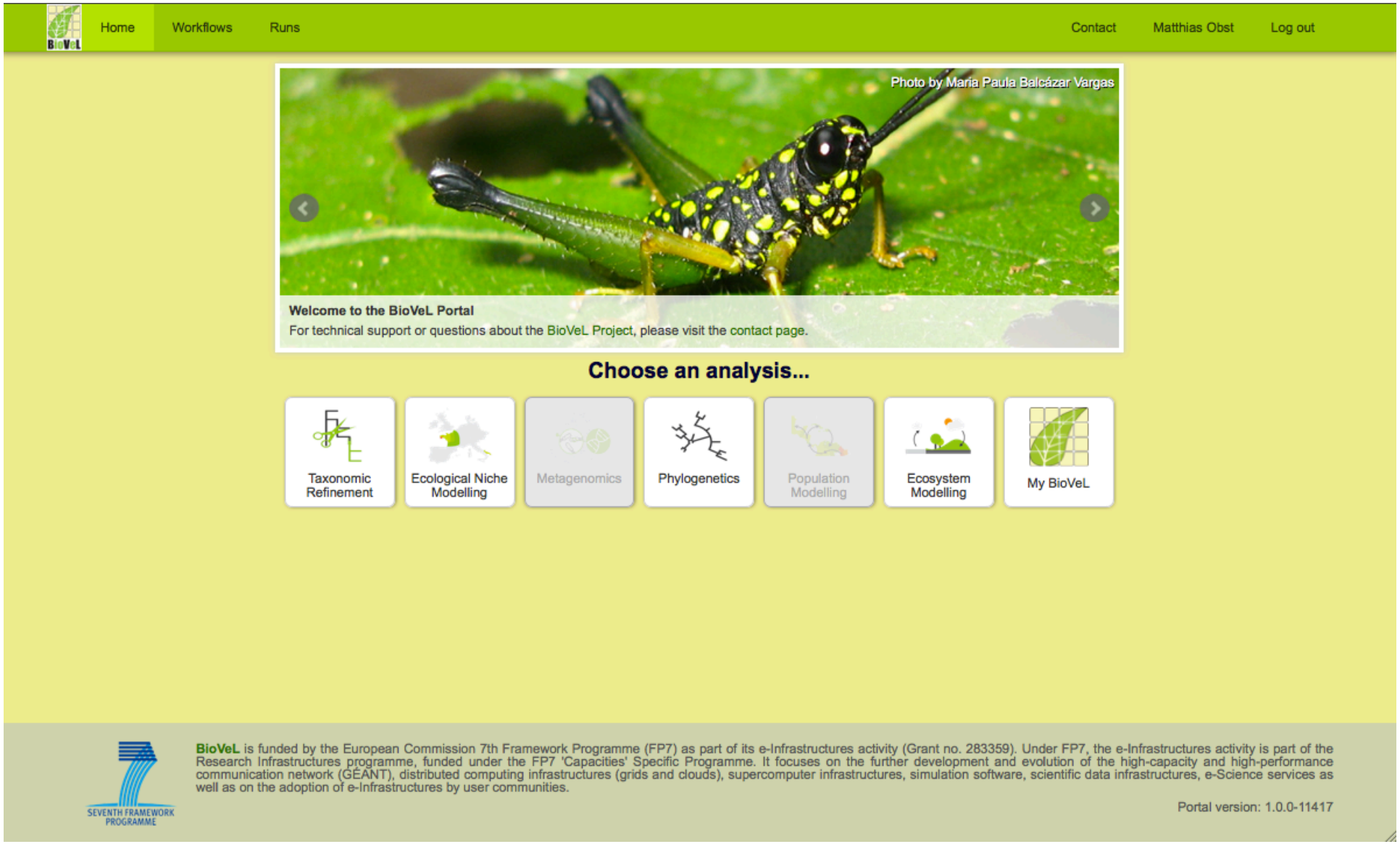


Build your own workflow on the Taverna workbench



Ecological niche modelling workflow

Running workflows from the portal



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

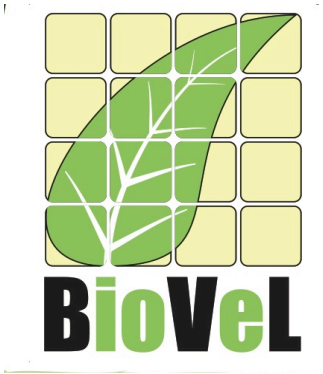
Statistics

Catalogue of Life

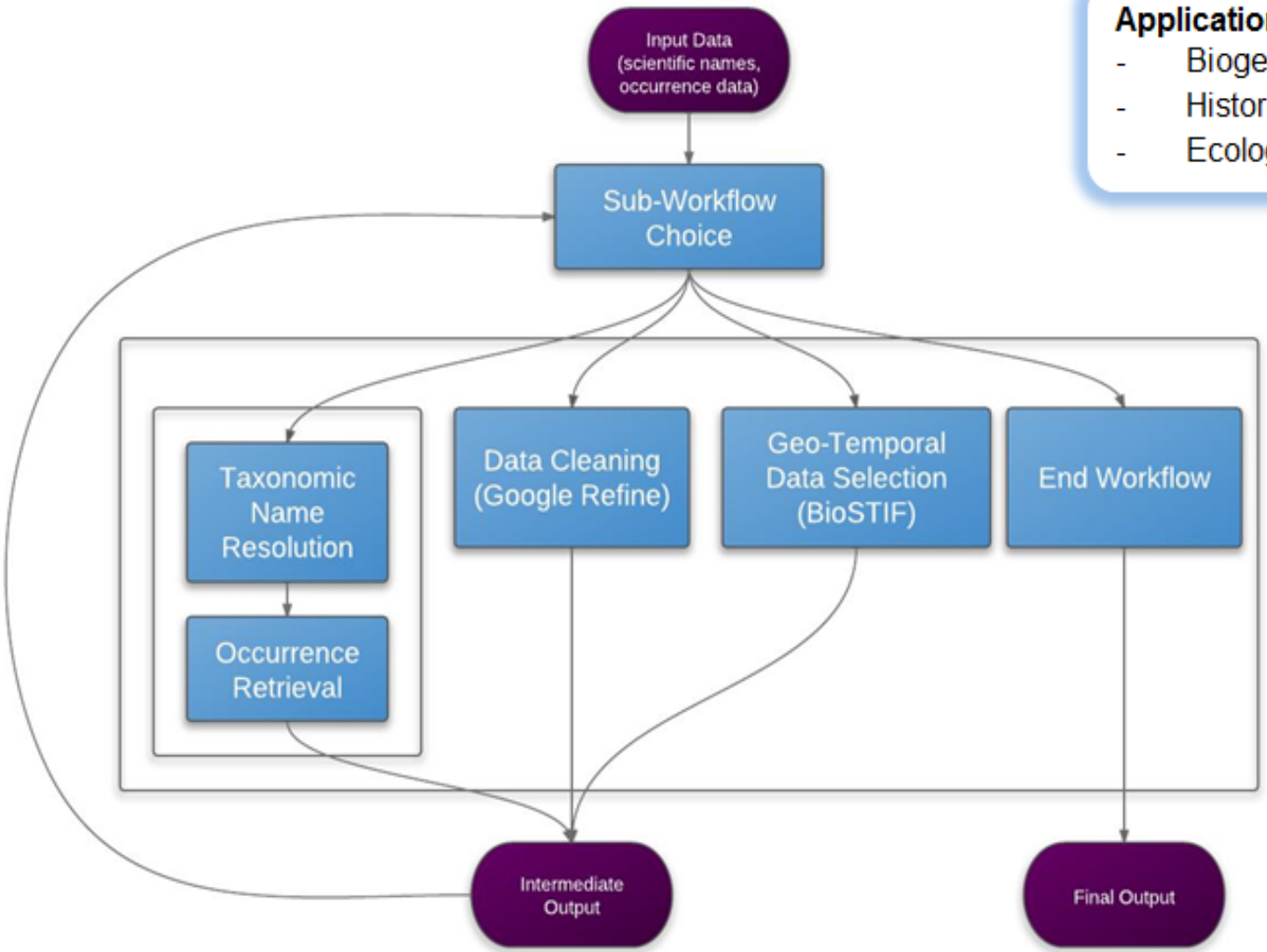
OpenRefine

BioSTIF (GIS)

Introduction to the Data Refinement Workflow and scientific applications



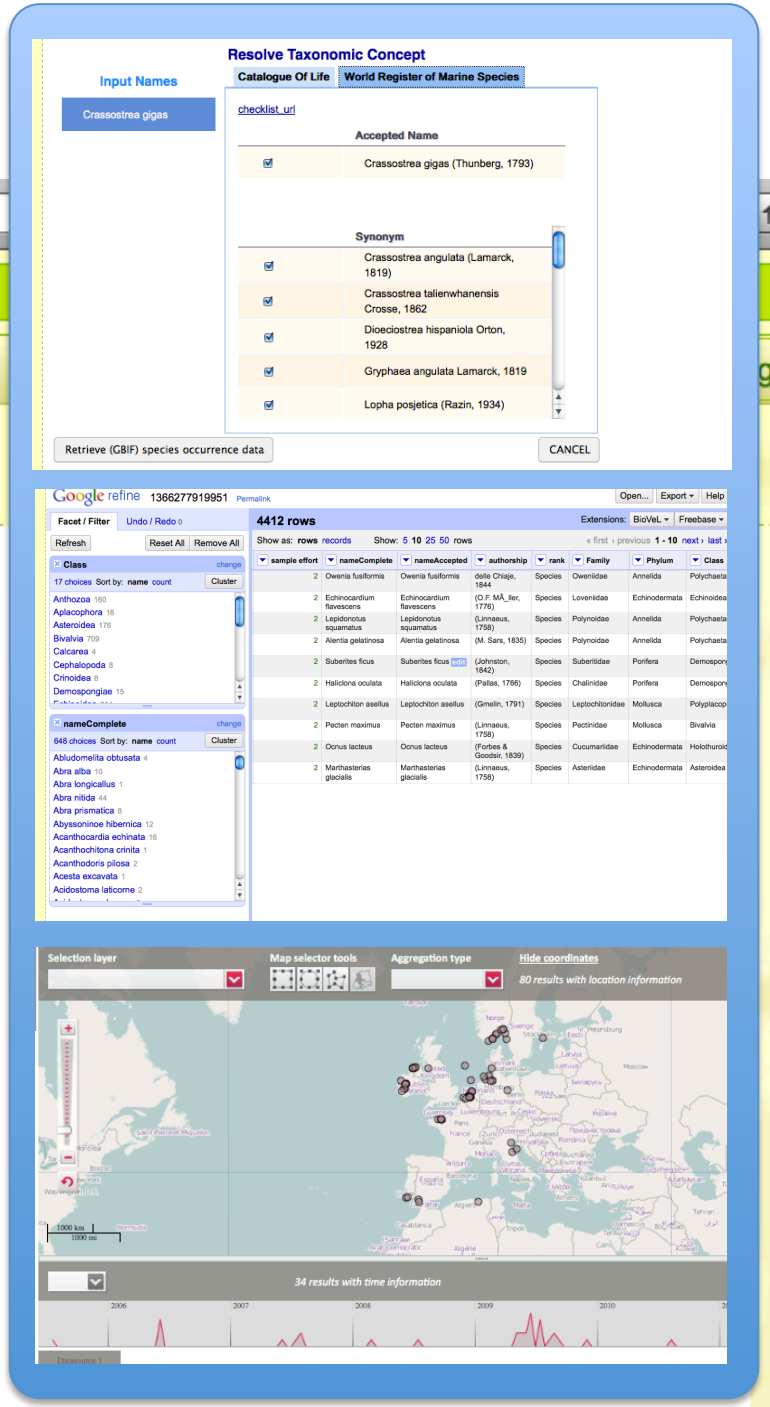
Data Refinement Workflow



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

Historical analyses of biodiversity

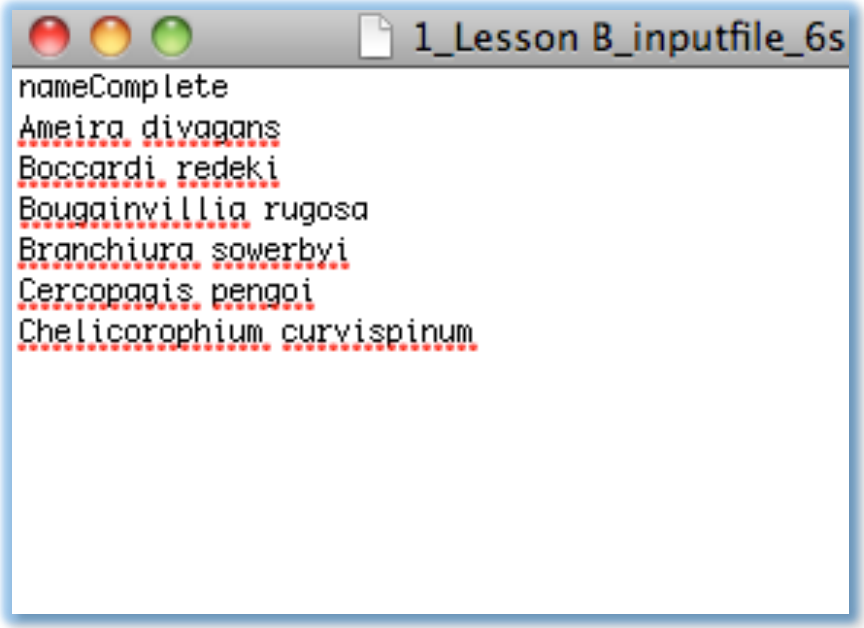
Register on the portal

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



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

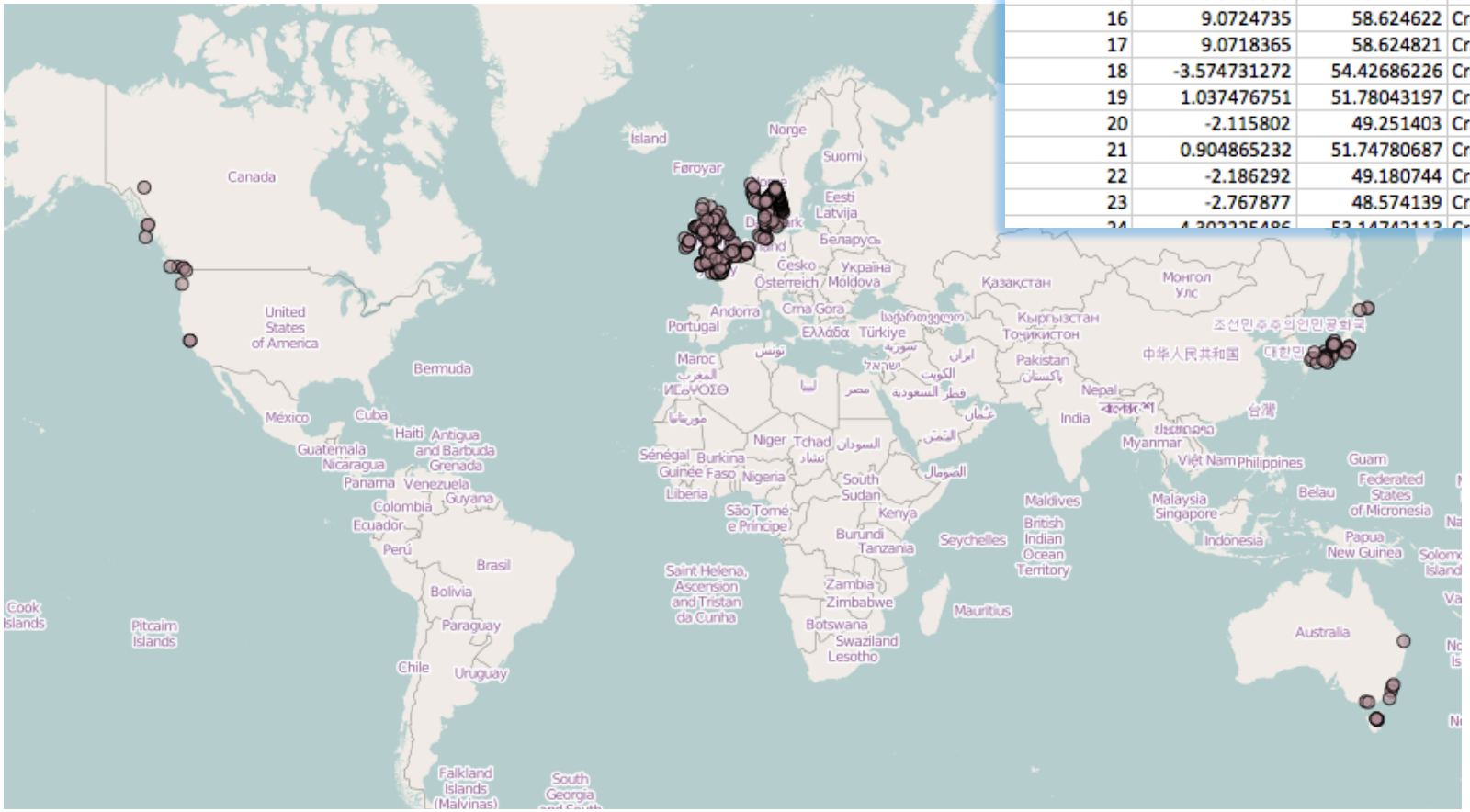
Lunch

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

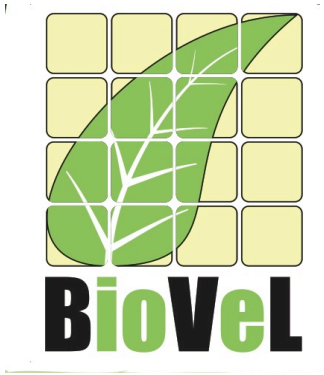
ENM input files with 4 columns

- 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



Introduction to Species Distribution Modeling



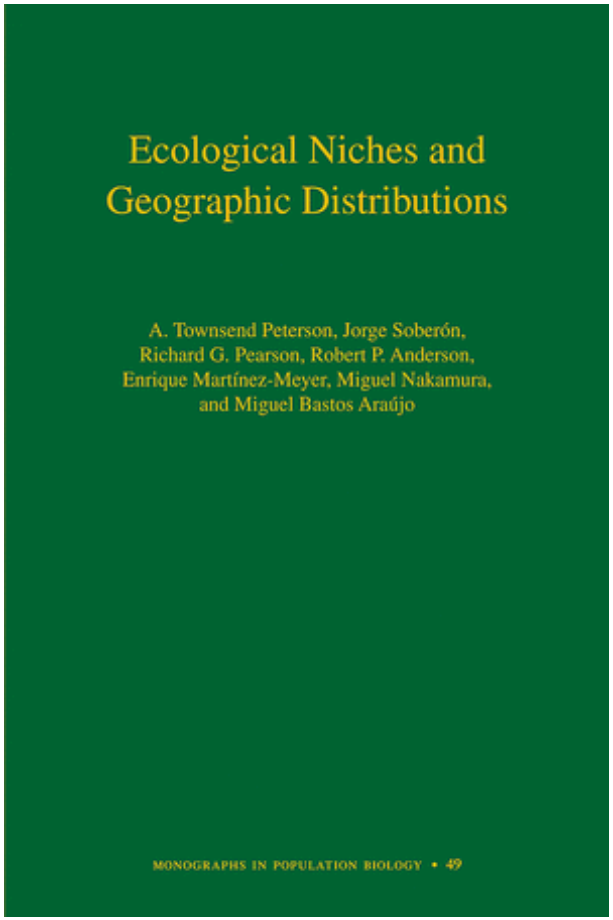
Literature

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.

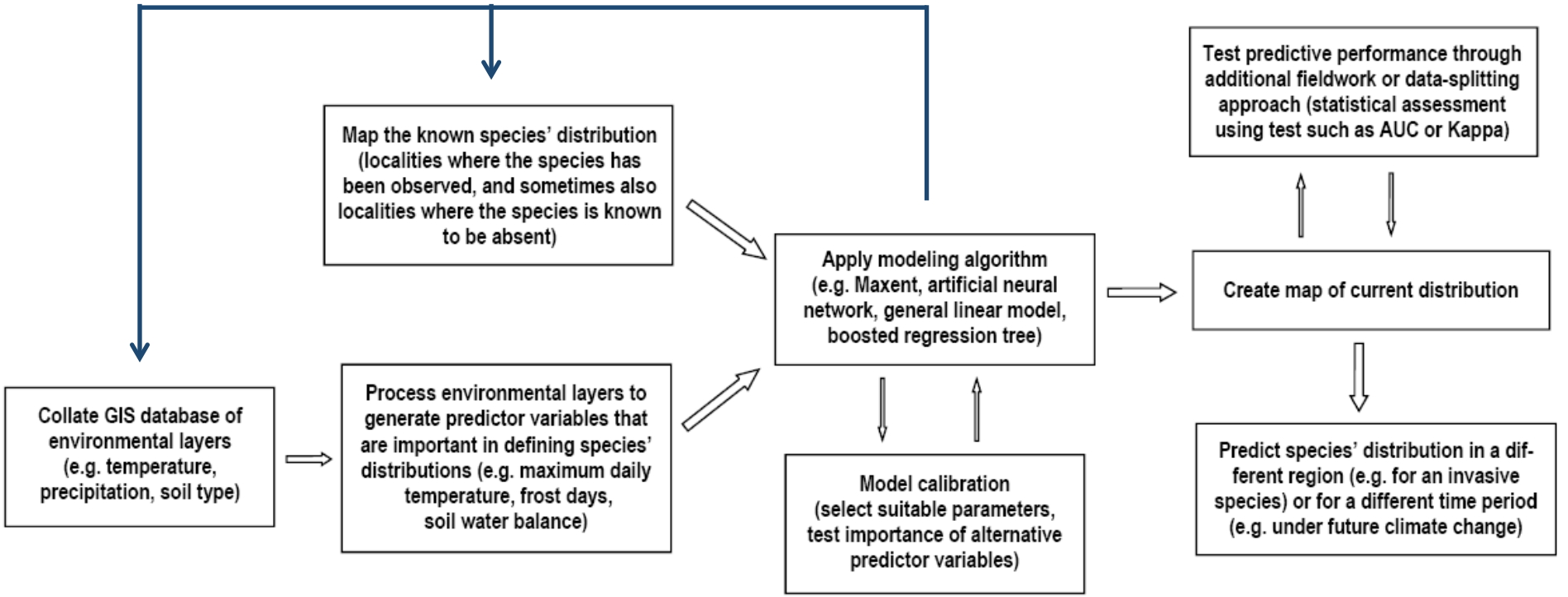


Model types

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

Cuddington et al. (2013) Ecosphere

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.

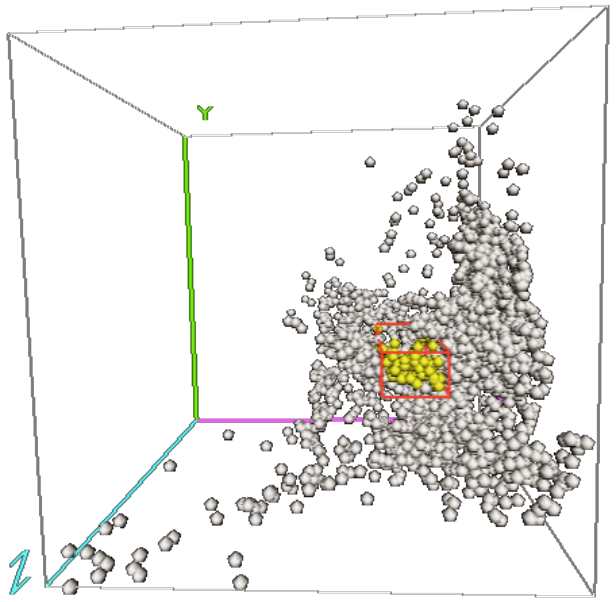
The fundamental niche may be thought of as an '*n*-dimensional hypervolume', every point in which corresponds to a state of the environment that would permit the species to exist indefinitely (Hutchinson, 1957)

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

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

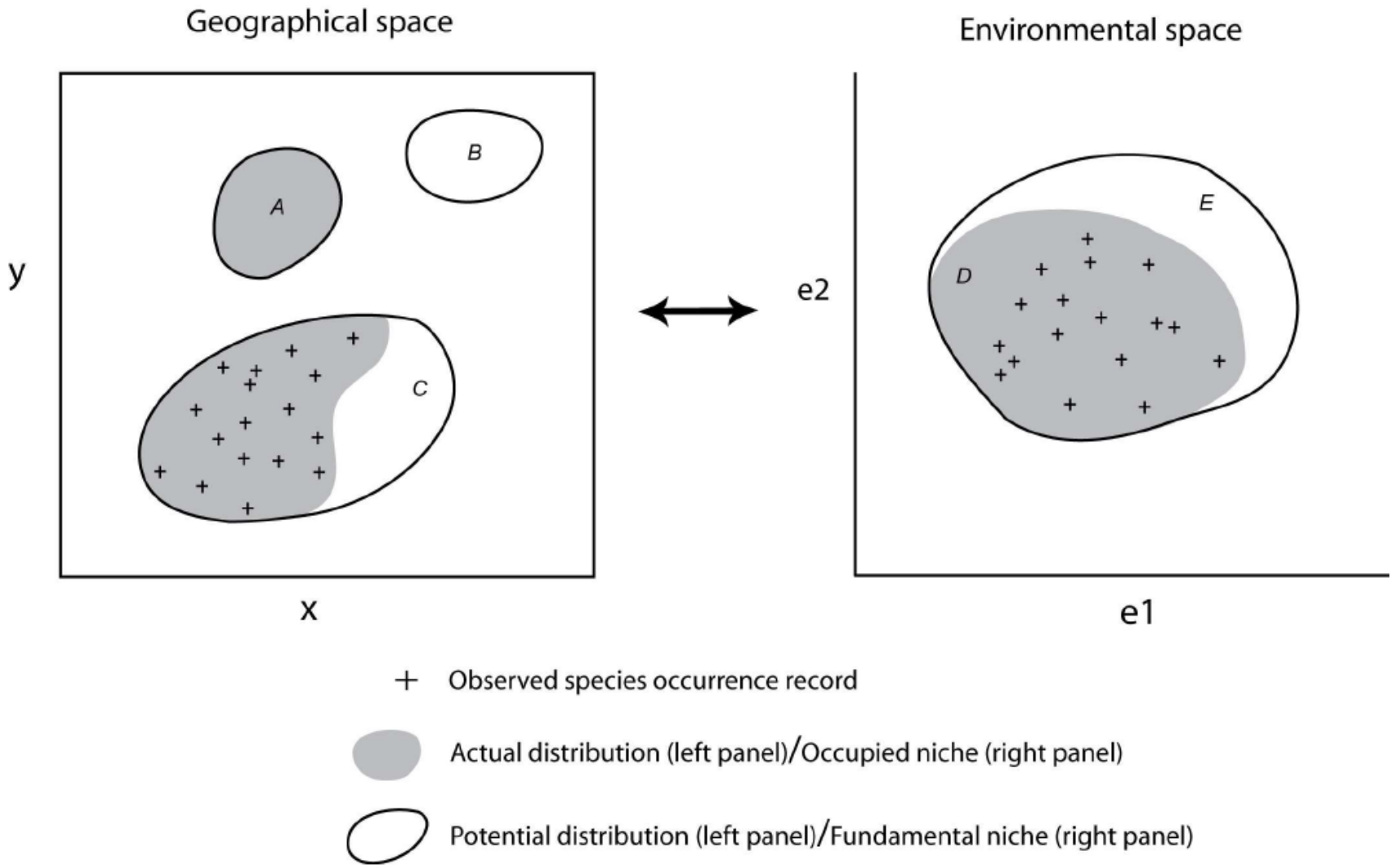
Constrains that influence the potential from actual distribution

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



Fundamental niche depicted in environmental-space

Geographical versus environmental space

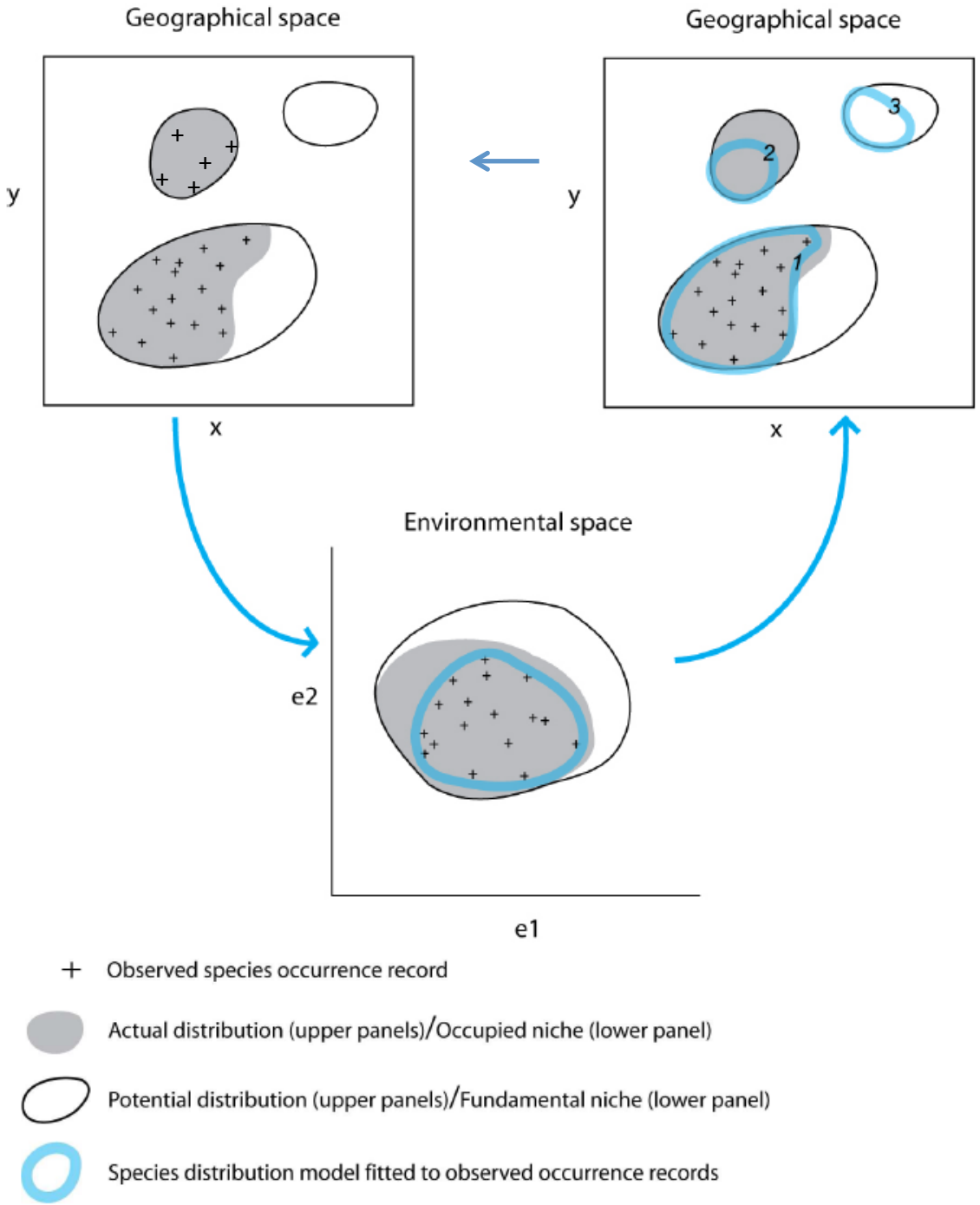


Species' distribution models may identify

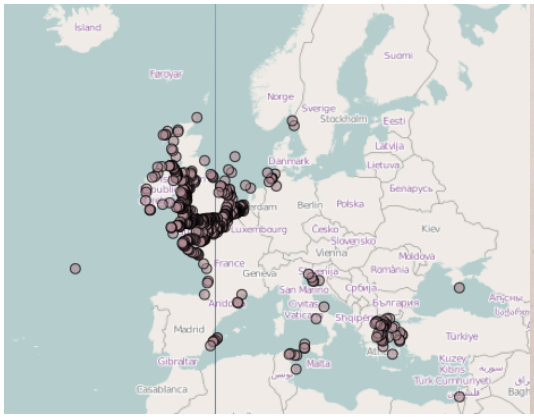
1) **Protection areas,** the area around the observed occurrence records that is expected to be occupied (area 1)

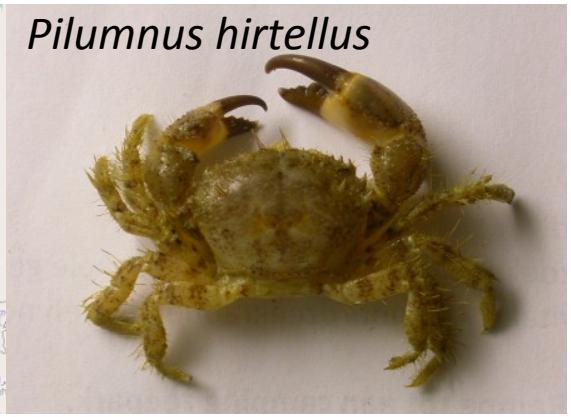
2) **Unobserved populations,** currently unknown distributions (area 2).

3) **Invasive or re-introduction areas,** potential distribution that is not occupied (area 3)



Species data





Enclosed sea problem (Ready et al., 2010)

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

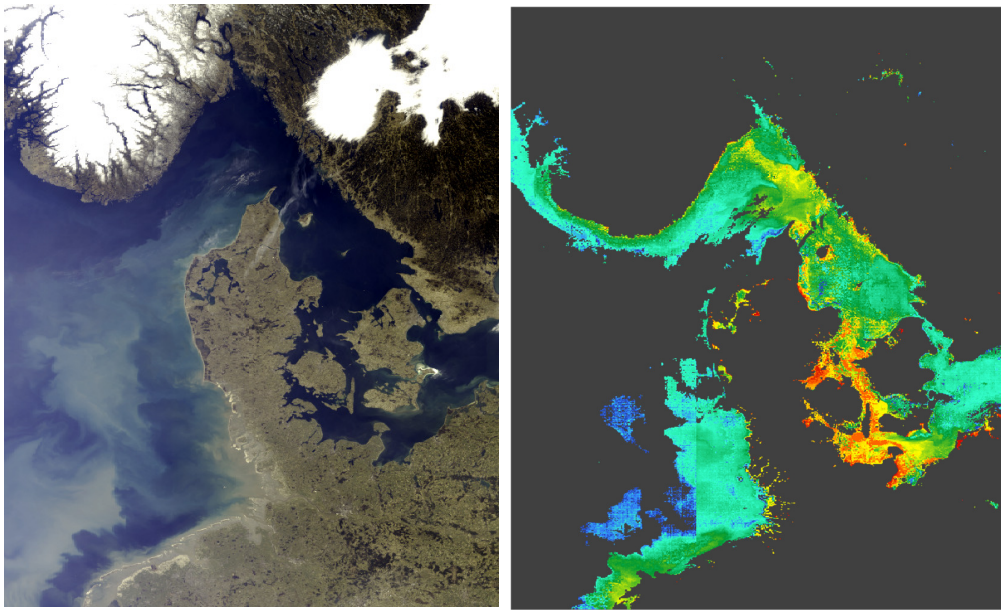
Species data sources

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

Sources of errors

- Are the species records sustained obervations (sink vs source)
- Incorrect identification
- Innacurate 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%.

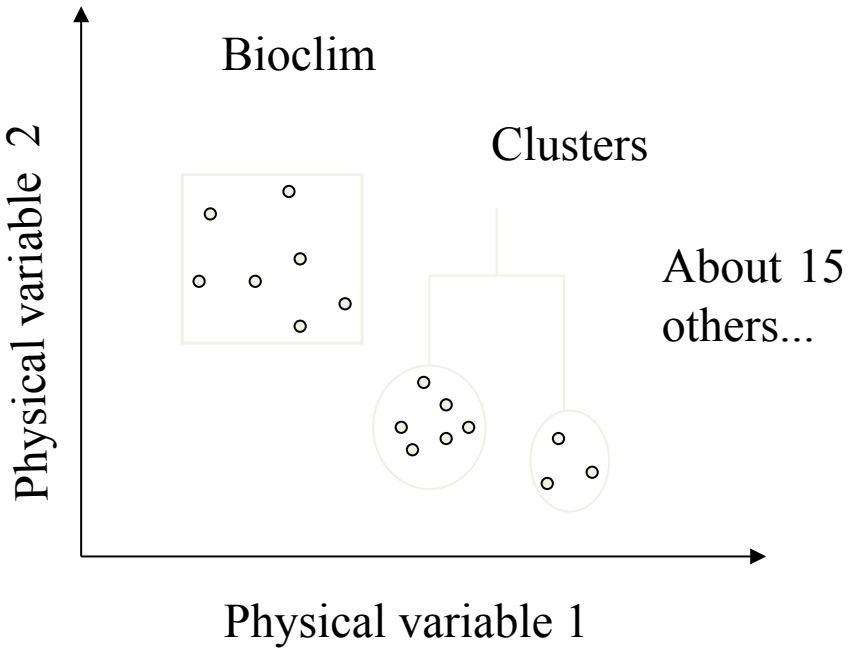


Table 4. Modelling methods implemented.

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

Elith & al. 2006

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

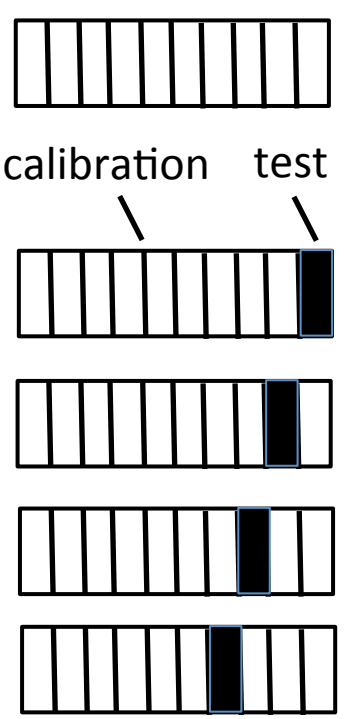
Bootstrapping

- 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**

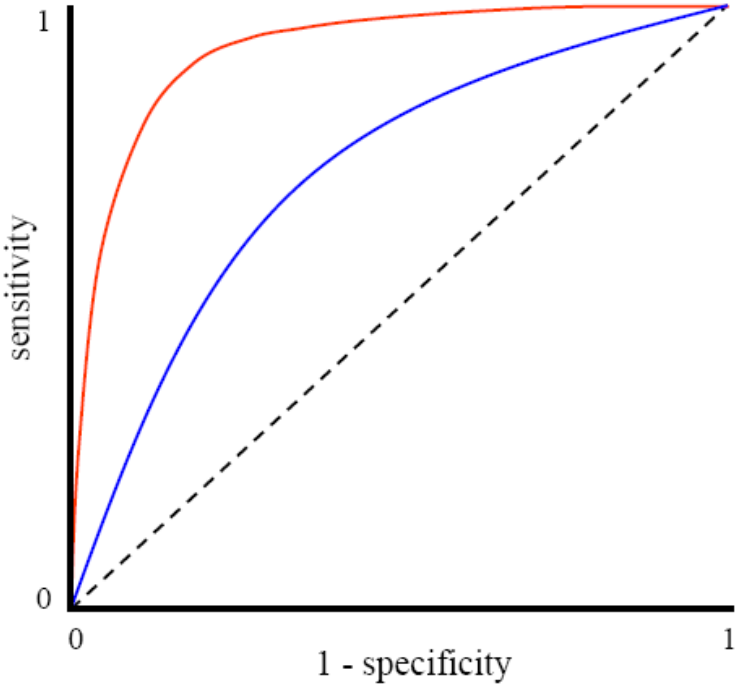
- data are split into *k* parts of roughly equal size and each part is used as a test set with the remaining (*k*-1) sets used for model calibration.

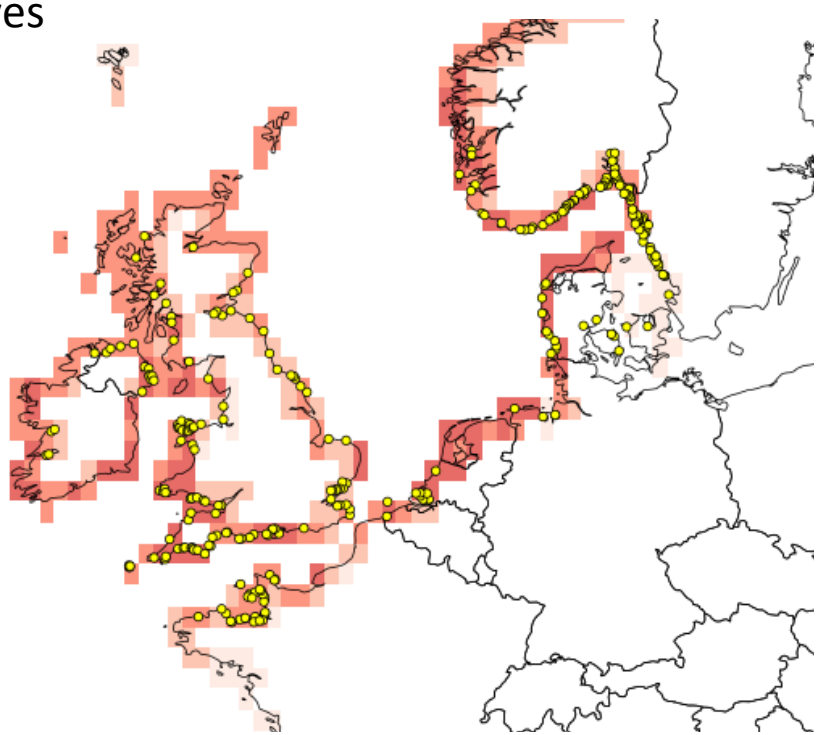
10-fold partitioning



Assessing predictive performance - validation statistics

Receiver Operating Characteristic (ROC) Curves





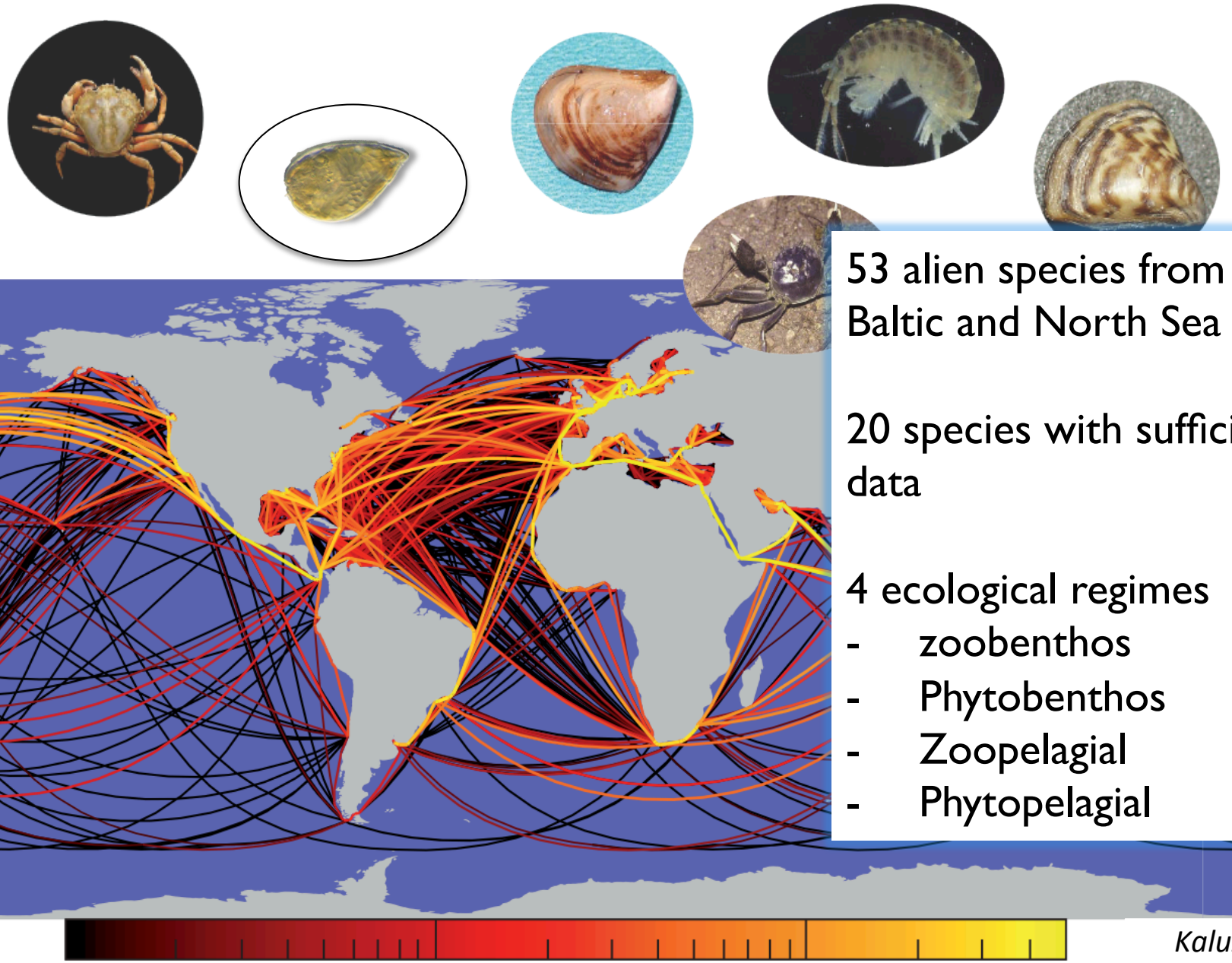
AUC (area under the ROC curve)

- 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
- Phytopelagial

Kaluza et al (2013)

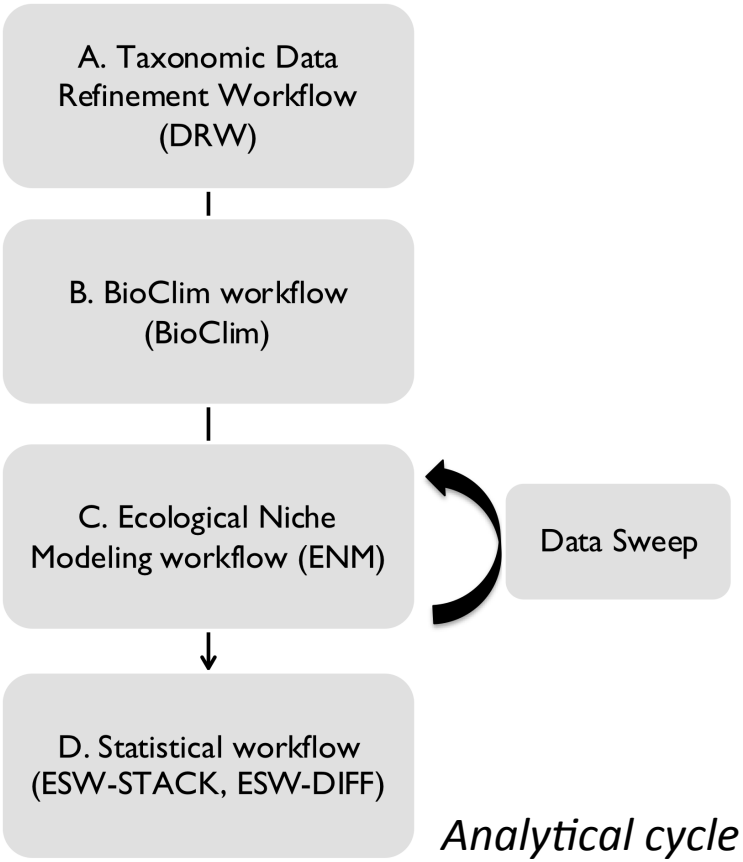
<10 20 50 100 200 500 1000 2000 >5000 journeys

Data discovery

Occurrence records for 31 species

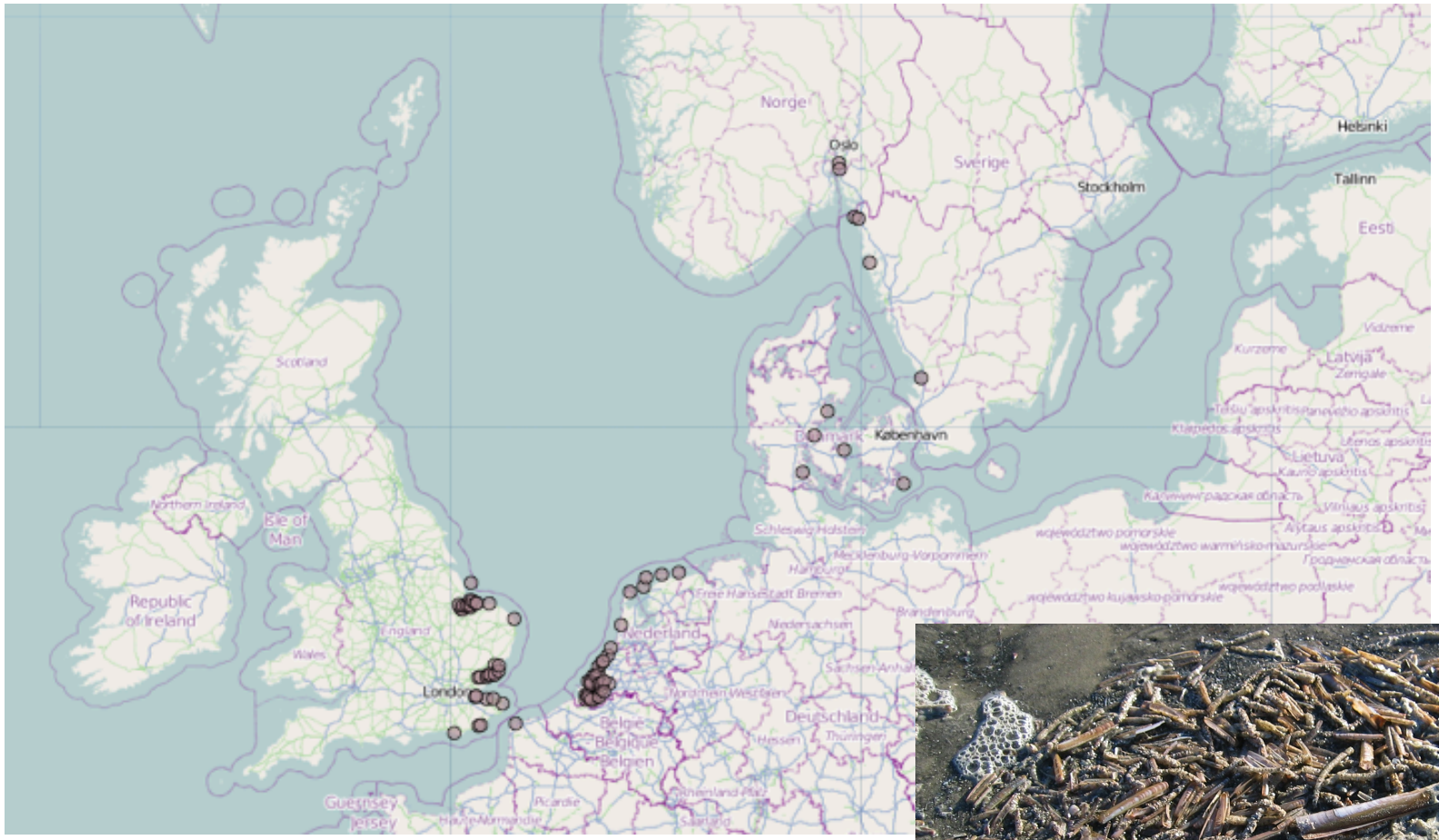
Sources

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



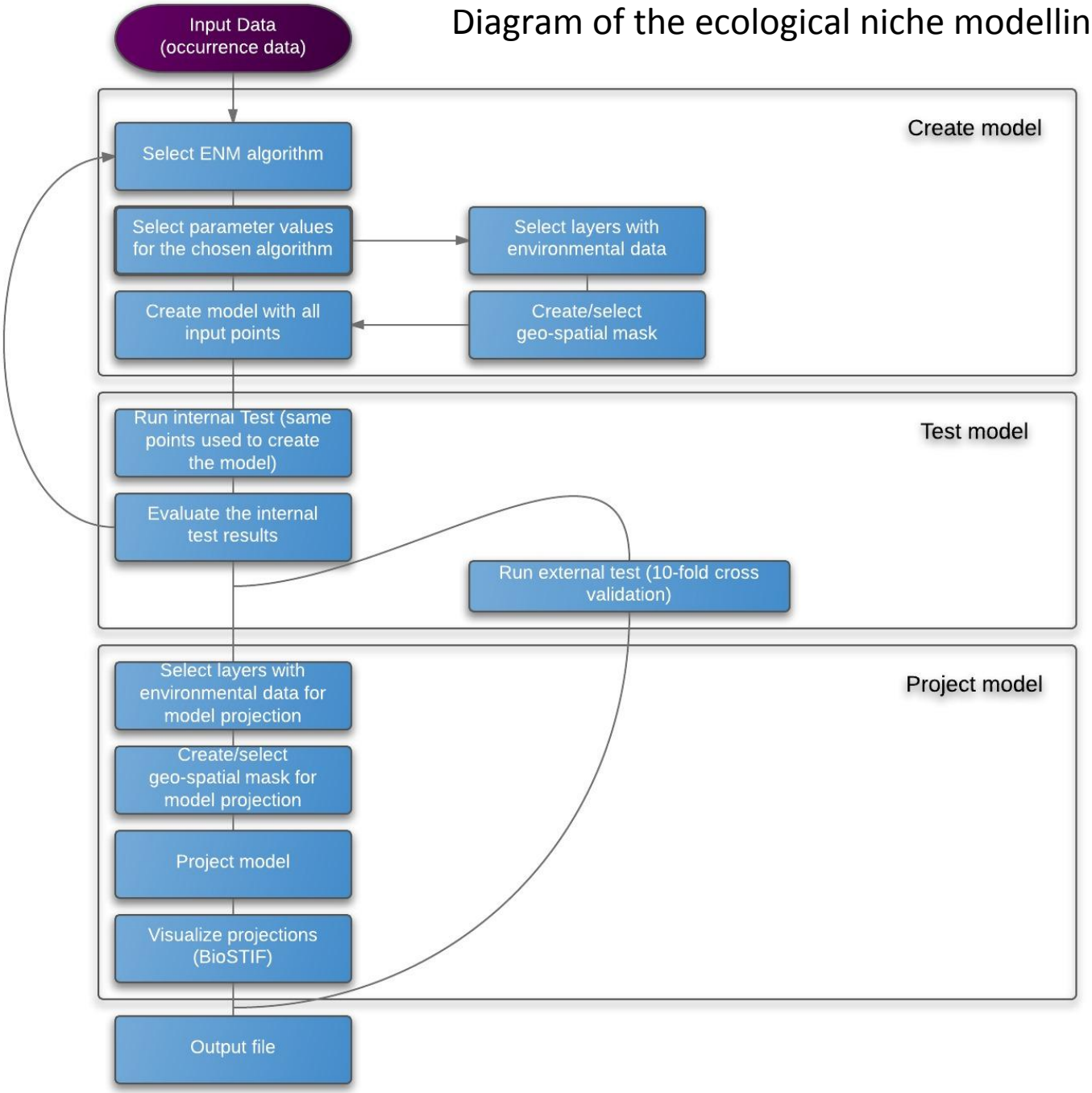
Analytical cycle

Species, Authors	Eco-group	Origin	Invasion Path	Introduction/ First observation		Total # of records	References of Occurrence data
				North Sea	Baltic Sea		
Austrominius modestus (Darwin, 1854)	ZB	S Pacific	S	1953	-	709	GBIF (709)
Crassostrea gigas (Thunberg, 1793)	ZB	NW Pacific	A, ST	1991	1980s	967	GBIF (967)
Ensis directus (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)
Eriocheir sinensis 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)
Gammarus tigrinus Sexton, 1939	ZB	NW Atlantic	ST	1965	1975/1985	1648	GBIF (1566), Berezina 2007 (2), Guszka 1999 (44), Jazdzwski et al. 2004 (6), Kotta et al. 2013 (26), Strode et al. 2013 (4)
Marenzellaria *viridis* (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)
Mytilopsis leucophaeata (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)
Pilmnus hirtellus (Linnaeus, 1761)	ZB	NW Atlantic	S	-	2004	1270	GBIF (1258), Berggren 2012 (10), www.frammandearter.se (2)
Potamopyrgus antipodarum	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

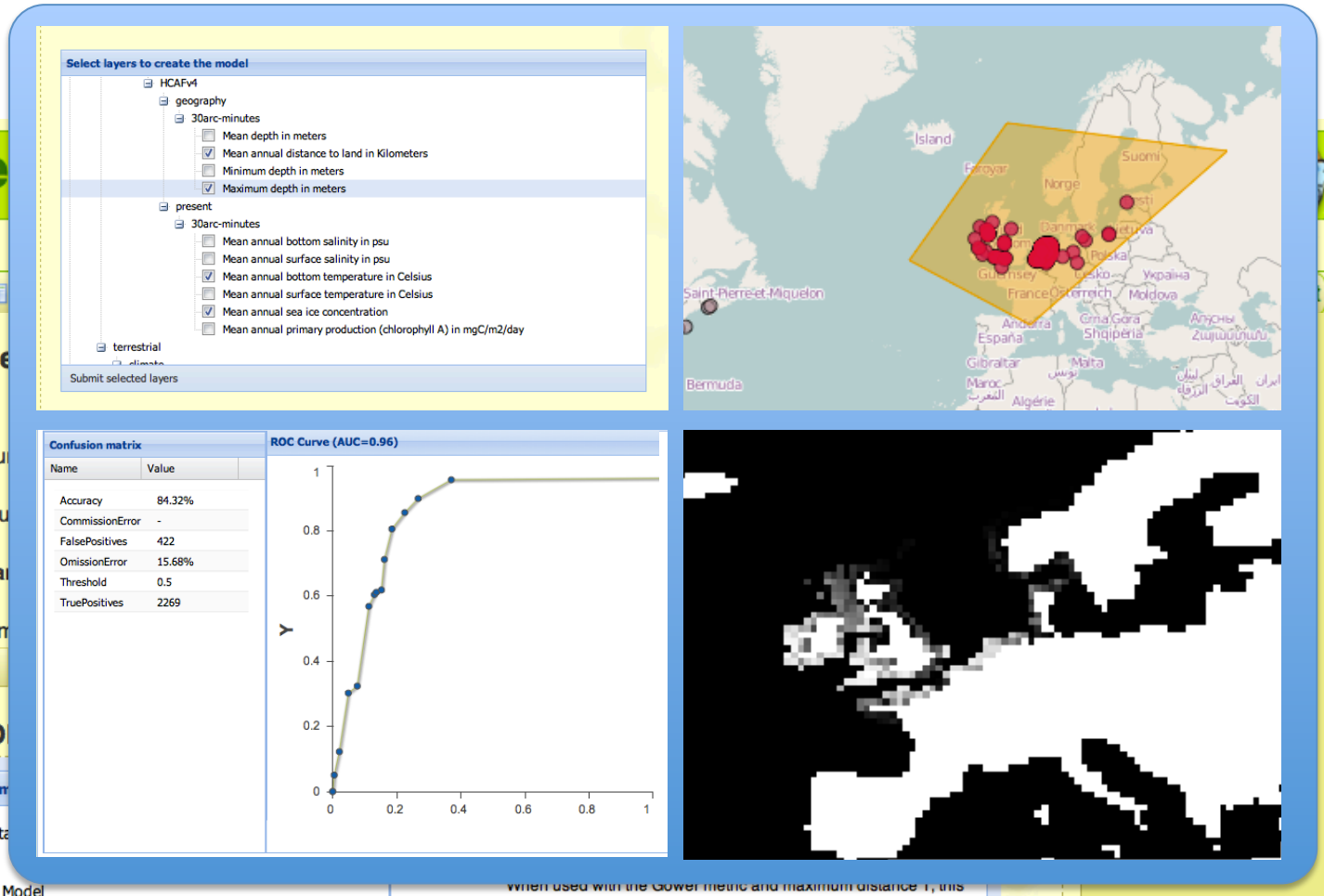
Test model:

- 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)



BioVeL Tave

BioVeL

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

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

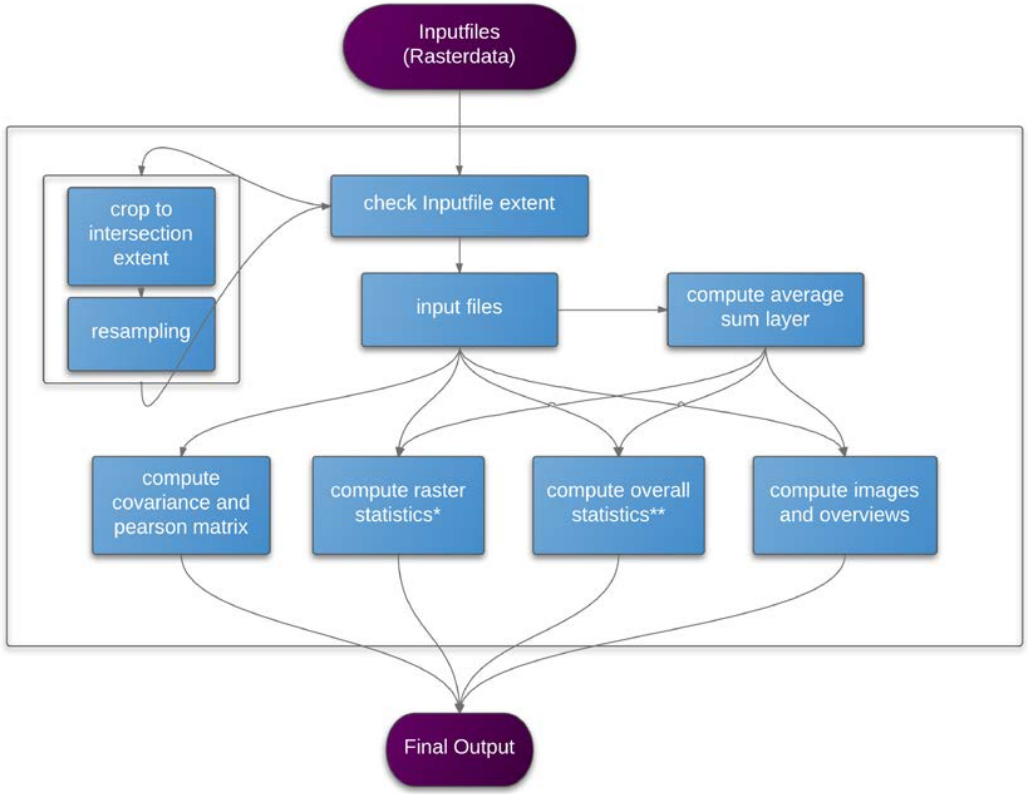
Bibliography Carpenter G, Gillison AN, Winter J (1993) DOMAIN: A flexible modeling procedure for mapping potential distributions of animals and plants. Biodiversity and Conservation 2: 667-680. Farber O & Kadmon R 2003. Assessment of alternative approaches for bioclimatic modeling with special emphasis on the Mahalanobis distance. Ecological Modelling 160: 115â130.

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

ENM Statistical Workflows

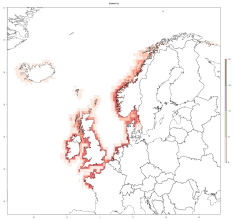
1) ESW DIFF
2) ESW STACK
3) ESW SHIFT

ESW STACK workflow using R



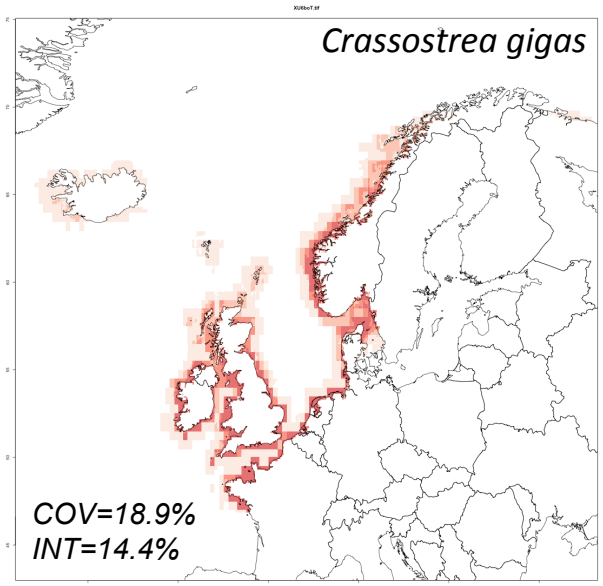
*computed raster statistics: number of cells, mean, median, coefficient of variation (cv), standard deviation (sd), min, max

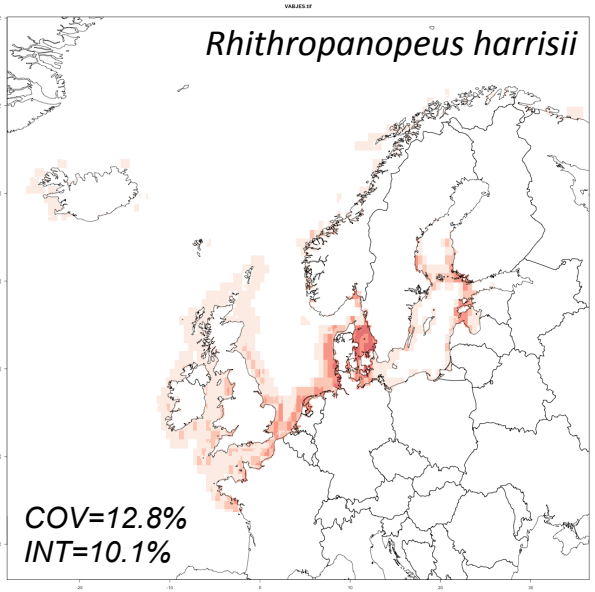
**computed overall statistics:
- overall coverage as the percentage of raster cells with values >0,
- overall intensity as the sum of all valued cells divided by the number of raster cells,
- differences between the coverage and intensity between the input files

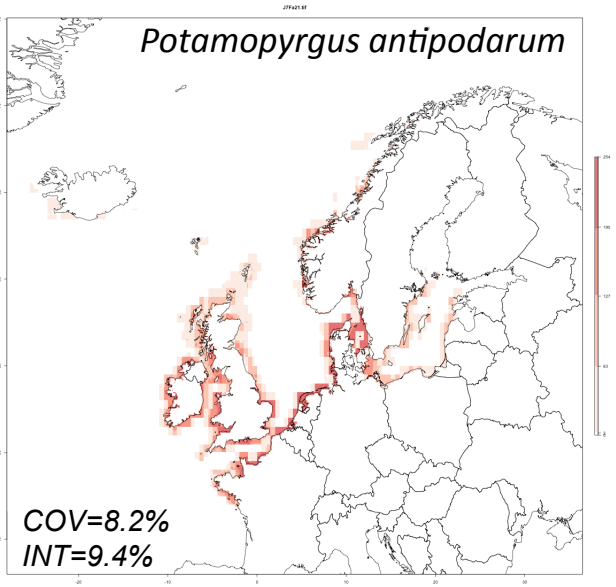


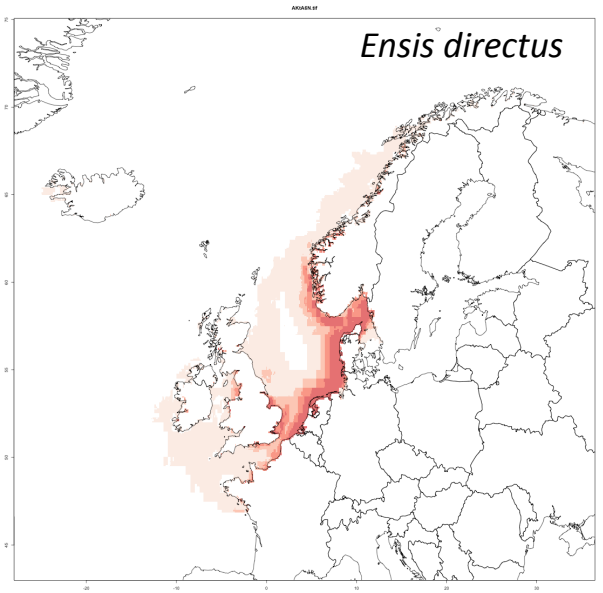
XX	Number of raster cells	Mean of all raster cell values	Median of all raster cell values	Coefficient of Variation
currentLayer	643104	2.889023	0	472.7624667
predictionLayer	643104	2.8119792	0	462.6982272
diffLayer	643104	-0.077043835	0	-11966.1249

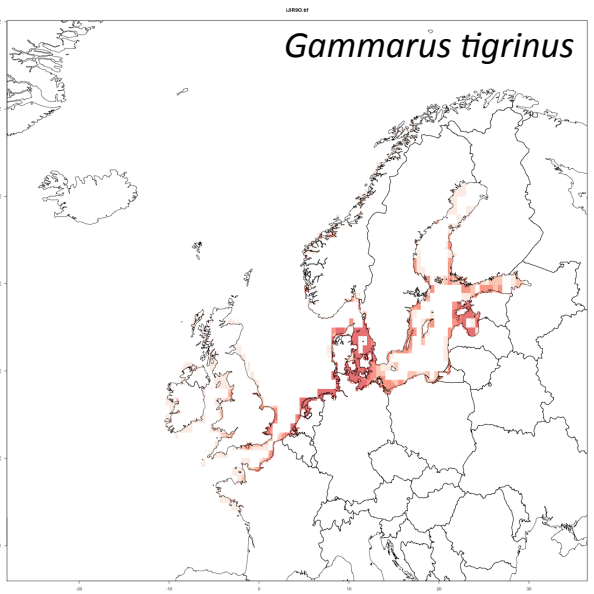
Invasive heatmaps

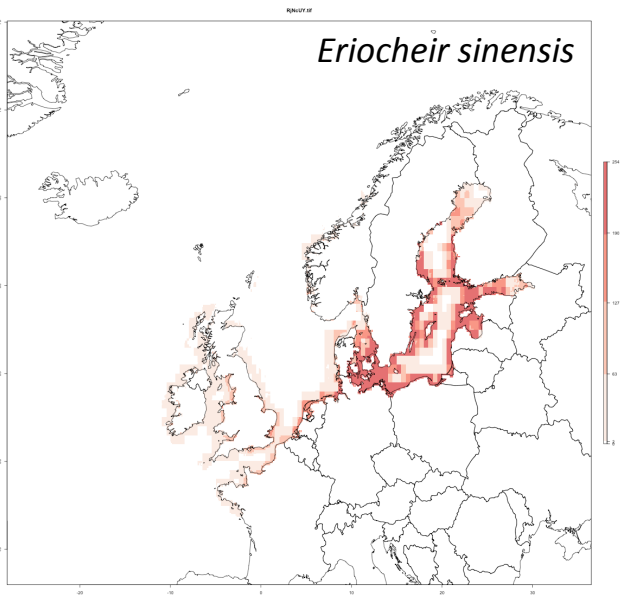




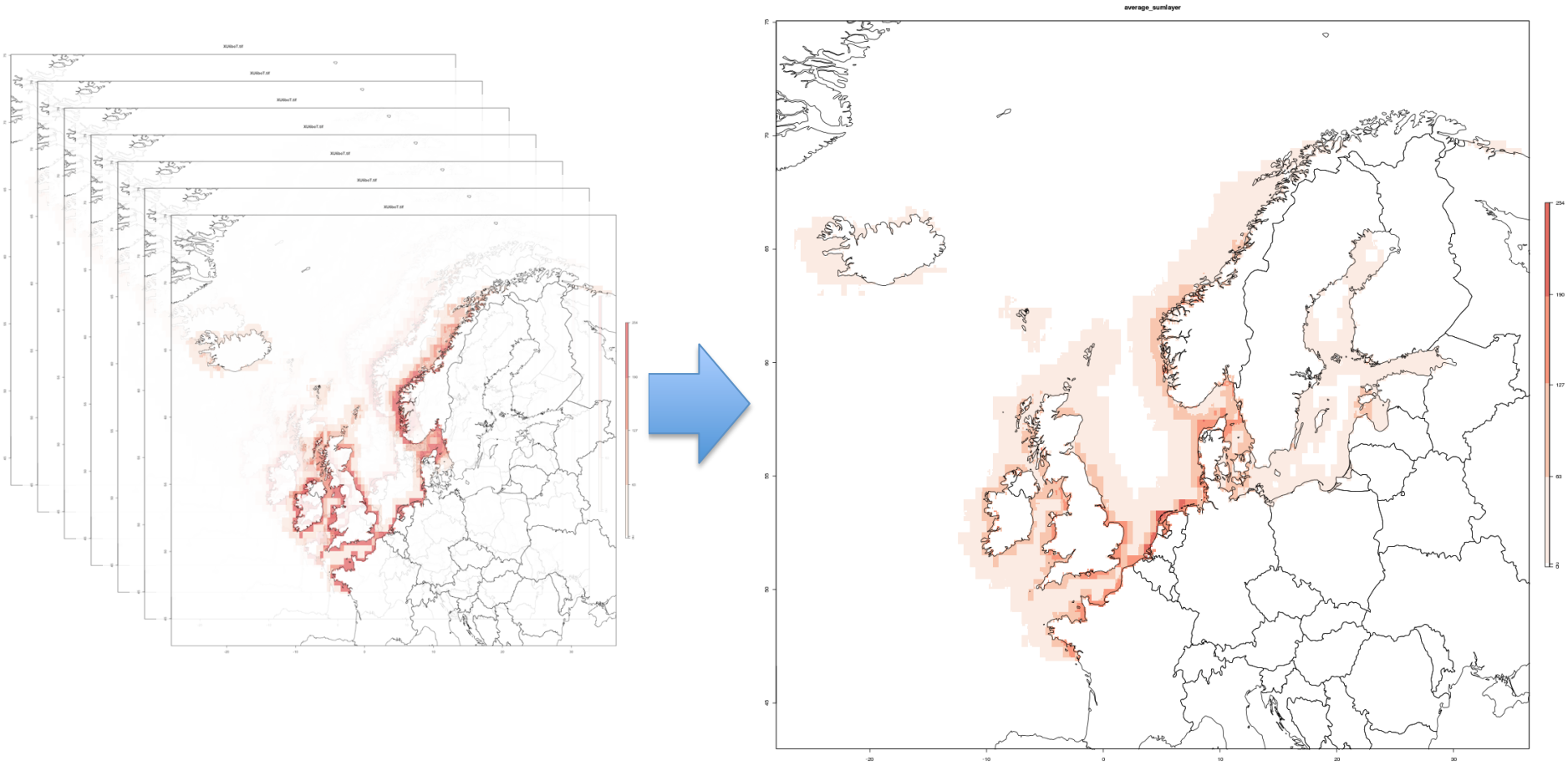






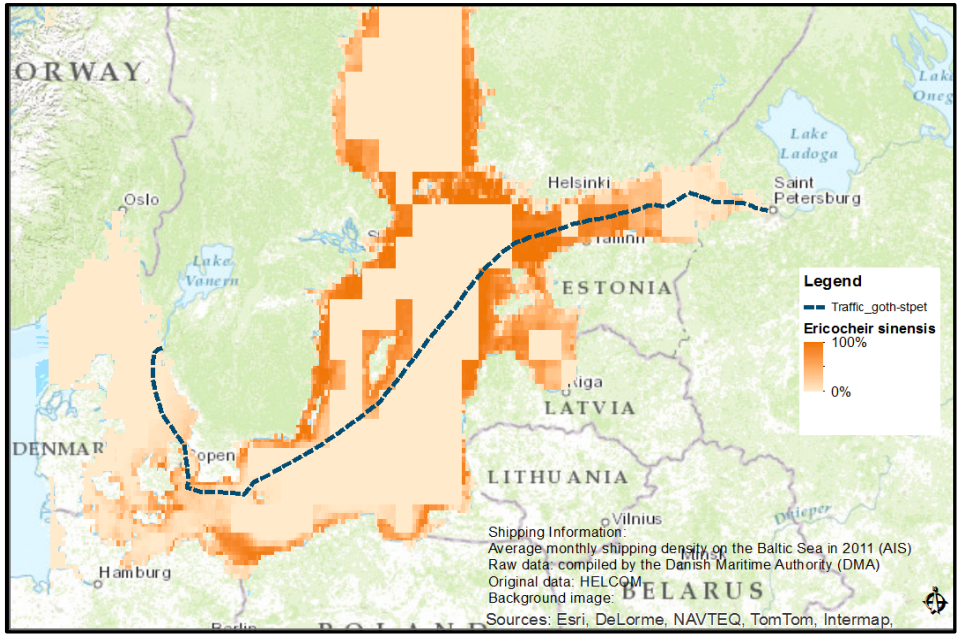


Accumulated invasive potential for ecological groups

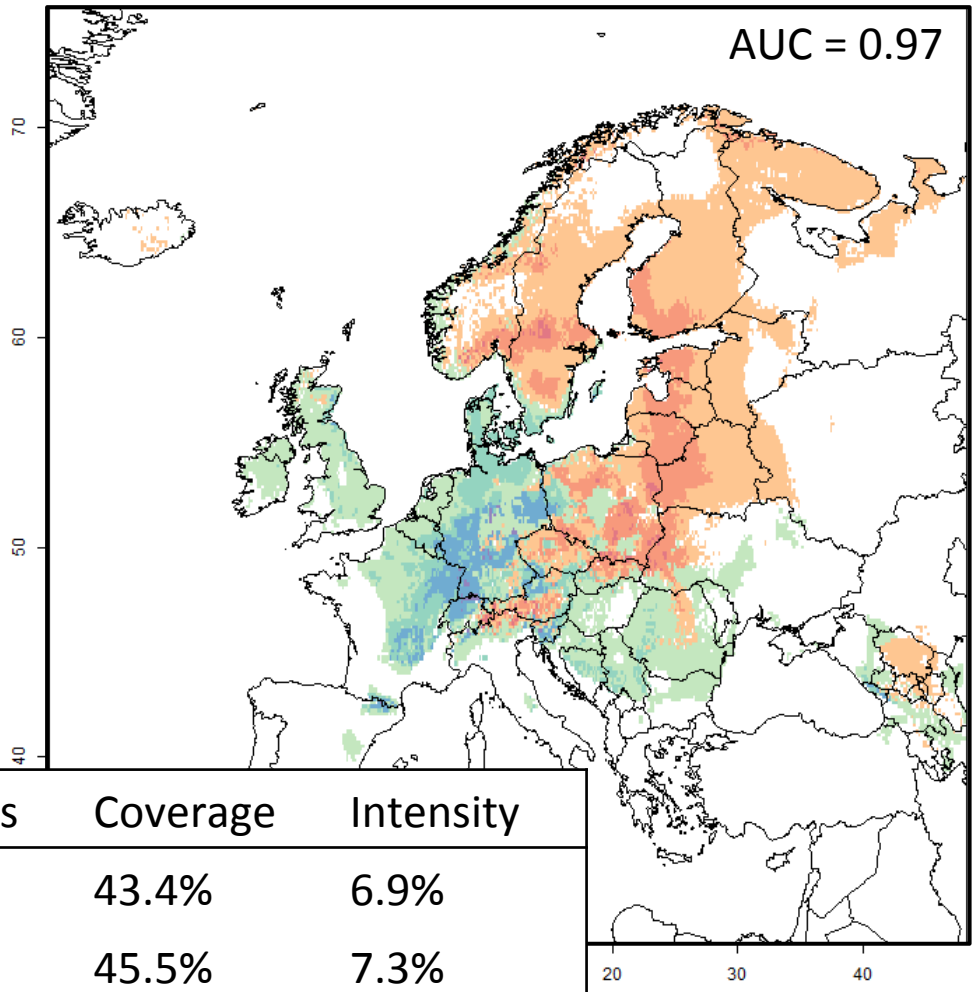


Stack of macrozoobenthic invasion heatmaps

Accumulated invasive potential



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



Projections	Coverage	Intensity
Today	43.4%	6.9%
2050	45.5%	7.3%
Difference	2.1%	0.4%


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

Create model

Algorithm: Environmental distance

Parameter values: 2, 0, 1

Environmental layers:

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

Geographic mask:

- GBIF_training_mask_1800arcsecs_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