Biosecurity
COMMONS

Species Distribution Modelling – Quick Start Guide

Last modified: 4 November 2024

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Species Distribution Modelling

Abiotic barriers that limit a species' potential distribution vary widely in nature and scale. They can include factors such as climate, disturbance regimes, and terrain attributes. On large geographic scales (e.g. global or continental), climate is believed to govern a species' potential distribution (Araújo and Rozenfeld 2014). Over the past several decades, global databases of climate and biological data have been developed, along with a wide range of statistical and mechanistic Species Distribution Models (SDMs). In invasive species management, SDMs are often parameterized using global climatic variables, the most readily available global environmental data, and are thus sometimes called "*climate suitability models*" (Camac et al. 2024). These models have become popular tools in biosecurity for quantifying potential areas of occupancy, which can inform threat prioritisation (McGeoch et al. 2016), post-border surveillance design (Camac et al. 2021, Camac et al. 2024), and estimates of expected economic impacts (Dodd et al. 2020, Stoeckl et al. 2023).

Biosecurity Commons provides users with a wide range of statistical SDM functionality that allows users to generate maps identifying where the environment may be suitable for a species based on climatic and/or habitat preferences.

Descriptions of all the SDMs can also be found on the Biosecurity Commons Support Portal.

SDM linkages to other workflows

Outputs of species distribution models can be used directly as inputs in many other workflows, such as:

- Informing abiotic layers in risk mapping
- informing suitability and carrying capacity layers in dispersal modelling
- informing occupancy layers in surveillance design

Creating a species distribution model

Step 1. Choose between Biosecurity Commons or EcoCommons model utility

When users select the Species Distribution Modelling workflow, they will be able to choose between Biosecurity Commons models and EcoCommons models (see screenshot below).

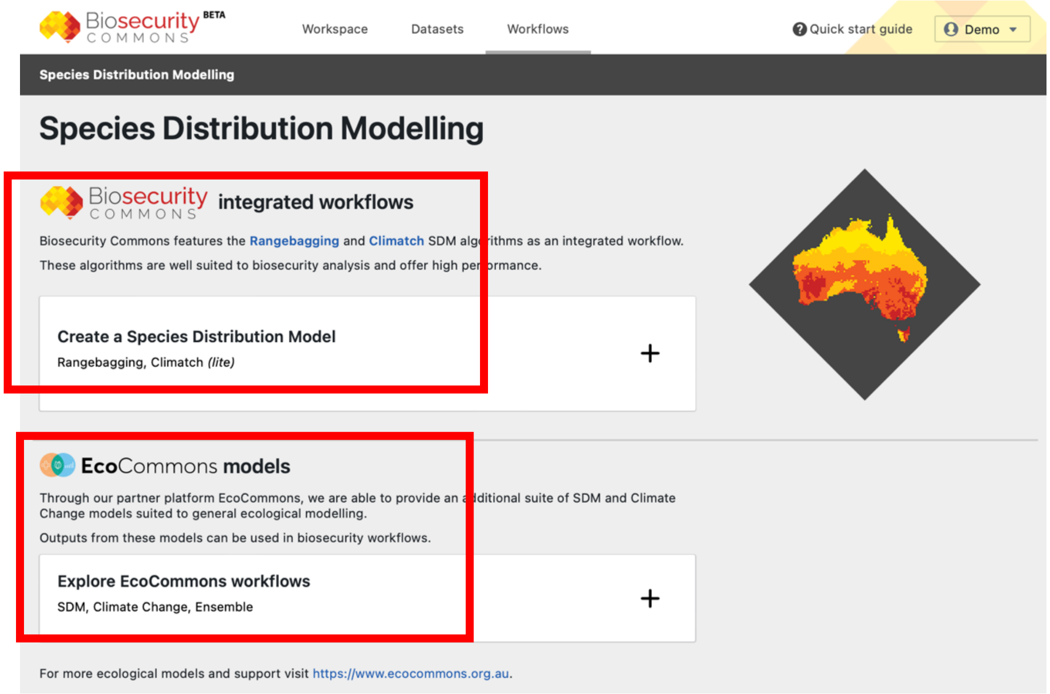
Biosecurity Commons integrated models

Biosecurity Commons provides direct integrated support for two profile (i.e. presence-only) models: Range-bagging and Climatch SDM algorithms commonly used for invasive species. These algorithms have seen recent applications to invasion biology and appear promising in the context of biosecurity. Part of their appeal is that no absences or background data are required – presence data are sufficient (Camac et al., 2020, Hill et al., 2022, Camac et al. 2024). This removes several subjective decisions required in the modelling process and focuses solely on the data commonly available for most threats – presence locations. Moreover, using Biosecurity Commons integrated models provides users with on-platform data cleaning routines powered by CoordinateCleaner (Zizka et al. 2019) – functionality not currently available on EcoCommons.

EcoCommons models

If users wish to utilise other SDM algorithms, they can directly access functionality available on our sister platform, EcoCommons. EcoCommons, a SDM specific platform, provides users with an additional 16 SDM algorithms spanning profile models (e.g. BIOCLIM), machine learning models (e.g. MaxEnt), statistical models (e.g. Generalised Additive Models) and geographic models (e.g. Convex and Voronoi hulls). While EcoCommons does not currently offer the data cleaning routines available on Biosecurity Commons, it does provide functionality for forecasting species distributions under climate change.

This guide focuses primarily on Biosecurity Commons integrated models, for details on how to use EcoCommons functionality, please see the BCCVL Modelling Wizard guide.



Species Distribution Modelling

Biosecurity COMMONS integrated workflows

Biosecurity Commons features the Rangebagging and Climatch SDM alg rithms as an integrated workflow. These algorithms are well suited to biosecurity analysis and offer high per ormance.

Create a Species Distribution Model
Rangebagging, Climatch *(lite)*

EcoCommons models

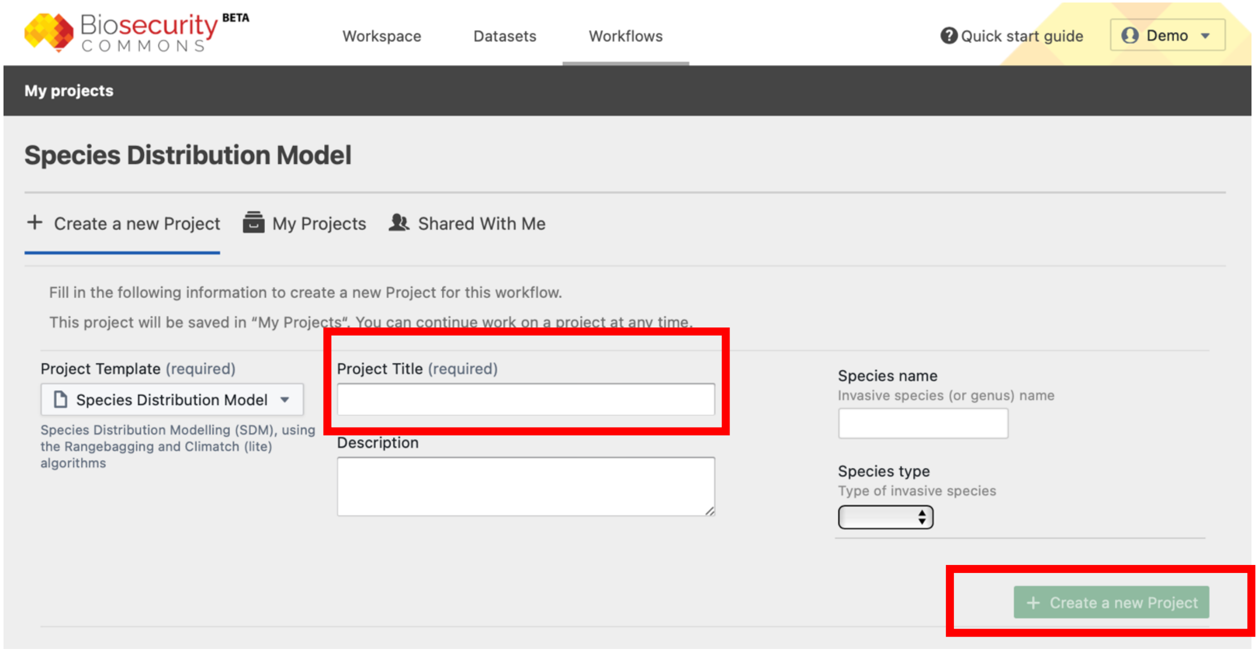
Through our partner platform EcoCommons, we are able to provide an a ditional suite of SDM and Climate Change models suited to general ecological modelling.
Outputs from these models can be used in biosecurity workflows.

Explore EcoCommons workflows
SDM, Climate Change, Ensemble

For more ecological models and support visit https://www.ecocommons.org.au.

Step 2. Create a Species Distribution Model project using Biosecurity Commons integrated models

Select create a Species Distribution Model (see screenshot above) and then give your project a title (screenshot below). Users can also optionally provide additional descriptive details under the Description, Species name and Species type tabs. Project title is the only required field to be completed. Once details have been provided select the green “Create a new Project” button in the bottom right-hand corner.



Species Distribution Model

Fill in the following information to create a new Project for this workflow.

This project will be saved in "My Projects". You can continue work on a project at any time.

Project Template (required): Species Distribution Model

Species Distribution Modelling (SDM), using the Rangebagging and Climatch (lite) algorithms

Project Title (required)

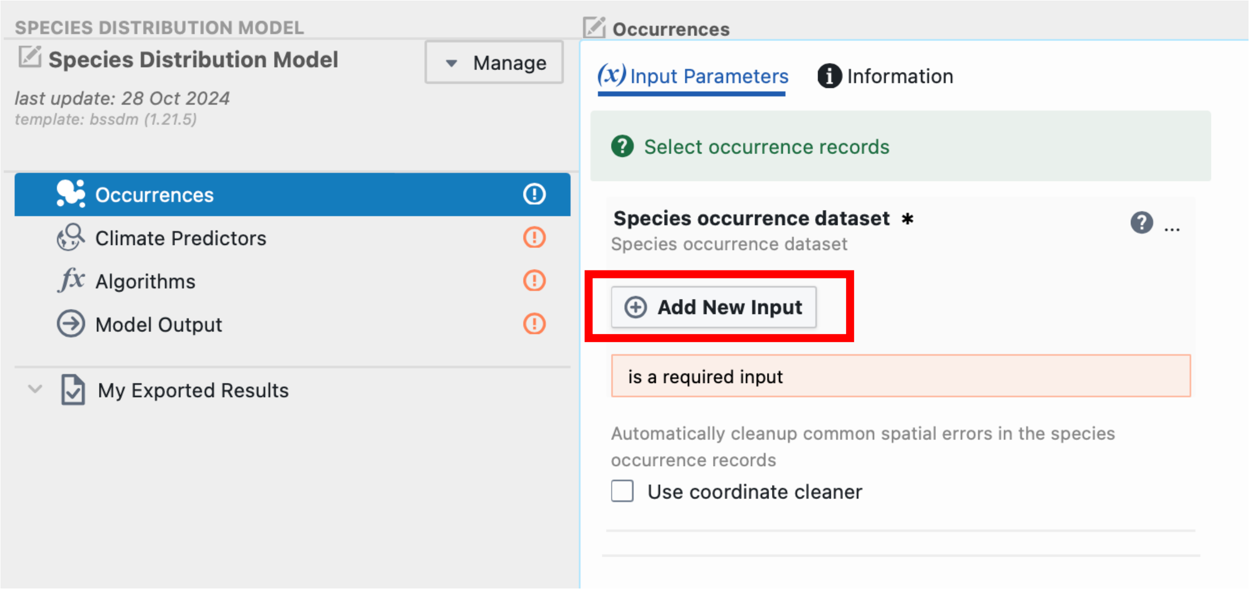
Description

Species name: Invasive species (or genus) name

Species type: Type of invasive species

Step 3. Select your species occurrence data

The two integrated species distribution models available on Biosecurity Commons are forms of correlative models. That is, they attempt to estimate environmental suitability as a function of spatial environmental data and known occurrence locations. As such, to fit these models, occurrence records are required. To add such data press "Add New Input".



Species Distribution Model

last update: 28 Oct 2024

template: bssdm (1.21.5)

Select occurrence records

Species occurrence dataset *

Species occurrence dataset

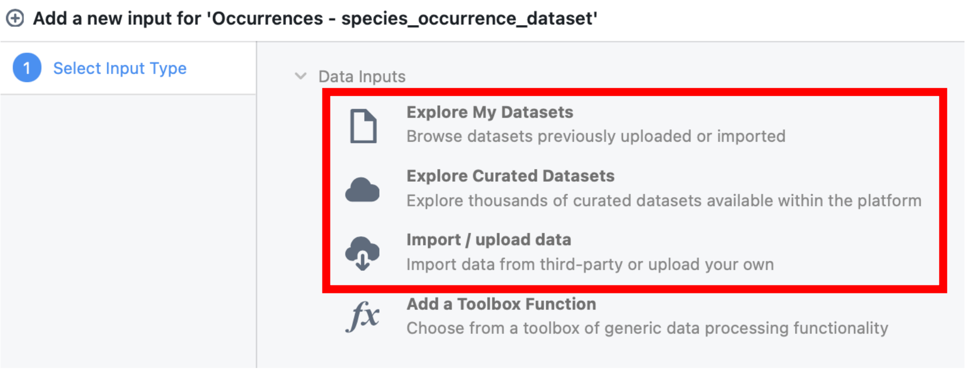
is a required input

Automatically cleanup common spatial errors in the species occurrence records

☐ Use coordinate cleaner

Users have four options to access or utilise occurrence records. They can:

- Search previously uploaded databases
- Search the curated database for pre-existing species-specific occurrences
- Upload their own georeferenced occurrence datasets
- Import data directly from third-party biodiversity databases, the Atlas of Living Australia (ALA), the Global Biodiversity Information Facility (GBIF), or for ocean species, Ocean Biogeographic Information System (OBIS).



⊕ Add a new input for 'Occurrences - species_occurrence_dataset'

1 Select Input Type

Data Inputs

Explore My Datasets
Browse datasets previously uploaded or imported

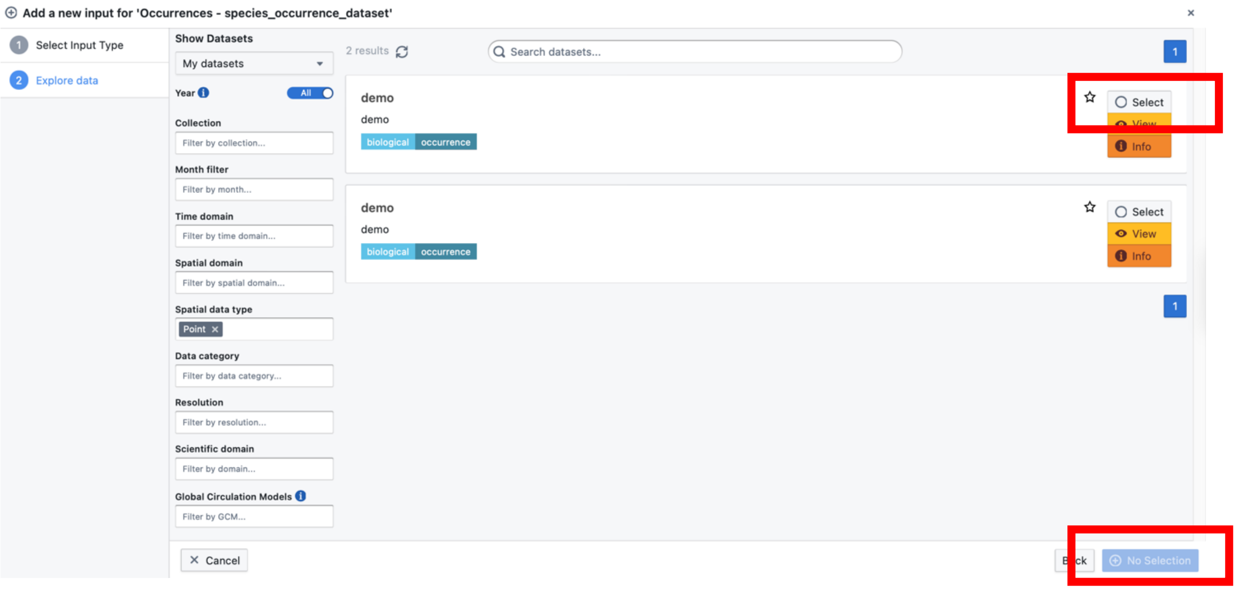
Explore Curated Datasets
Explore thousands of curated datasets available within the platform

Import / upload data
Import data from third-party or upload your own

Add a Toolbox Function
Choose from a toolbox of generic data processing functionality

1. Search your previously uploaded datasets

To search for occurrence records you've previously uploaded click "Explore My Datasets". This will load up a window allowing users to search through datasets they have previously uploaded (see screenshot below).



⊕ Add a new input for 'Occurrences - species_occurrence_dataset'

1 Select Input Type

2 Explore data

Show Datasets: My datasets

Year: All

Spatial data type: Point

2 results

demo
demo
biological occurrence

demo
demo
biological occurrence

Users can then use the search to enter keywords to find the relevant dataset. Note, if users have many uploaded datasets, it is recommended they use the filtering options on the left to narrow down searches (see below for more details).

Once the relevant dataset is selected, simply click “Select” to the right of the dataset, and then click the blue “Add” button in the bottom right of the screen.

2. Search for data on the Biosecurity Commons curated database

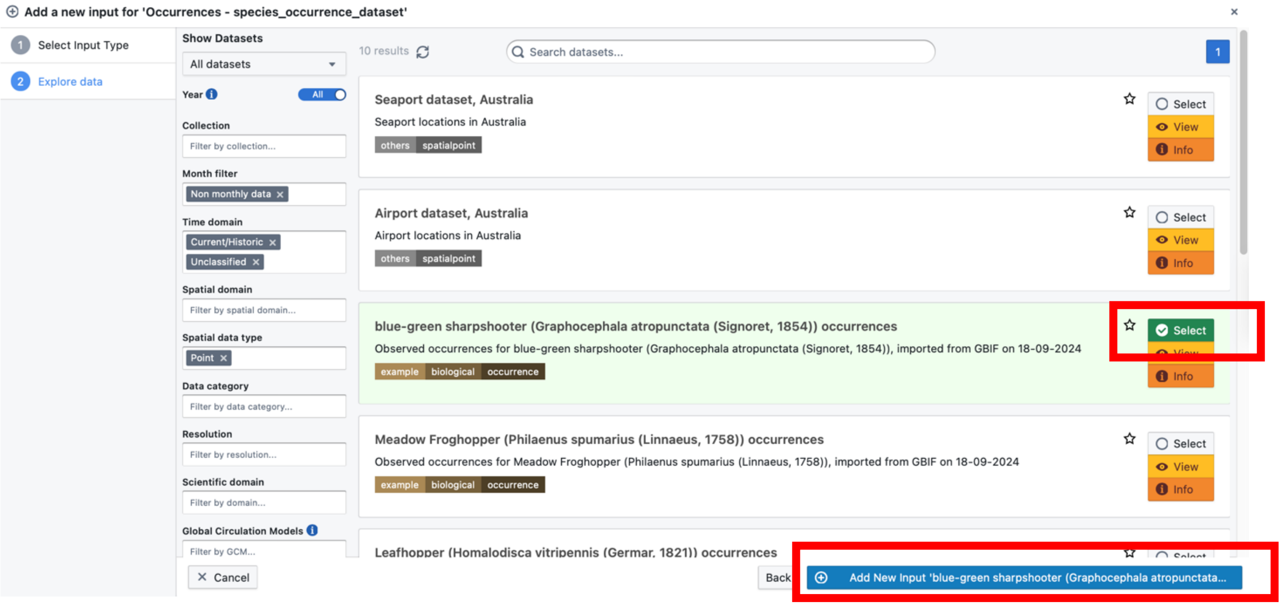
Users may wish to search through the curated datasets publicly available on Biosecurity Commons. To do this, select “Explore curated datasets”. This will load up a similar window to the screenshot above, however, this time users will be able to search the entire curated database.

Biosecurity Commons has thousands of datasets that users can access. As such, it can sometimes be challenging to find the dataset of interest. We **strongly recommend** using the filtering functionality to the left to navigate for appropriate datasets.
For occurrence records, we recommend users add the following filtering options:

Spatial data type = Point
Data category = Biological

These filtering options should narrow down the search to just occurrence point data that are available on the platform.

Once the relevant dataset is selected, simply click “Select” to the right of the dataset, and then click the blue “Add” button in the bottom right of the screen.


Add a new input for 'Occurrences - species_occurrence_dataset'

Show Datasets: All datasets

Year: All

Month filter: Non monthly data

Time domain: Current/Historic, Unclassified

Spatial data type: Point

10 results

Seaport dataset, Australia
Seaport locations in Australia

Airport dataset, Australia
Airport locations in Australia

blue-green sharpshooter (Graphocephala atropunctata (Signoret, 1854)) occurrences
Observed occurrences for blue-green sharpshooter (Graphocephala atropunctata (Signoret, 1854)), imported from GBIF on 18-09-2024

Meadow Froghopper (Philaenus spumarius (Linnaeus, 1758)) occurrences
Observed occurrences for Meadow Froghopper (Philaenus spumarius (Linnaeus, 1758)), imported from GBIF on 18-09-2024

Leafhopper (Homalodisca vitripennis (Germar, 1821)) occurrences

Add New Input 'blue-green sharpshooter (Graphocephala atropunctata...

3. Upload own data

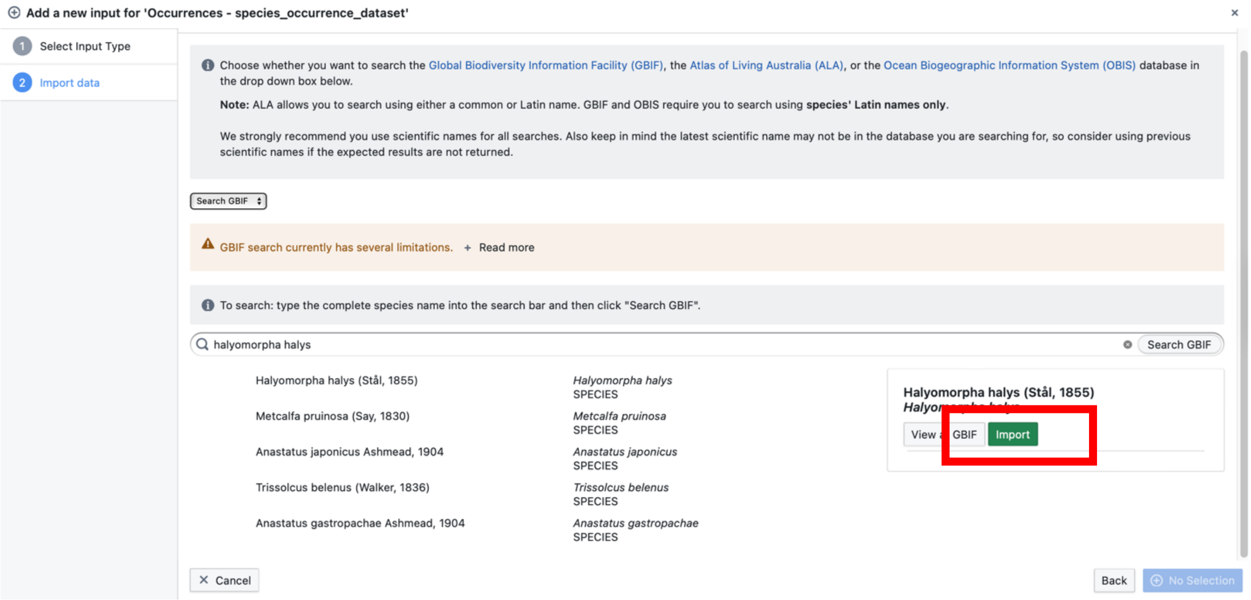
To upload your own data, click on import/upload data and follow these instructions.

4. Import occurrences directly from third-party

Biosecurity Commons also allows users to directly search and import occurrence data from Atlas of Living Australia (ALA), the Global Biodiversity Information Facility (GBIF) and the Ocean Biogeographic Information System (OBIS).

To do this, click Import/Upload data, then click “Import from third party” and then click “Species Occurrence”.

Users can select the database they wish to search from a dropdown menu. Species can then be searched using the search query. Note that both GBIF and OBIS require Latin species names. By contrast, ALA allows common names or Latin names. We strongly recommend searching using species Latin names, to minimise potential inconsistencies in naming.



Choose whether you want to search the Global Biodiversity Information Facility (GBIF), the Atlas of Living Australia (ALA), or the Ocean Biogeographic Information System (OBIS) database in the drop down box below.

Note: ALA allows you to search using either a common or Latin name. GBIF and OBIS require you to search using **species' Latin names only**.

We strongly recommend you use scientific names for all searches. Also keep in mind the latest scientific name may not be in the database you are searching for, so consider using previous scientific names if the expected results are not returned.

GBIF search currently has several limitations. + Read more

To search: type the complete species name into the search bar and then click "Search GBIF".

halyomorpha halys

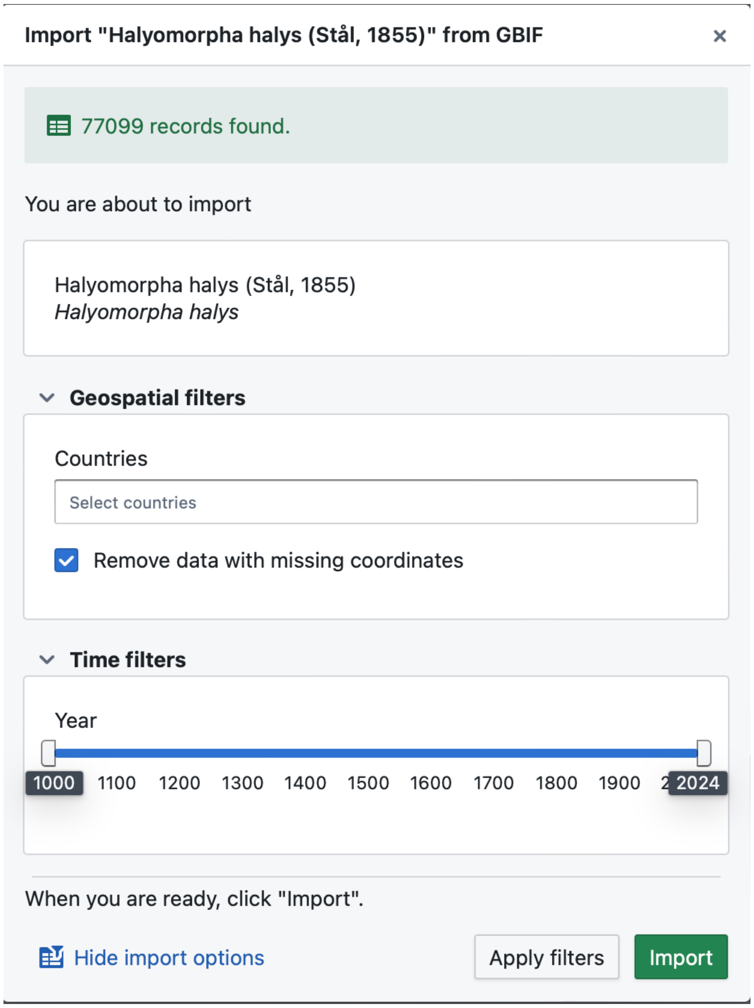
Halyomorpha halys (Stål, 1855)	*Halyomorpha halys* SPECIES
Metcalfa pruinosa (Say, 1830)	*Metcalfa pruinosa* SPECIES
Anastatus japonicus Ashmead, 1904	*Anastatus japonicus* SPECIES
Trissolcus belenus (Walker, 1836)	*Trissolcus belenus* SPECIES
Anastatus gastropachae Ashmead, 1904	*Anastatus gastropachae* SPECIES

Halyomorpha halys (Stål, 1855)
Halyomorpha halys

When the search is complete, users can select the relevant records they wish to import.

For terrestrial exotic threats, GBIF is likely to be the primary database used to access global occurrence records. When a user finds appropriate records on GBIF, they can click the green "Import" button.

This will open a mini window that notifies the user of the number of records found, tells the users how many records (e.g. below there are 77,099 records).



Import "Halyomorpha halys (Stål, 1855)" from GBIF

77099 records found.

You are about to import

Halyomorpha halys (Stål, 1855)
Halyomorpha halys

Geospatial filters

Countries: Select countries

☑ Remove data with missing coordinates

Time filters

Year: 1000 – 2024

When you are ready, click "Import".

CAUTION: Users should take careful note of the record number, as GBIF currently has a cap of 100,000 records that can be directly imported onto the platform. This means that for species with more than 100,000 records, then records cannot be imported directly into the platform without some form of filtering the results in records falling below this number.

Irrespective of record number, we recommend users make appropriate use of the import Geospatial and Time filters. Specifically, we recommend users include countries where the pest has known to be established (i.e. attempt to remove transient records) and set the temporal period that is in alignment with period of the climate data (e.g. for WorldClim data, records post 1970). Once filters have been applied, click “Apply filters”. This will update the number of records to be imported. If less than 100,000 the platform will allow you to import. If greater than 100,000 we recommend sourcing the records directly from the GBIF website and then upload them to the platform.

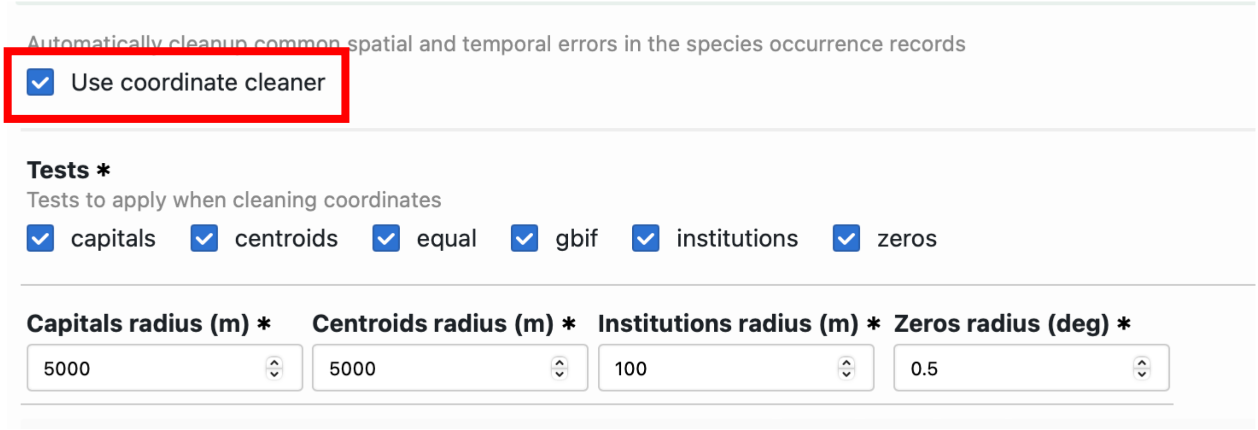
Importing records directly from databases such as GBIF may take some time depending on the demand on their servers. Please be patient.

Step 4. Clean your occurrences

Once an occurrence dataset has been selected, users have the option to clean these data using some inbuilt automated cleaning functionality available in the R package CoordinateCleaner. Specifically, Biosecurity Commons offers the following set of cleaning routines:

- **Capital centroids**: Remove records within a user-defined radius of capital centroids
- **Country centroids**: Remove records within a user-defined radius of a country centroid
- **Equal**: Remove records with equal latitude and longitude
- **Institutions**: Remove records within a user-defined radius from known biodiversity institutions (e.g. museums, herbariums, universities, botanic gardens)
- **gbif**: Remove records within 1 degree of GBIF headquarters in Copenhagen, Denmark.
- **Zeros**: Remove records with coordinates 0,0 or within a given radius of those coordinates
- **Seas:** Remove records with coordinates located in the ocean

To run these cleaning routines, simply click “Use coordinate cleaner”, then select the cleaning tests required, and if required, the test-specific radius.



Automatically cleanup common spatial and temporal errors in the species occurrence records

☑ Use coordinate cleaner

Tests *

Tests to apply when cleaning coordinates

☑ capitals ☑ centroids ☑ equal ☑ gbif ☑ institutions ☑ zeros

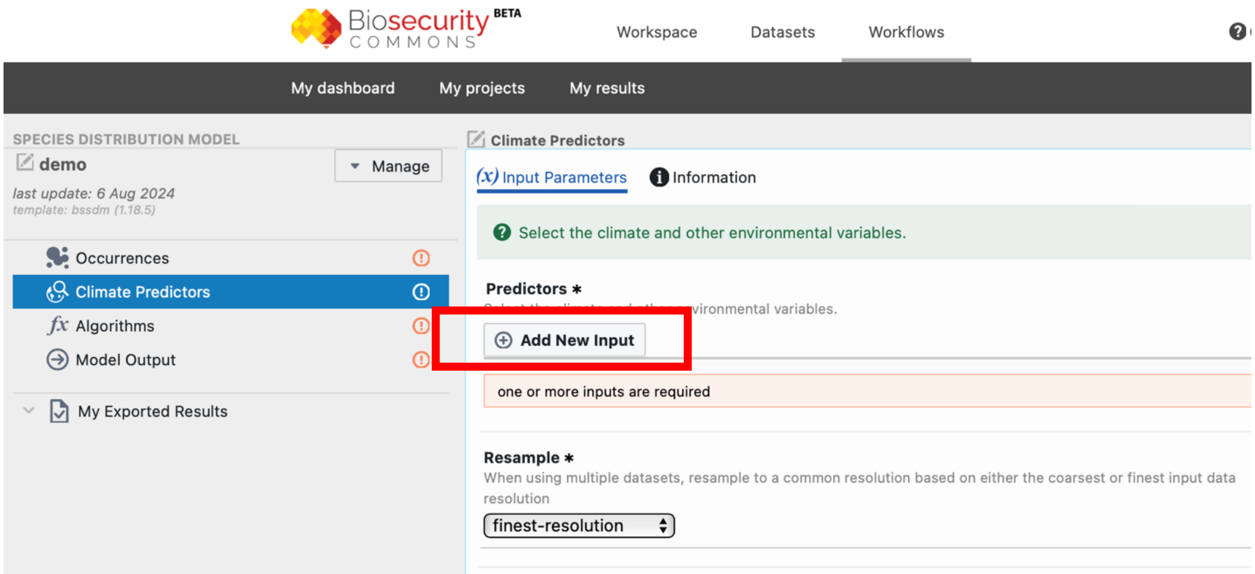
Capitals radius (m) *	Centroids radius (m) *	Institutions radius (m) *	Zeros radius (deg) *
5000	5000	100	0.5

Once desired setting has been selected, click save at the bottom of the screen.

You are now ready to move onto the climate predictor stage.

Step 5. Select climate predictors

Biosecurity Commons and its sister platform, EcoCommons, have a vast array of spatial datasets that can be used in species distribution models to infer suitability. To search this database, click “Add New Input”.



last update: 6 Aug 2024
template: bssdm (1.18.5)

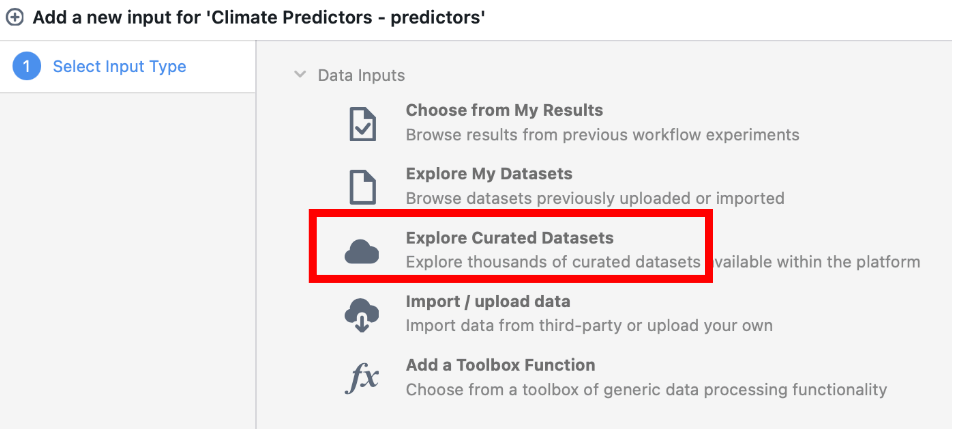
Select the climate and other environmental variables.

Predictors *
vironmental variables.

one or more inputs are required

Resample *
When using multiple datasets, resample to a common resolution based on either the coarsest or finest input data resolution
finest-resolution

Then select “Explore curated datasets”.



Choose from My Results
Browse results from previous workflow experiments

Explore My Datasets
Browse datasets previously uploaded or imported

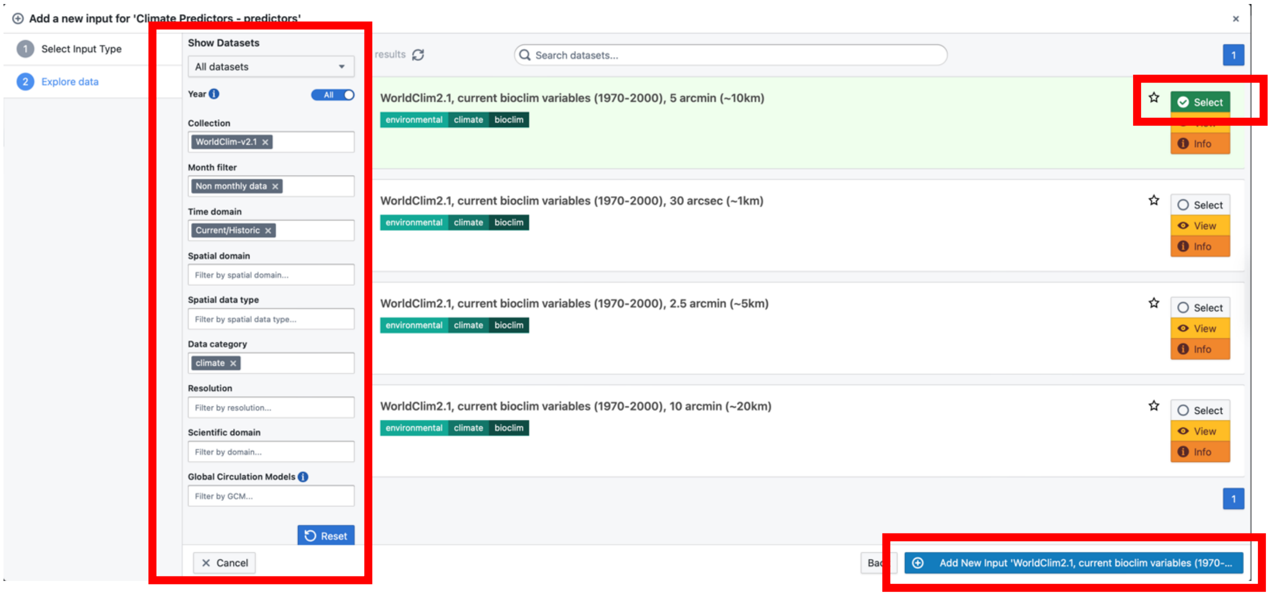
Explore Curated Datasets
Explore thousands of curated datasets available within the platform

Import / upload data
Import data from third-party or upload your own

Add a Toolbox Function
Choose from a toolbox of generic data processing functionality

As the database contains over 50,000 datasets, we **strongly recommend** users utilise the filtering options to the left. Specifically, use the “Collection” filter to select the collection of data they wish to use.

For example, if a user wishes to use long-term average historical WorldClim BIOCLIM predictor data, we recommend that users first select “WorldClim-v2.1” in the “Collection” dropdown menu, ensure “Non monthly data” is specified in the Month filter, and “climate” is selected in the Data category. This should show the different WorldClim climate datasets available and their associated resolutions.



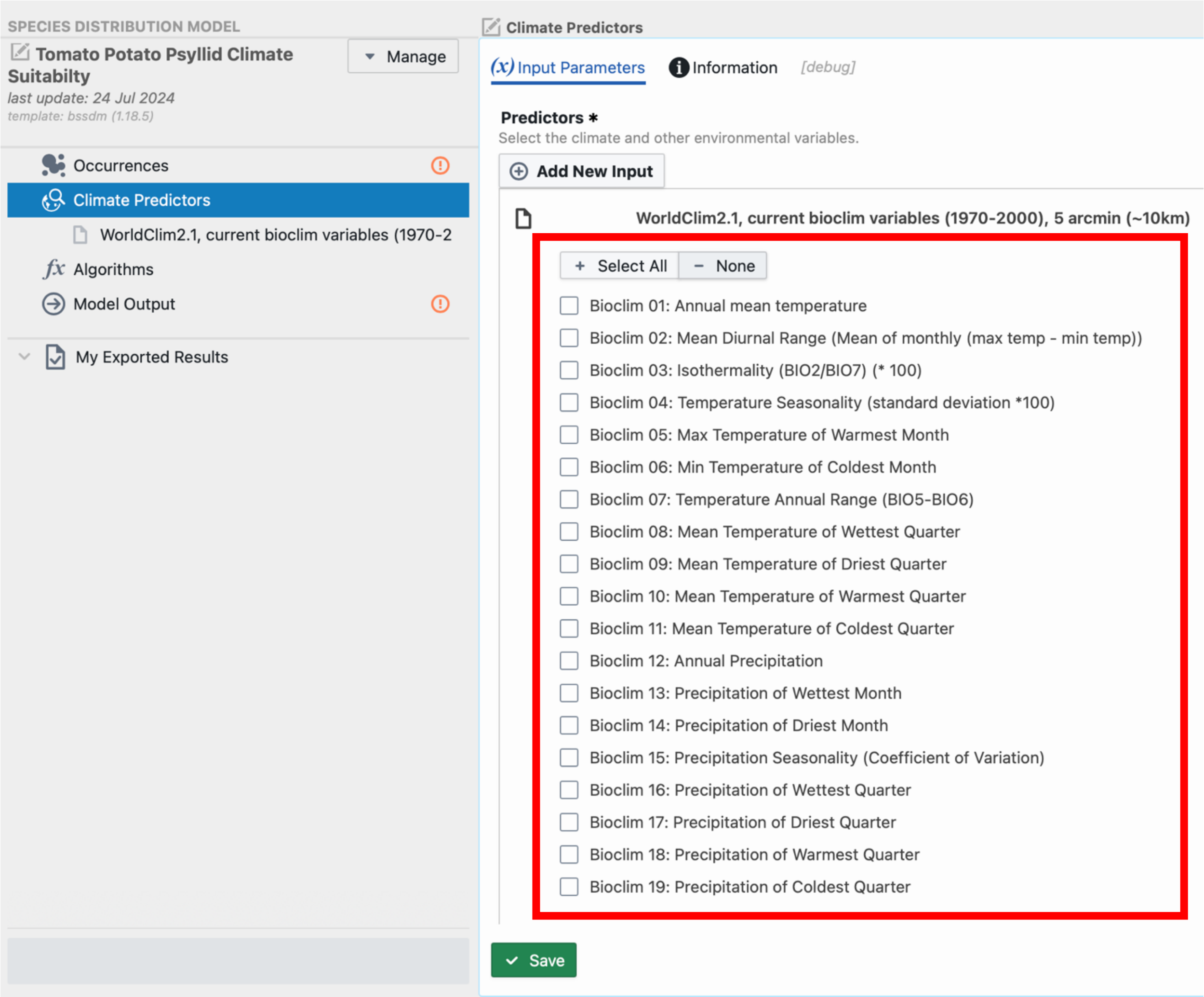
Add a new input for 'Climate Predictors - predictors'

Show Datasets: All datasets
Year: All
Collection: WorldClim-v2.1
Month filter: Non monthly data
Time domain: Current/Historic
Data category: climate

WorldClim2.1, current bioclim variables (1970-2000), 5 arcmin (~10km) — environmental, climate, bioclim
WorldClim2.1, current bioclim variables (1970-2000), 30 arcsec (~1km) — environmental, climate, bioclim
WorldClim2.1, current bioclim variables (1970-2000), 2.5 arcmin (~5km) — environmental, climate, bioclim
WorldClim2.1, current bioclim variables (1970-2000), 10 arcmin (~20km) — environmental, climate, bioclim

Once the relevant dataset is selected, simply click “Select” to the right of the dataset, and then click the blue “Add” button in the bottom right of the screen.

When you have selected your dataset, you will be able to choose from a list of climate and environmental variables (screenshot below). Select the layers that are related to your target species.



Tomato Potato Psyllid Climate Suitabilty
last update: 24 Jul 2024
template: bssdm (1.18.5)

Predictors *
Select the climate and other environmental variables.

WorldClim2.1, current bioclim variables (1970-2000), 5 arcmin (~10km)

- ☐ Bioclim 01: Annual mean temperature
- ☐ Bioclim 02: Mean Diurnal Range (Mean of monthly (max temp - min temp))
- ☐ Bioclim 03: Isothermality (BIO2/BIO7) (* 100)
- ☐ Bioclim 04: Temperature Seasonality (standard deviation *100)
- ☐ Bioclim 05: Max Temperature of Warmest Month
- ☐ Bioclim 06: Min Temperature of Coldest Month
- ☐ Bioclim 07: Temperature Annual Range (BIO5-BIO6)
- ☐ Bioclim 08: Mean Temperature of Wettest Quarter
- ☐ Bioclim 09: Mean Temperature of Driest Quarter
- ☐ Bioclim 10: Mean Temperature of Warmest Quarter
- ☐ Bioclim 11: Mean Temperature of Coldest Quarter
- ☐ Bioclim 12: Annual Precipitation
- ☐ Bioclim 13: Precipitation of Wettest Month
- ☐ Bioclim 14: Precipitation of Driest Month
- ☐ Bioclim 15: Precipitation Seasonality (Coefficient of Variation)
- ☐ Bioclim 16: Precipitation of Wettest Quarter
- ☐ Bioclim 17: Precipitation of Driest Quarter
- ☐ Bioclim 18: Precipitation of Warmest Quarter
- ☐ Bioclim 19: Precipitation of Coldest Quarter

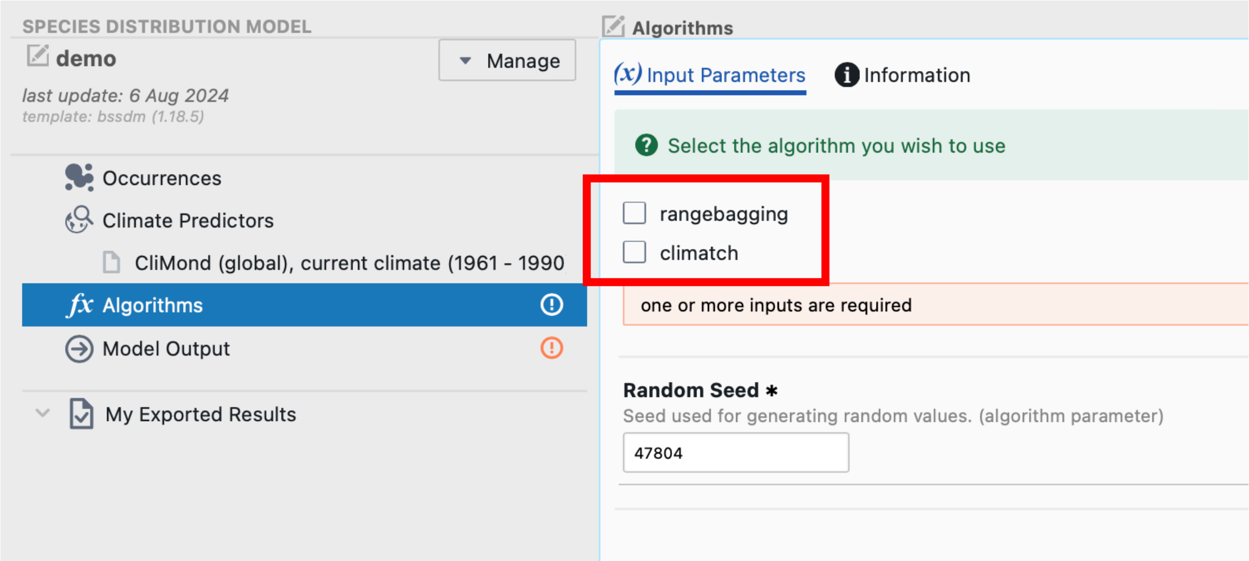
Note that users can select multiple datasets. If multiple datasets are selected and these are at different resolutions, the platform will automatically resample coarser resolution data inputs to the finest resolution selected – ensuring all input predictors are on a common resolution.

Users can change this setting to resample finer resolution inputs to the coarsest resolution by changing “Resample” from “finest-resolution” to “coarsest-resolution.

When you are ready, click save and move to the algorithms stage.

Step 6. Choose your SDM algorithm

Users can choose either Range Bagging or Climatch, or both. Both models are profile models. That is, they only use presence records and do not use absence or background data in model fitting. These models simply describe the environmental conditions found across all the areas the species is known to occur.



SPECIES DISTRIBUTION MODEL

demo

last update: 6 Aug 2024

template: bssdm (1.18.5)

Algorithms

Select the algorithm you wish to use

☐ rangebagging

☐ climatch

one or more inputs are required

Random Seed *

Seed used for generating random values. (algorithm parameter)

47804

Range Bagging

Range bagging is an algorithm that estimates the environmental limits of a species' habitat by calculating convex hulls around environmental conditions at occurrence locations. Environments that fall within the hull are defined as suitable, whereas those that fall outside are considered unsuitable. This process is then repeated using random subsets of both occurrence records as well as available environmental covariates (e.g. annual rainfall, mean annual temperature, etc.). The number of covariates included in a replicate is defined by the user. Suitability is then defined for each raster cell as the proportion of replicates that define the location as suitable. For example, a suitability score of 0.1 would indicate only 10% of the estimated convex hulls ensembled deemed that location suitable. By contrast, a score of 0.9 would indicate that 90% of estimated convex hulls deemed that location climatically suitable.

Advantages:

- Quick and easy profile method
- It is likely more robust than other profile methods due to 'bagging'
- Increasing evidence that algorithm performs well
- Ensemble of many models

Limitations:

- Only uses continuous predictor variables

Assumptions:

- No assumptions are made about the distributions of the environmental variables.

Climatch

Climatch is a software tool developed by the Australian Bureau of Agricultural and Resource Economics and Sciences (ABARES). It assesses the climatic suitability of different geographic regions for a particular species by comparing the climate of a target region with the climate of regions where the species is already known to exist. Climatch analyses various climatic variables, such as temperature and precipitation, to predict the potential distribution of species, particularly invasive species, under current and future climate scenarios.

The software uses Euclidean distances to estimate climatic suitability. It calculates the Euclidean distance between the climate variables of the target region and those of the known regions. Smaller Euclidean distances indicate higher climatic similarity and thus higher suitability for the species. This method helps identify areas that are climatically suitable for the establishment and spread of species of interest, making Climatch a valuable tool for biosecurity, conservation planning, and managing invasive species risks.

Disclaimer: *Please note that Biosecurity Commons implements the Climatch algorithm (Euclidean). As Biosecurity Commons allows users to input different climate predictor datasets, outputs will differ to those created using the official ABARES version. Details of the Climatch algorithm can be found in the Climatch manual Climatch (agriculture.gov.au).*

Advantages:

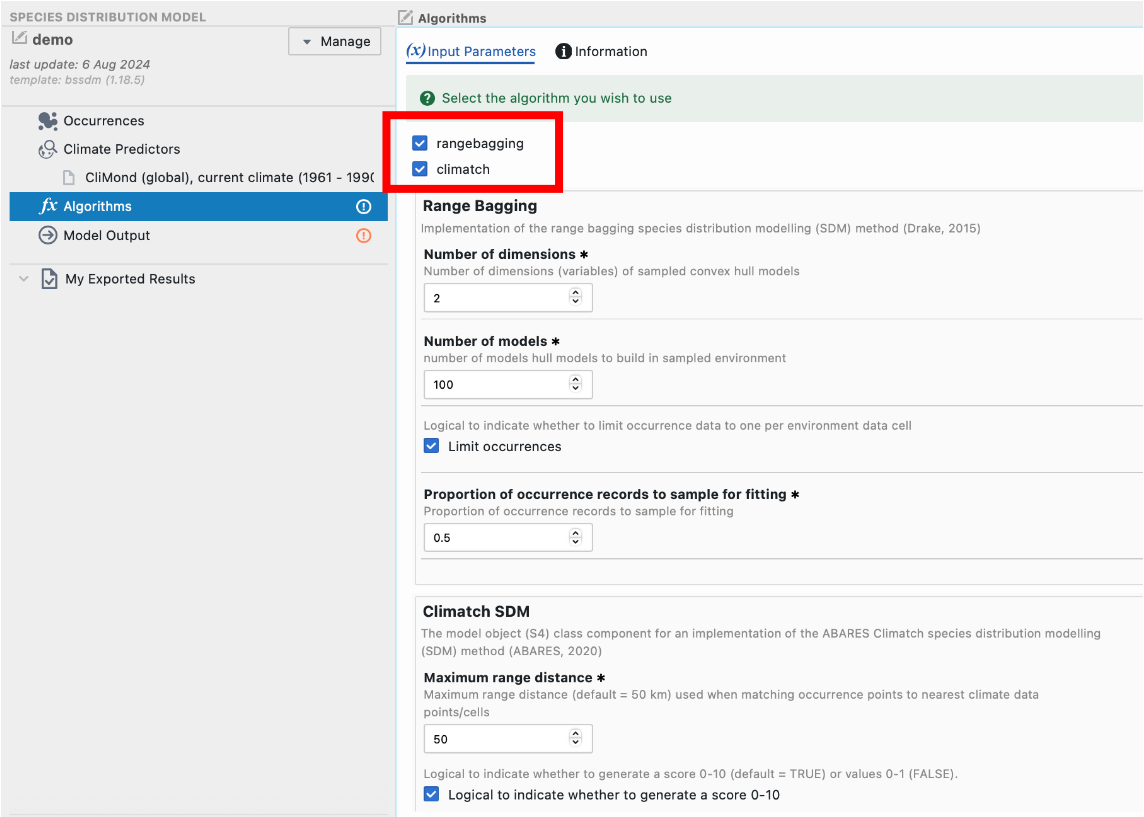
- Quick and easy way to identify environmental space used by selected pests
- Only requires presence occurrence data included within a gridded study area
- Algorithm has been widely used in pest and weed biosecurity risk analyses
- Again, due to use of grid data on our platform the matching is not like the official Climatch algorithm which compares target and source point locations

Limitations:

- Simple and less sophisticated approach than other SDM methods
- Does not allow model ensembling (i.e. is reliant on single model fit)
- Only uses continuous predictor variables

Users can select one or both algorithms. When both are selected, users will obtain two outputs, one per algorithm.

Once algorithms are selected, users may modify algorithm specific parameters (screenshot below).



last update: 6 Aug 2024
template: bssdm (1.18.5)

Select the algorithm you wish to use

☑ rangebagging
☑ climatch

Range Bagging

Implementation of the range bagging species distribution modelling (SDM) method (Drake, 2015)

Number of dimensions *
Number of dimensions (variables) of sampled convex hull models
2

Number of models *
number of models hull models to build in sampled environment
100

Logical to indicate whether to limit occurrence data to one per environment data cell
☑ Limit occurrences

Proportion of occurrence records to sample for fitting *
Proportion of occurrence records to sample for fitting
0.5

Climatch SDM

The model object (S4) class component for an implementation of the ABARES Climatch species distribution modelling (SDM) method (ABARES, 2020)

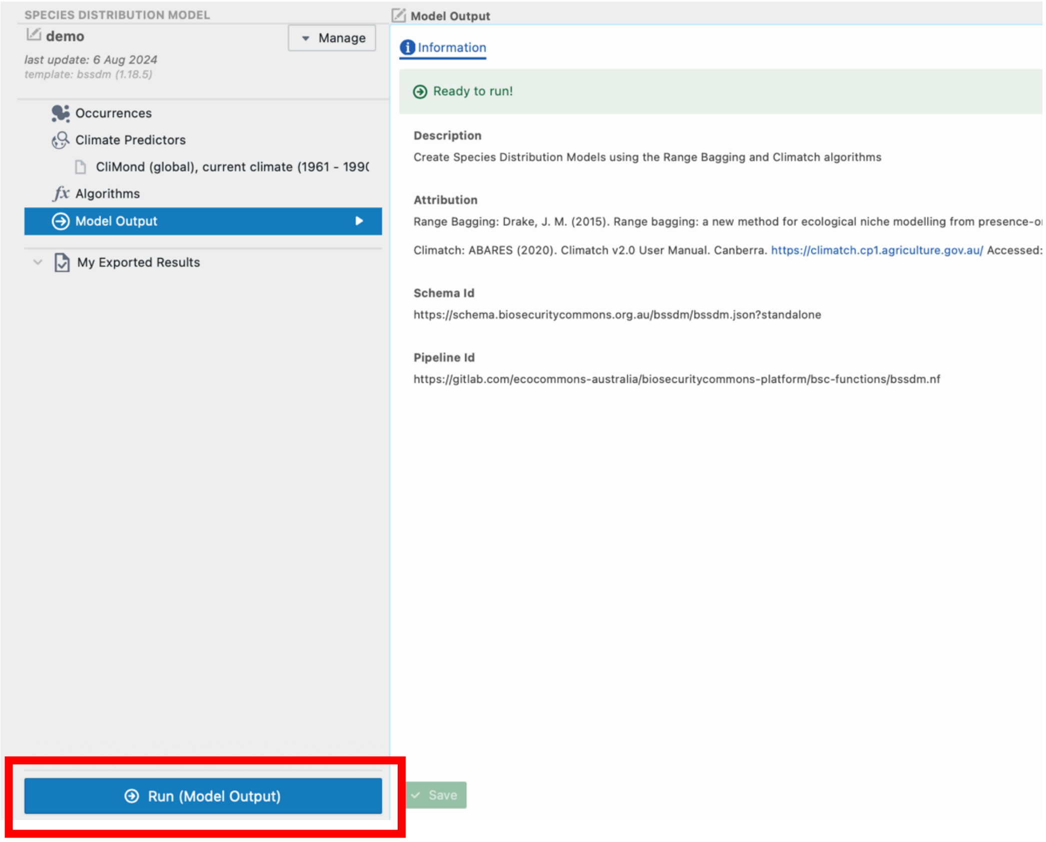
Maximum range distance *
Maximum range distance (default = 50 km) used when matching occurrence points to nearest climate data points/cells
50

Logical to indicate whether to generate a score 0-10 (default = TRUE) or values 0-1 (FALSE).
☑ Logical to indicate whether to generate a score 0-10

When you are ready, click save and move to model output.

Step 7. Model outputs

If all required inputs have been specified, you will see the ‘ready to run’ message in green.



Ready to run!

Description
Create Species Distribution Models using the Range Bagging and Climatch algorithms

Attribution
Range Bagging: Drake, J. M. (2015). Range bagging: a new method for ecological niche modelling from presence-o
Climatch: ABARES (2020). Climatch v2.0 User Manual. Canberra. https://climatch.cp1.agriculture.gov.au/ Accessed:

Schema Id
https://schema.biosecuritycommons.org.au/bssdm/bssdm.json?standalone

Pipeline Id
https://gitlab.com/ecocommons-australia/biosecuritycommons-platform/bsc-functions/bssdm.nf

Click the blue ‘Run’ button in the bottom left to run your project. The output page will be updated as the job processes from “Created”, “Submitted”, “Started” and “Success”.


Model Output-Rangebagging-09-Aug-2024-02:06:08.795267

Pipeline: *https://gitlab.com/ecocommons-australia/biosecuritycommons-platform/bsc-functions/rangebagging.nf*

Version: *1.18.5*

CREATED

Model Output-Rangebagging-09-Aug-2024-02:06:08.795267

Pipeline: *https://gitlab.com/ecocommons-australia/biosecuritycommons-platform/bsc-functions/rangebagging.nf*

Version: *1.18.5*

SUBMITTED

Model Output-Rangebagging-09-Aug-2024-02:06:08.795267

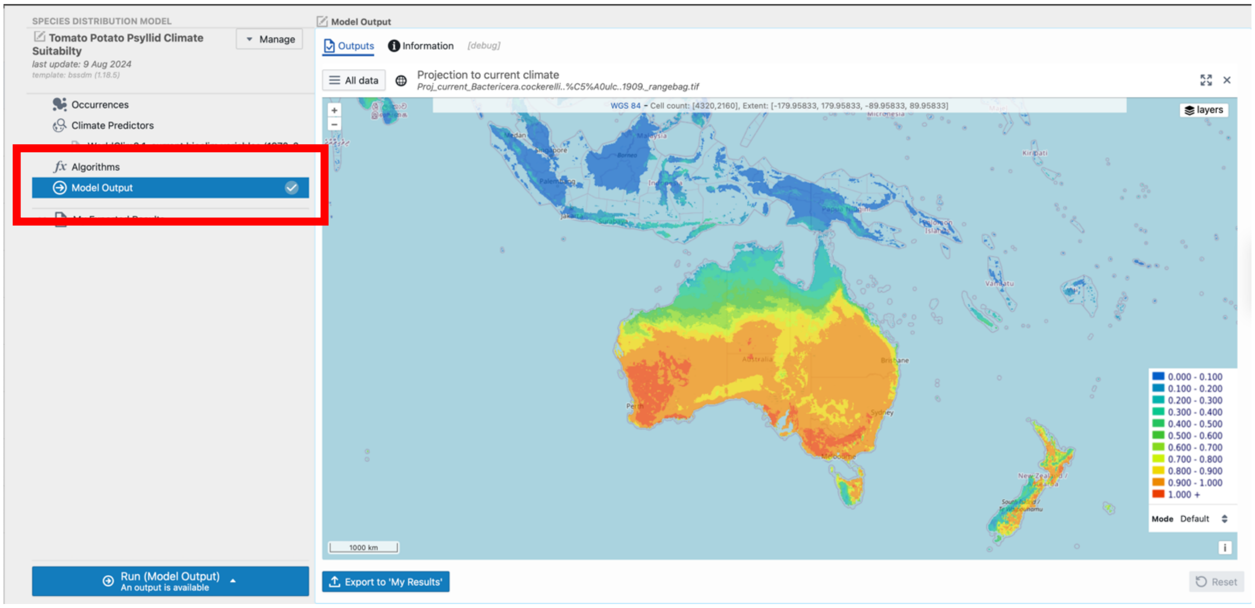
Pipeline: *https://gitlab.com/ecocommons-australia/biosecuritycommons-platform/bsc-functions/rangebagging.nf*

Version: *1.18.5*

STARTED

Once the models, or model, have finished, a green tick will appear next to Model Outputs.

If users only selected one algorithm, the model output will automatically be displayed as a global heat map will be viewable in the interactive map pane. Users can zoom in or out of regions of interest. Interactive maps also allow users to change the type of legend displayed.



SPECIES DISTRIBUTION MODEL

Tomato Potato Psyllid Climate Suitabilty

last update: 9 Aug 2024

template: bssdm (1.18.5)

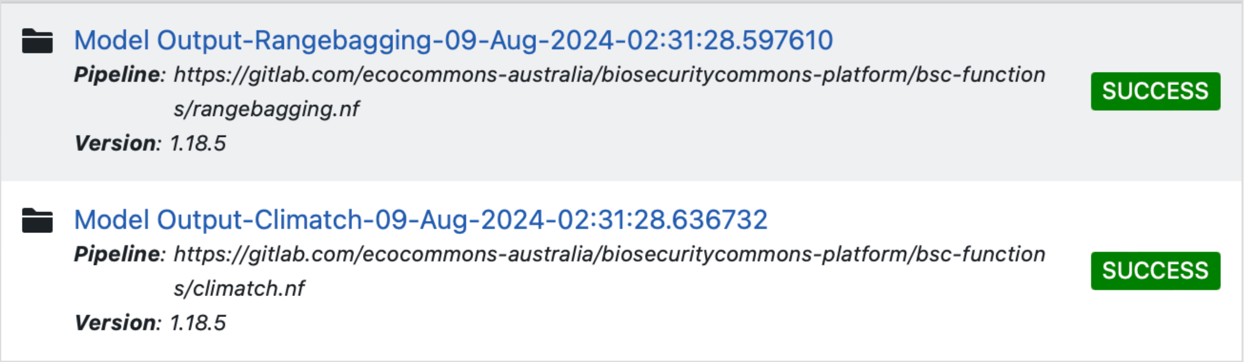
Model Output

Projection to current climate

Proj_current_Bactericera.cockerelli..%C5%A0ulc..1909._rangebag.tif

WGS 84 - Cell count: [4320,2160], Extent: [-179.95833, 179.95833, -89.95833, 89.95833]

If users selected both algorithms, the heat map will not be automatically displayed. Rather, users need to select one of the two outputs.



Model Output-Rangebagging-09-Aug-2024-02:31:28.597610

Pipeline: *https://gitlab.com/ecocommons-australia/biosecuritycommons-platform/bsc-functions/rangebagging.nf*

Version: *1.18.5*

SUCCESS

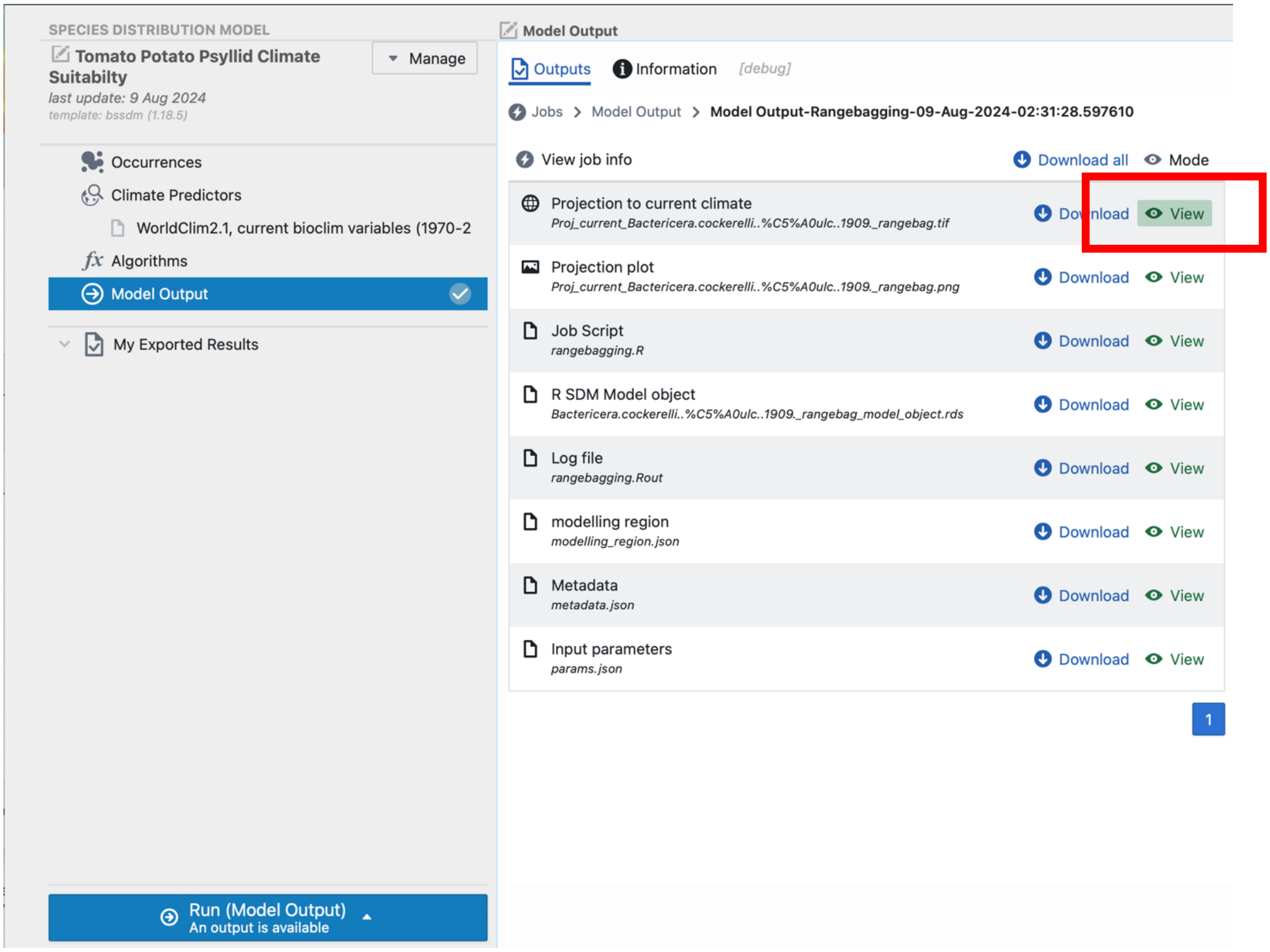
Model Output-Climatch-09-Aug-2024-02:31:28.636732

Pipeline: *https://gitlab.com/ecocommons-australia/biosecuritycommons-platform/bsc-functions/climatch.nf*

Version: *1.18.5*

SUCCESS

And then select “View” on the file named “Projection to current climate”.



Projection to current climate *Proj_current_Bactericera.cockerelli..%C5%A0ulc..1909._rangebag.tif*	Download	View
Projection plot *Proj_current_Bactericera.cockerelli..%C5%A0ulc..1909._rangebag.png*	Download	View
Job Script *rangebagging.R*	Download	View
R SDM Model object *Bactericera.cockerelli..%C5%A0ulc..1909._rangebag_model_object.rds*	Download	View
Log file *rangebagging.Rout*	Download	View
modelling region *modelling_region.json*	Download	View
Metadata *metadata.json*	Download	View
Input parameters *params.json*	Download	View

Note also, that model outputs also contain a variety of other outputs including:

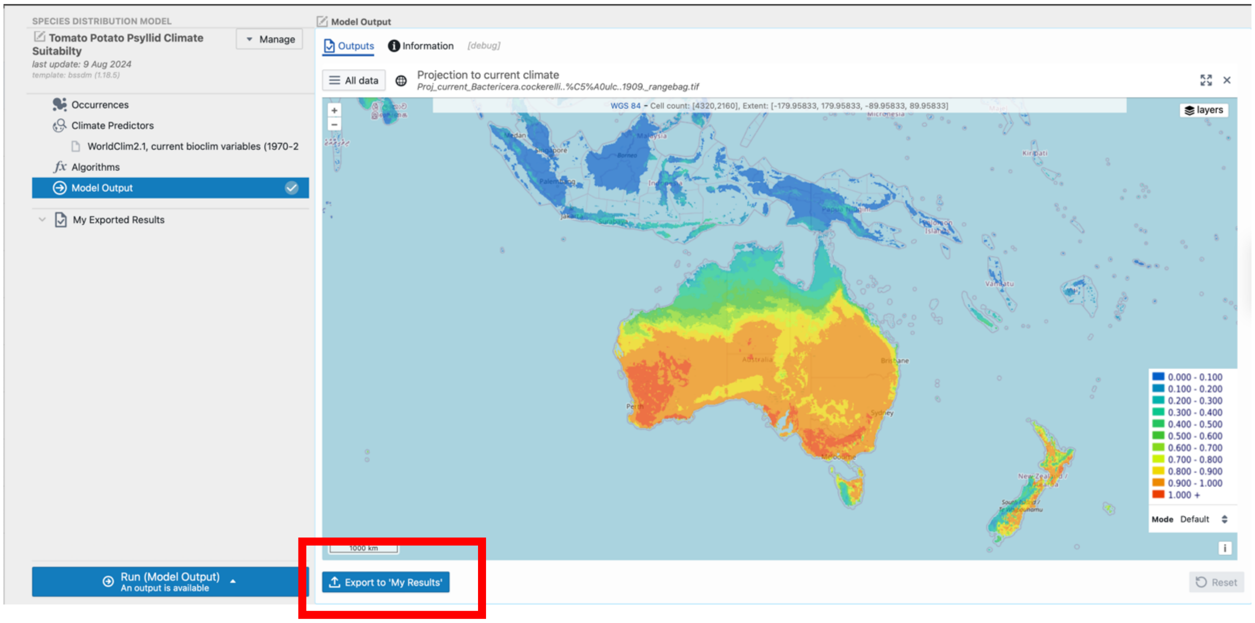
- **Projection plot:** A .png global heat map of predicted suitability
- **Job Script**: A copy of the R script used to build the model

- **R SDM Model object**: A .rds file containing the model object
- **Log file**: A text data file containing processes, messages, and other details associated with model runs.
- **Modelling region**: A .json file defining the extent of the projections (this is always global extent)
- **Metadata:** A .json file containing the metadata required to run the model on Biosecurity Commons
- **Input parameters**: Input parameters required to run the Job Script.

Users can download outputs by selecting the “Download” button.

Step 8. Exporting outputs for use in other workflows

Users may wish to export outputs for use in other projects or other workflows.
To do this, view the output of interest, and select in the bottom left corner of the interactive map “Export to My Results”. This output will now be discoverable in the users “My results” database, which in turn, makes the layer available for use in other workflows.



SPECIES DISTRIBUTION MODEL

Tomato Potato Psyllid Climate Suitabilty
last update: 9 Aug 2024
template: bssdm (1.18.5)

Projection to current climate
Proj_current_Bactericera.cockerelli..%C5%A0ulc..1909._rangebag.tif

WGS 84 - Cell count: [4320,2160], Extent: [-179.95833, 179.95833, -89.95833, 89.95833]