



Biosecurity
COMMONS

Risk Mapping – Quick Start Guide



Last modified: 4 November 2024

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Risk Mapping

A robust and effective biosecurity system hinges on identifying regions most vulnerable to the introduction, establishment, and spread of biological threats. To guide this process, biosecurity experts commonly develop maps of establishment potential – commonly referred to as risk maps (albeit these are not true risk maps as they do not incorporate consequences). These establishment potential maps are routinely used to guide where to focus finite surveillance resources, determine the potential extent of suitable area, inform statistical models of likelihoods of threat absence, and prioritise threats.

Biosecurity Commons provides extensive flexibility in how establishment potential maps can be created. This workflow is largely based on the work conducted in [Camac et al 2020](#), [2021](#) and summarised in [Camac et al. 2024](#).

In the ideal case, threat establishment potential should be quantified by explicitly considering three spatial criteria, where all three must be met for establishment to occur (Fig 1):

- Can the threat reach the location of interest (i.e. propagule pressure)?
- Are abiotic conditions suitable (e.g. climate suitability)?
- Are biotic conditions suitable (e.g. presence of host or required habitat/food source)?

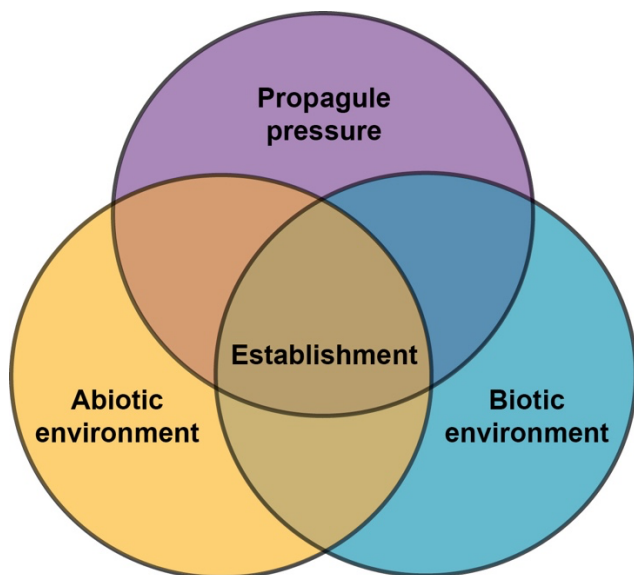


Figure 1: The three main elements governing the likelihood of establishment of exotic species in the introduced region (Derived from [Camac et al. 2024](#))

Biosecurity Commons allows users to create risk maps that account for all, or a subset of the above three constraints, providing critical functionality that can be applied to any threat. It does this by providing access to a wide range of climate, environmental and social (e.g. human population, points of entry) geospatial datasets that can be easily used to construct estimates of climate suitability, biotic suitability or how entry risk may vary across geographic space for different pathways.

For more details about the risk mapping workflow please see the [Risk Mapping workflow overview](#) support article. A [demonstration video](#) is also available for this workflow.

Linkages to other workflows

Outputs of Risk Mapping can be used directly as inputs in many other workflows, such as:

- Informing [Dispersal Modelling](#) by:
 - Stochastic seeding of incursions based on establishment likelihoods
 - Constraining geographic spread based on threat suitability
 - Constraining carrying capacity based on threat suitability (in population spread models)
 - Informing location attractiveness via threat suitability
- Informing [Surveillance Design](#) for early detection by identifying areas of high establishment likelihood
- Informing [Proof of Area Freedom](#) by combining risk mapping and surveillance design to determine confidence or likelihood of threat absence.

Creating a Risk Map

Step 1. Create a new project

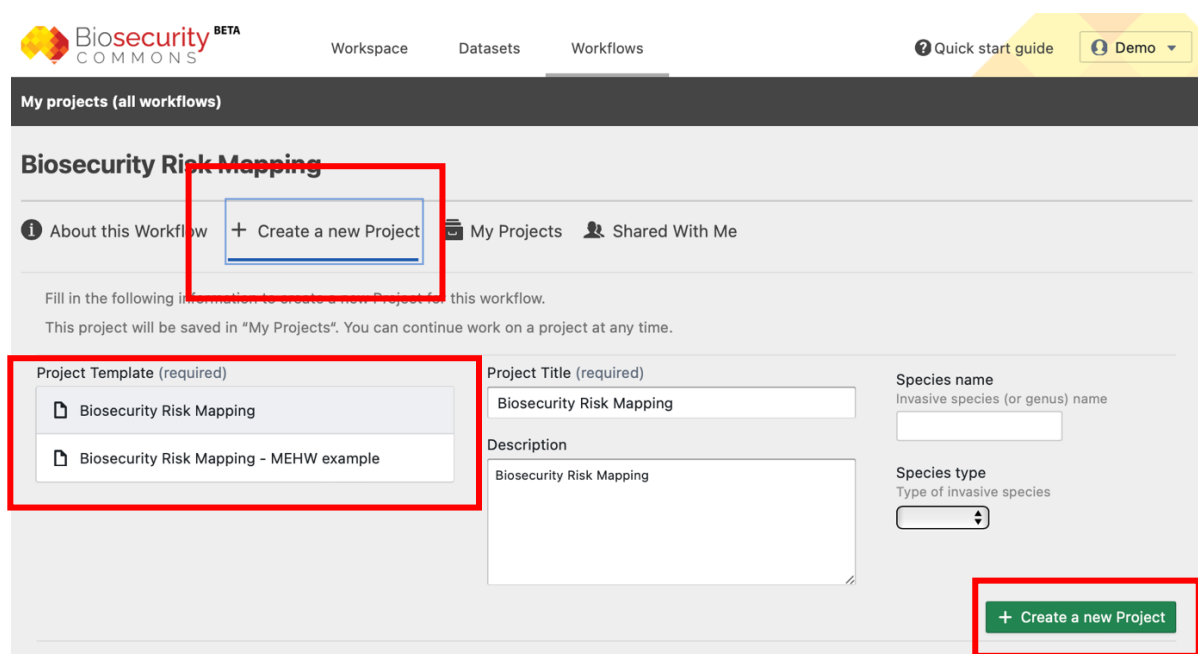
Select the Risk Mapping workflow and then select “Create a new Project” (see screenshot below).

When creating a new risk mapping project, users have the option to select an empty template, “Biosecurity Risk Mapping”, or one of a range of prepopulated templates that have been constructed as examples of the workflow or based on previous case studies (e.g. “Mouse-ear hawkweed (*Pilosella officinarum*)”).

The empty template is ideal for those wishing to create a brand-new risk map as it contains:

- The basic structure of the Risk Mapping workflow
- No preloaded datasets (except for the default region, albeit this can be easily changed)

By contrast, example templates provide users with the opportunity to see a completed demonstration of how risk maps can be produced, or if based on a real-world case study, how others have attempted to derive maps of establishment potential.



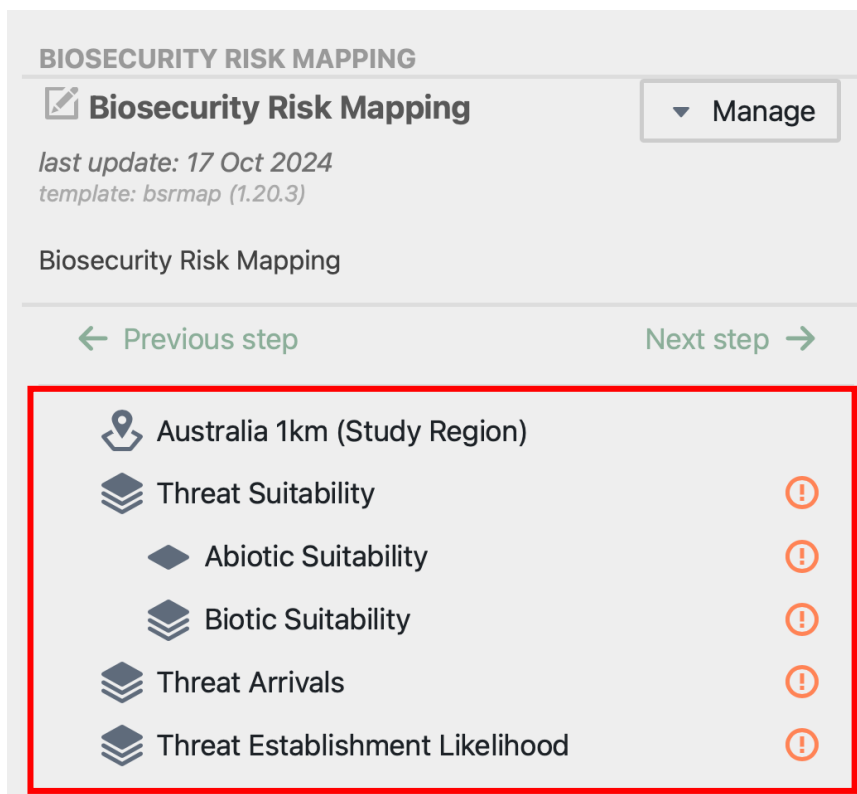
The screenshot shows the 'Biosecurity Risk Mapping' project creation interface. At the top, there is a navigation bar with 'Workspace', 'Datasets', and 'Workflows' tabs, along with a 'Quick start guide' and a 'Demo' button. Below this, the page title is 'My projects (all workflows)'. The main heading is 'Biosecurity Risk Mapping'. There are three tabs: 'About this Workflow', '+ Create a new Project' (highlighted with a red box), and 'My Projects'. Below the tabs, there is a text prompt: '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.' The form consists of several fields: 'Project Template (required)' with two options: 'Biosecurity Risk Mapping' and 'Biosecurity Risk Mapping - MEHW example' (both highlighted with a red box); 'Project Title (required)' with the value 'Biosecurity Risk Mapping'; 'Description' with the value 'Biosecurity Risk Mapping'; 'Species name' with the label 'Invasive species (or genus) name' and an empty input field; and 'Species type' with the label 'Type of invasive species' and a dropdown menu. A green '+ Create a new Project' button (highlighted with a red box) is located at the bottom right of the form.

Select a template and then give your project a title. Users can optionally provide additional descriptive details under the Description, Species name and Species type fields. These metadata are presently unused but will provide future flexibility in filtering and summarising projects.

Once details have been provided, click the green “Create a new Project” button in the bottom right-hand corner to continue.

When you start a Risk Mapping workflow from an empty template you will be presented with the core elements of the workflow on the left side of the screen – Study Region, Threat Suitability (which comprises Abiotic & Biotic Suitability), Threat Arrivals and Threat Establishment Likelihood. Orange exclamation points indicate steps that require

attention and, as you progress through the project, these change to green ticks when complete.



BIOSECURITY RISK MAPPING

Biosecurity Risk Mapping Manage

last update: 17 Oct 2024
template: bsrmap (1.20.3)

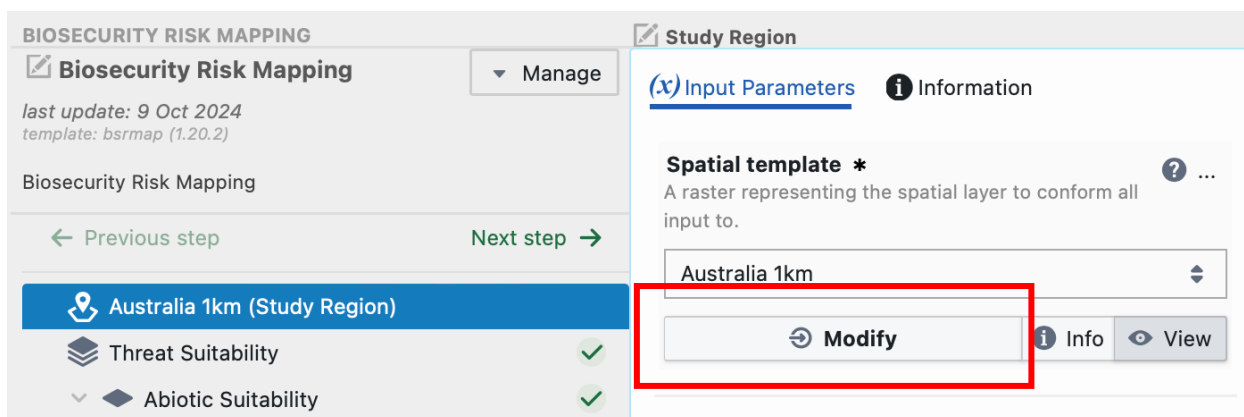
Biosecurity Risk Mapping

← Previous step Next step →

- 📍 Australia 1km (Study Region)
- 📄 Threat Suitability !
 - ◆ Abiotic Suitability !
 - 📄 Biotic Suitability !
- 📄 Threat Arrivals !
- 📄 Threat Establishment Likelihood !

Step 2. Choose your study region

By default, Biosecurity Commons will load a template raster encompassing the extent of Australia, at 1km resolution, to define the study region. However, this can easily be changed to either a different region or sub-region by clicking the “Modify” button.



BIOSECURITY RISK MAPPING

Biosecurity Risk Mapping Manage

last update: 9 Oct 2024
template: bsrmap (1.20.2)

Biosecurity Risk Mapping

← Previous step Next step →

- 📍 Australia 1km (Study Region)
- 📄 Threat Suitability ✓
- ▼ ◆ Abiotic Suitability ✓

Study Region

[\(x\) Input Parameters](#) **i** Information

Spatial template * ? ...

A raster representing the spatial layer to conform all input to.

Australia 1km

Modify **i** Info **👁** View

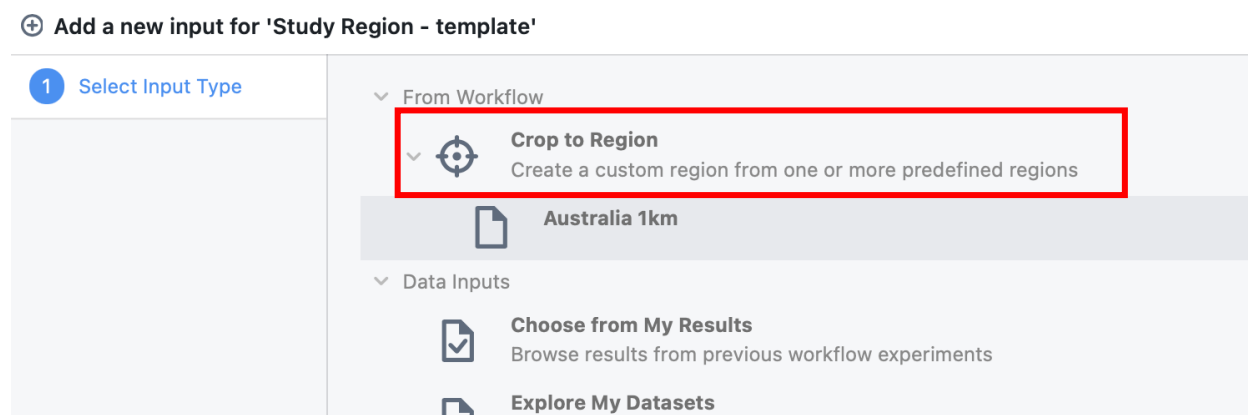
When users click “Modify” followed by “Select an alternative input” they can either:

- Crop to Region: For selecting a sub region within Australia
- Select an alternative raster input from available results and curated datasets or upload a new raster file defining the study region extent, resolution, and coordinate system.

1. Crop to Region

The first option available to users in the “Select an alternative input” menu is “Crop to Region” (see screenshot below).

This tool allows users to crop the study region. Select “Crop to Region” and then select the blue “Add New Input” button.



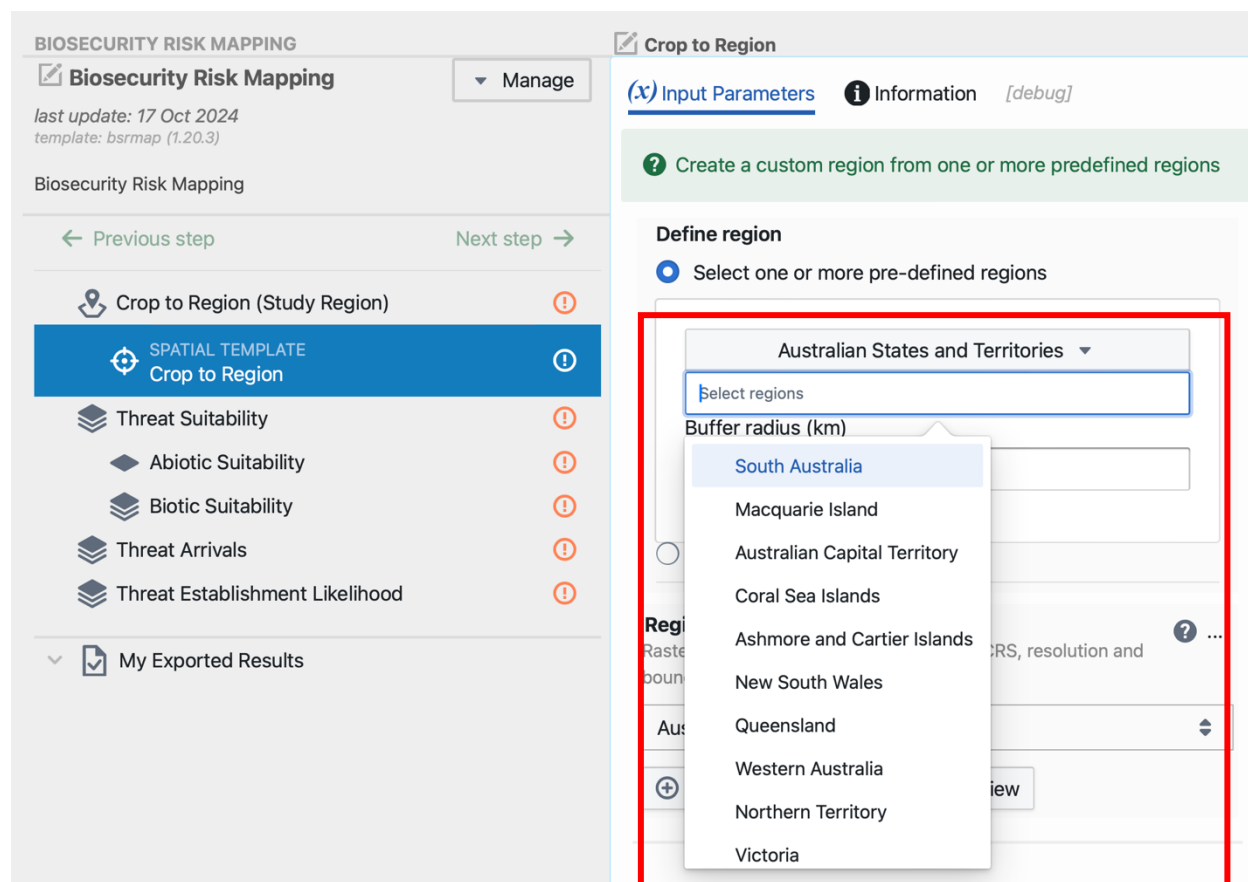
A “Crop to Region” sub-step will appear in the tree on the left-hand side which allows users to define their custom region.

After clicking on this sub-step, users can select one of several pre-defined Australian regions from the drop-down menu. Predefined regions include:

- Local Government Areas
- National Resource Management Regions (NRMs)
- Australian state and territories
- IBRA regions
- River regions
- Drainage Divisions (Level 1 or 2)
- Marine Ecoregions of the world
- IMCRA provincial or meso-scale bioregions

For more details about these and other datasets please consult the [Atlas of Living Australia](#).

Once selected, users can then specify one or more subclasses to define their study region. For example, if a user selected “Australian States and Territories” and they wished to constrain their study region to Victoria and New South Wales, they can simply select both states from the dropdown menu.

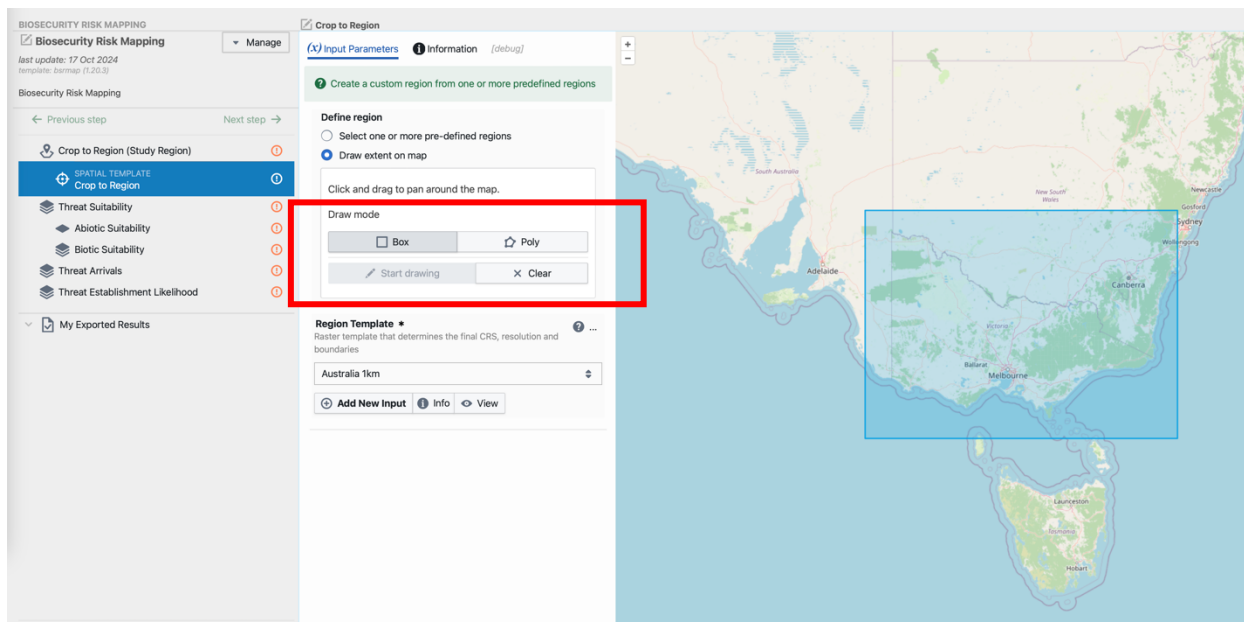


The screenshot shows the 'BIOSECURITY RISK MAPPING' interface. On the left, a sidebar lists various spatial templates and risk mapping components, with 'Crop to Region (Study Region)' selected. The main panel is titled 'Crop to Region' and includes tabs for 'Input Parameters', 'Information', and 'debug'. A green banner prompts the user to 'Create a custom region from one or more predefined regions'. Under the 'Define region' section, the user has selected 'Select one or more pre-defined regions'. A dropdown menu is open, showing a list of Australian states and territories: South Australia, Macquarie Island, Australian Capital Territory, Coral Sea Islands, Ashmore and Cartier Islands, New South Wales, Queensland, Western Australia, Northern Territory, and Victoria. The 'South Australia' option is highlighted. Below the dropdown, there is a 'Buffer radius (km)' input field.

Once selected, users can also add a buffer (units in km) to their pre-defined regions. Adding a buffer can sometimes be useful to ensure complex boundaries (e.g. coastlines) are appropriately captured within the study region.

Where a predefined region is not available users can manually draw their extent on the provided map. To do this, select “Draw extent on map”. Users can then either draw a box around the region of interest or draw their own complex polygon over the region of interest. Simply specify the draw mode (Box or Poly) required, then press “Start

Drawing”. Then draw your extent on the map the map provided. If you wish to undo a drawing, simply press “Clear”.



1a. Define Region Template

Irrespective of whether a pre-defined or drawn extent is used, users must specify the study region coordinate system and resolution that the workflow will use to construct the risk map. This is specified under the subheading “Region Template”.

By default, Biosecurity Commons uses a 1km Australian Albers (equal area) projection layer. Extents are rasterized using the coordinate system and resolution defined in “Region Template”.

Users can select a finer Australian Albers template from the dropdown menu.

Region Template *

Raster template that determines the final CRS, resolution and boundaries



✓ Australia 1km

Australia 500m

Australia 200m

Australia 100m

Australia 50m

However, if users wish to use a different coordinate system, they are required to select “Add New Input” and select a raster with the desired coordinate system and resolution either from previously uploaded datasets or results, or from existing curated datasets, or else upload a new raster for this purpose using the import/upload option.

▼ Data Inputs



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

2. Choose your own study region

Users may also opt to specify their own study region by providing the workflow with an existing raster object. In the “Select an alternative input” menu, users have several ways to choose their own study region raster (see screenshot below).

⊕ Add a new input for 'Study Region - template'

1
Select Input Type

▼ From Workflow

▼ Crop to Region
Create a custom region from one or more predefined regions

📄 Australia 1km

▼ Data Inputs

📄 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

Custom label

✕ Cancel

- **Choose from My Results:** Choose a study region from your results if you have completed previous projects.
- **Explore My Datasets:** To search for datasets you have previously uploaded. This will load a window allowing you to search through datasets you have previously uploaded. 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.
- **Explore Curated Datasets:** Search the curated datasets available on Biosecurity Commons. Given the vast number of datasets provided by the platform, we **strongly recommend** using the filtering functionality to navigate for appropriate datasets. 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.
- **Import/Upload data:** Use this option to upload your own study region in GeoTIFF format. Select this option and then select “Upload my own data”. Select your data type (see first screenshot below) and then choose the file you want to upload. Click the blue “Next” button and then you will be required to add a title, description, and information regarding the rights associated with the dataset (see second screenshot below). Finally, click “Finish” and your dataset will be imported (see third screenshot below). Select the uploaded dataset and then click the blue “Add new Input” button.

⊕ Add a new input for 'Study Region - template'

1 Select Input Type < Select data source Select data type

2 Import data

Please select the type of data you are about to upload:

Species Occurrence	CSV (lat, lon, month?)
Species Absence	CSV (lat, lon, month?)
Multi-Species Occurrence	CSV (lat, lon, month, species)
Multi-Species Absence	CSV (lat, lon, month, species)
Species Trait	CSV (lat, lon, species)
Generic Spatial Points	CSV (lat, lon, ...)
Generic Aspatial	CSV (...)
Generic Spatial Raster	GeoTiff
Current Climate	GeoTiff
Future Climate	GeoTiff
Environmental	GeoTiff
Future Environmental	GeoTiff
Bias or Targeted Background File	GeoTiff

⊕ Add a new input for 'Study Region - template' x

1 Select Input Type < Upload data Provide metadata

2 Import data

Title (required)

Description (required)

Rights

Type of Dataset (required)
Continuous ▾

CRS
EPSG:4283

Resolution
[250.00000,-250.00000]

Extent
[8560218.01535,8502218.01535,680630.23500,727380.23500]

Fill in the metadata for this Generic Spatial Raster dataset.
Once all metadata has been filled in, click "Finish".

→ Finish

Cancel

Back No Selection

⊕ Add a new input for 'Study Region - template' x

1 Select Input Type

2 Import data

Show Datasets 1 result 1

My datasets

Year All

Collection
Filter by collection...

Month filter
Filter by month...

Demo

Demo study region

others spatial-raster

Select

View

Info

1

Step 3. Threat Suitability

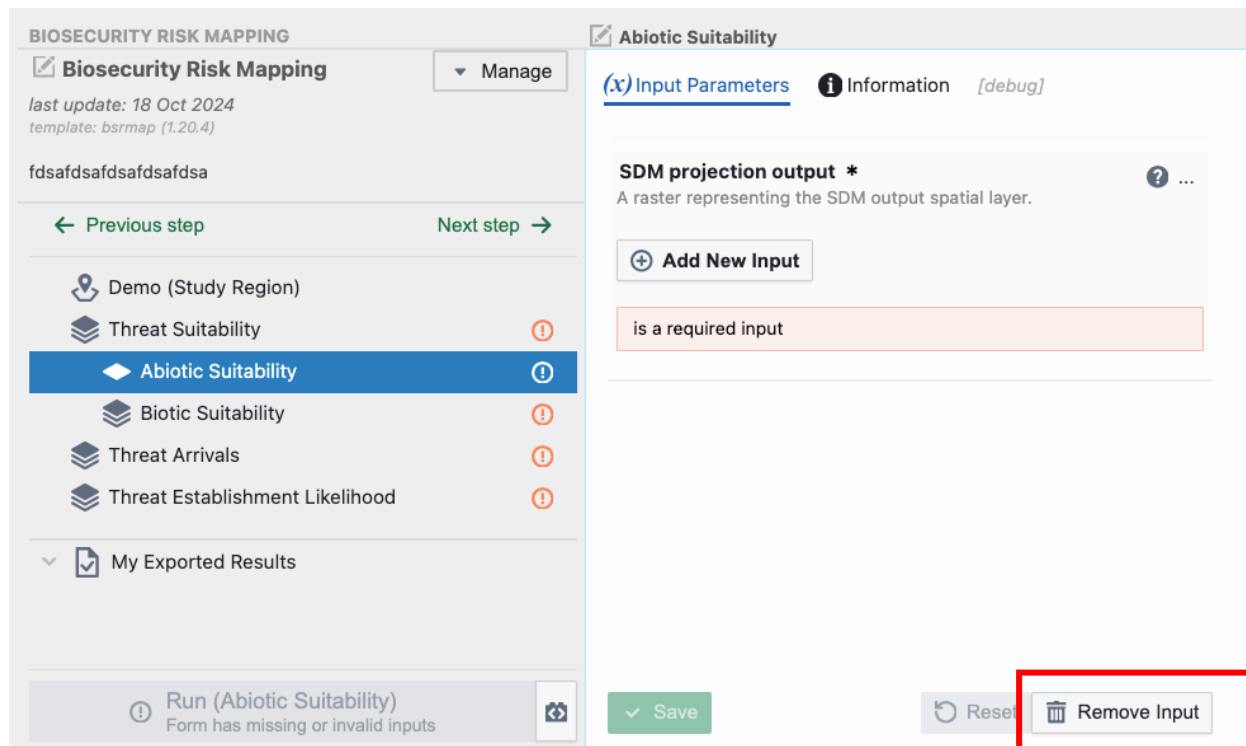
The Threat Suitability step is by default made up of two components:

- **Abiotic suitability:** A spatial layer that defines the suitability of the abiotic environment (i.e. non-living factors such as climate) that may be conducive for threat survival and establishment
- **Biotic suitability:** A spatial layer that defines the suitability of the biotic environment (i.e. living environment, such as habitat or host availability) that may be conducive for threat survival and establishment.

While both factors are often critical barriers to threat establishment, there may be cases where a threat may not be exposed to ambient climatic conditions (e.g. pests of stored produce) making the abiotic environment an unnecessary component. Alternatively, some Species Distribution Models may explicitly account for both biotic and abiotic factors, and thus, remove the need to separate both forms of suitability.

If only one of these two factors is relevant, the platform allows users to easily remove a factor. To do this, simply select “Abiotic Suitability” or “Biotic Suitability” and then click “Remove Input” at the bottom of the screen. This will remove the requirement for this component to be completed within the workflow.

NOTE: *The risk mapping workflow combines abiotic suitability, biotic suitability, and arrival pathways by multiplying the layers together. It is therefore important to carefully consider how each layer is constructed and the values it contains. Using the approach specified in Camac et al. 2021, each layer should ideally represent the relative probability of either suitability or arrival. Thus, each component should be on the proportional scale if assuming equal weighting of components. To maximise flexibility in use (and allow for differential weighting to each component), Biosecurity Commons does not enforce these layers to be bounded between (0 and 1).*



The screenshot shows the 'Biosecurity Risk Mapping' interface. On the left is a sidebar with a navigation menu containing 'Demo (Study Region)', 'Threat Suitability', 'Abiotic Suitability' (highlighted), 'Biotic Suitability', 'Threat Arrivals', 'Threat Establishment Likelihood', and 'My Exported Results'. The main area is titled 'Abiotic Suitability' and shows 'SDM projection output *' with a description: 'A raster representing the SDM output spatial layer.' Below this is an 'Add New Input' button and a message 'is a required input'. At the bottom, there is a 'Run (Abiotic Suitability)' button with a warning icon and the text 'Form has missing or invalid inputs', a green 'Save' button, a 'Reset' button, and a 'Remove Input' button which is highlighted with a red box.

In the following sections, we briefly outline how each suitability component can be defined and included in a risk map workflow.

1. Abiotic Suitability

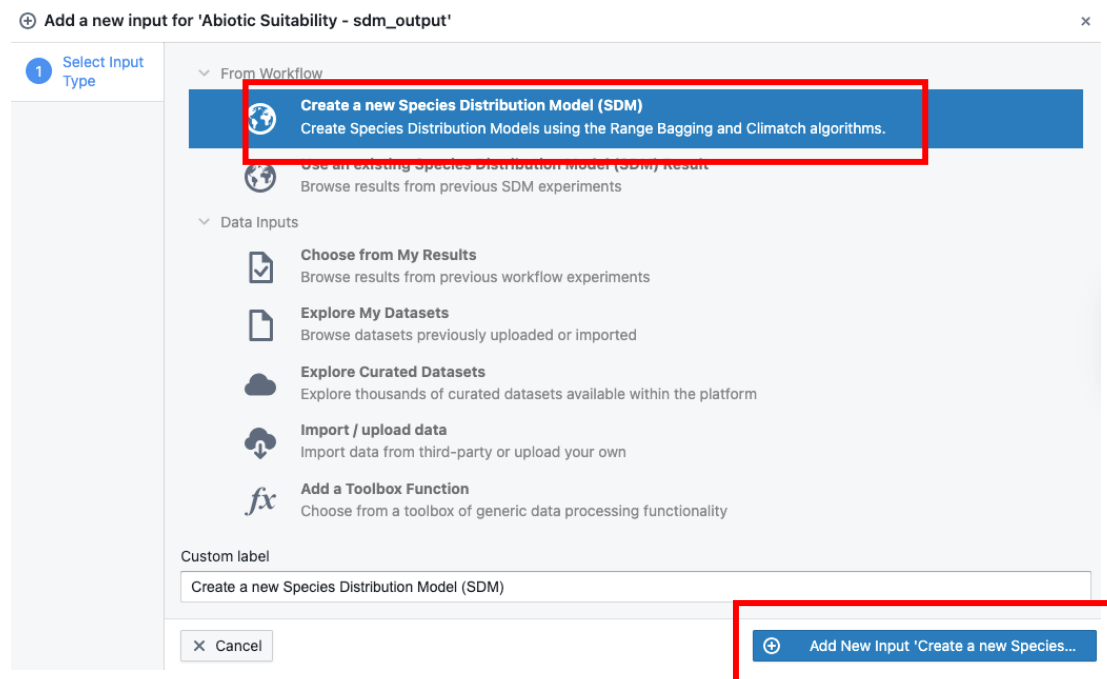
In most cases, the abiotic suitability layer refers to the climatic suitability for a threat. Commonly this is derived from some form of species distribution model.

Within the risk mapping workflow, users can define this component in four primary ways:

- Create a new abiotic layer using SDM functionality within the risk mapping workflow
- Import an existing SDM created in a SDM project
- Upload a SDM output built off-platform, or import from “Curated Datasets” or “My Datasets”
- Create a custom suitability layer by combining spatial layers using Toolbox Functionality

1a. Create a new Species Distribution Model (SDM) within the Risk Mapping workflow

The first option is to fit a SDM directly within the risk map project. To do this, select “Create a new Species Distribution Model (SDM)” and then click the blue “Add New Input” button.



This feature allows users to create a SDM within the Risk Mapping workflow. When selected, several sub-steps will appear in the tree (see screenshot below).

BIOSECURITY RISK MAPPING

Biosecurity Risk Mapping ▼ Manage

last update: 8 Oct 2024
template: bsrmap (1.19.3)

Biosecurity Risk Mapping

← Previous step Next step →

- Australia 1km (Study Region)
- Threat Suitability ⓘ
- Abiotic Suitability ⓘ
- ⓘ
 - SDM PROJECTION OUTPUT**
 - Create a new Species Distribution Model (SDM)**
 - Occurrences ⓘ
 - Climate Predictors ⓘ
 - Algorithms ⓘ
- Biotic Suitability ⓘ
- Threat Arrivals ⓘ
- Threat Establishment Likelihood ⓘ

▼ My Exported Results

Create a new Species Distribution Model (SDM)

Information

ⓘ 3 or more inputs may contain missing input

Description
Create Species Distribution Models using the Range

Attribution
Range Bagging: Drake, J. M. (2015). Range bagging: presence-only data. *Journal of the Royal Society Interface*. doi:10.1098/rsif.2015.0086
Climatch: ABARES (2020). Climatch v2.0 User Manual. Accessed: November 2021.

Schema Id
https://schema.biosecuritycommons.org.au/bssdm/t

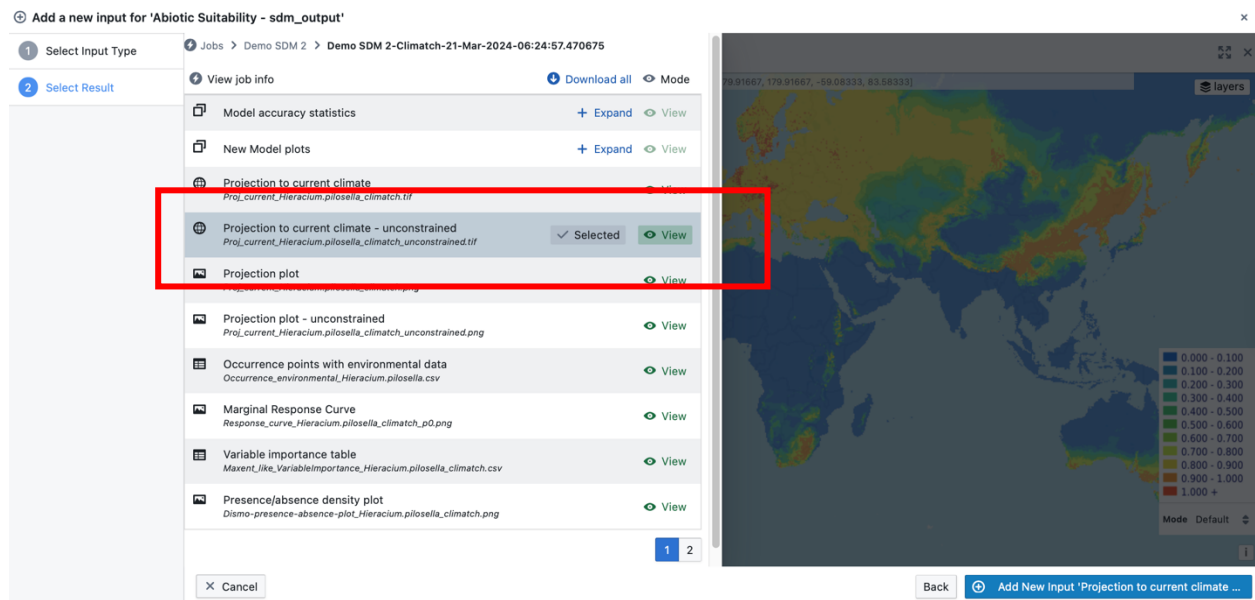
Pipeline Id
https://gitlab.com/ecocommons-australia/biosecurity

To produce a successful SDM, please follow the instructions in our [SDM start guide](#).

1b. Use an existing Species Distribution Model (SDM) result

The second option is to import an existing SDM project output created on Biosecurity Commons. To do this, select “Use an existing Species Distribution Model (SDM) Result” and then click the blue “Next” button.

This allows users to choose a SDM from their results. Find the relevant project, click on it and then select the output file named “Projection to current climate – unconstrained”. Once this is done, click the blue “Add New Input” button. This will import the SDM into the Risk Mapping workflow.



1c. Upload a SDM output built off-platform or import from “Curated Datasets” or “My Datasets”

If a user has created a SDM file offline or off-platform, it can be uploaded and used within the risk mapping workflow by doing the following:

“Select Add New Input” > “Import / upload data” > “Upload my own data”, then specify the data type (often Generic Spatial Raster) and upload a GeoTIFF of your abiotic suitability layer.

Alternatively, as in most cases, users can explore their own previously uploaded datasets or available curated datasets for specifying abiotic suitability.

1d: Create a custom suitability layer by combining spatial layers using Toolbox functionality (*ADVANCED USERS*)

Biosecurity Commons also provides advanced users the ability to combine and modify existing raster objects in many ways to construct new spatial objects that can be used in a variety of contexts, including informing abiotic and biotic suitability. To use this functionality, select “Add a Toolbox Function”.








Users will then be able to select from a range of raster manipulation options (see below).

⊕ Add a new input for 'Abiotic Suitability - sdm_output'

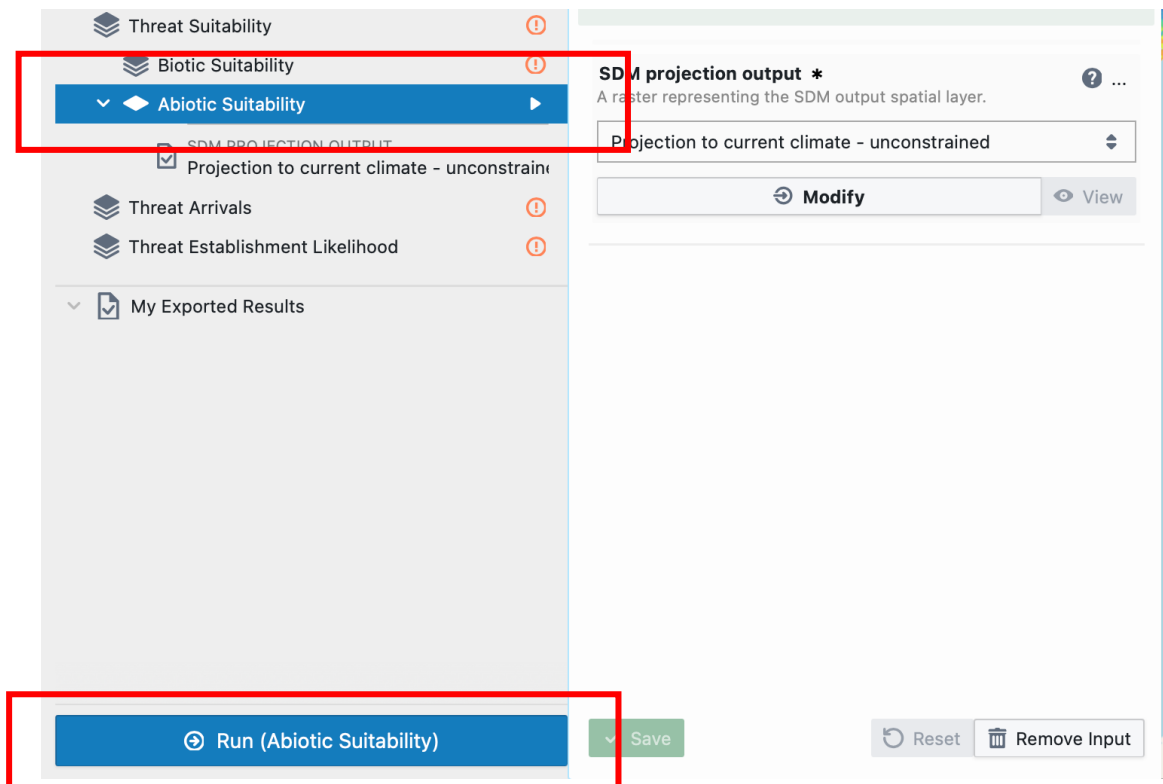
1 Select Input Type

2 Select Function

From Workflow

-  **Buffers & Hulls**
Create a hull or apply buffers to a spatial points
-  **Conform Layer**
Normalize or binarize a layer. The output will be conformed to the project 'study region'.
-  **Crop To Region**
Crop a raster by applying a custom bounding box or predefined region
-  **Combine Layers**
Combines multiple spatial layers via (optionally weighted) cell-wise multiplication, addition, or union (via complements), and optionally binarizes the output.
-  **Transform Layer**
Transforms a spatial layer via a variety of operations, including the application of: linear, exponential, or logarithmic expressions; or lower or upper thresholds; to layer values.
-  **Select Categories**
Aggregate any categorical data
-  **Distance Weight Layer**
Calculates a distance-weighted (negative exponential function) probability where cells surrounding a focal cell are given lower probability values as the radial distance from the focal cell increases.

Once a user has specified their abiotic layer and pressed the green save button, they can then click the “Abiotic Suitability” tab on the left-hand panel and click the “Run” button in the lower left-hand corner to complete this step in the tree (see screenshot below).



The screenshot shows a workflow tree on the left and a detailed view of the 'SDM projection output *' step on the right. The 'Abiotic Suitability' step is highlighted with a red box. At the bottom, the 'Run (Abiotic Suitability)' button is also highlighted with a red box. Other buttons like 'Save', 'Reset', and 'Remove Input' are visible at the bottom right.

2. Biotic Suitability

Biotic suitability often refers to the suitability of the living environment at a location. This can be defined in many ways, including:

- Fitting a separate SDM for a host species, or habitat type
- Inferring suitability based on vegetation or land use or other landscape attributes

Broadly the biotic suitability component follows a similar path as the abiotic suitability section stepped through above. However, there are a few unique differences.

First when users select biotic suitability and then select “Add New Inputs”, they have easy access to high resolution land use and vegetation classification rasters that are commonly used in biotic suitability approximations (see below).

⊕ Add a new input for 'Biotic Suitability - predictors'

1 Select Input Type


From Workflow

Combine Layers


fx **Land Use - Secondary (ACLUM/ABARES)**
Catchment Scale Land Use of Australia, ABARES, Secondary Categories, 2 arcsec (~50m)


fx **Land Use - Tertiary (ACLUM/ABARES)**
Catchment Scale Land Use of Australia, ABARES, Tertiary Categories, 2 arcsec (~50m)


fx **NVIS Vegetation Types**
Australia, National Vegetation Information System (NVIS) V6.0


 **Australian NDVI (Normalised Difference Vegetation Index)**
Normalised Difference Vegetation Index, October 2018 - March 2019

Data Inputs

 **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

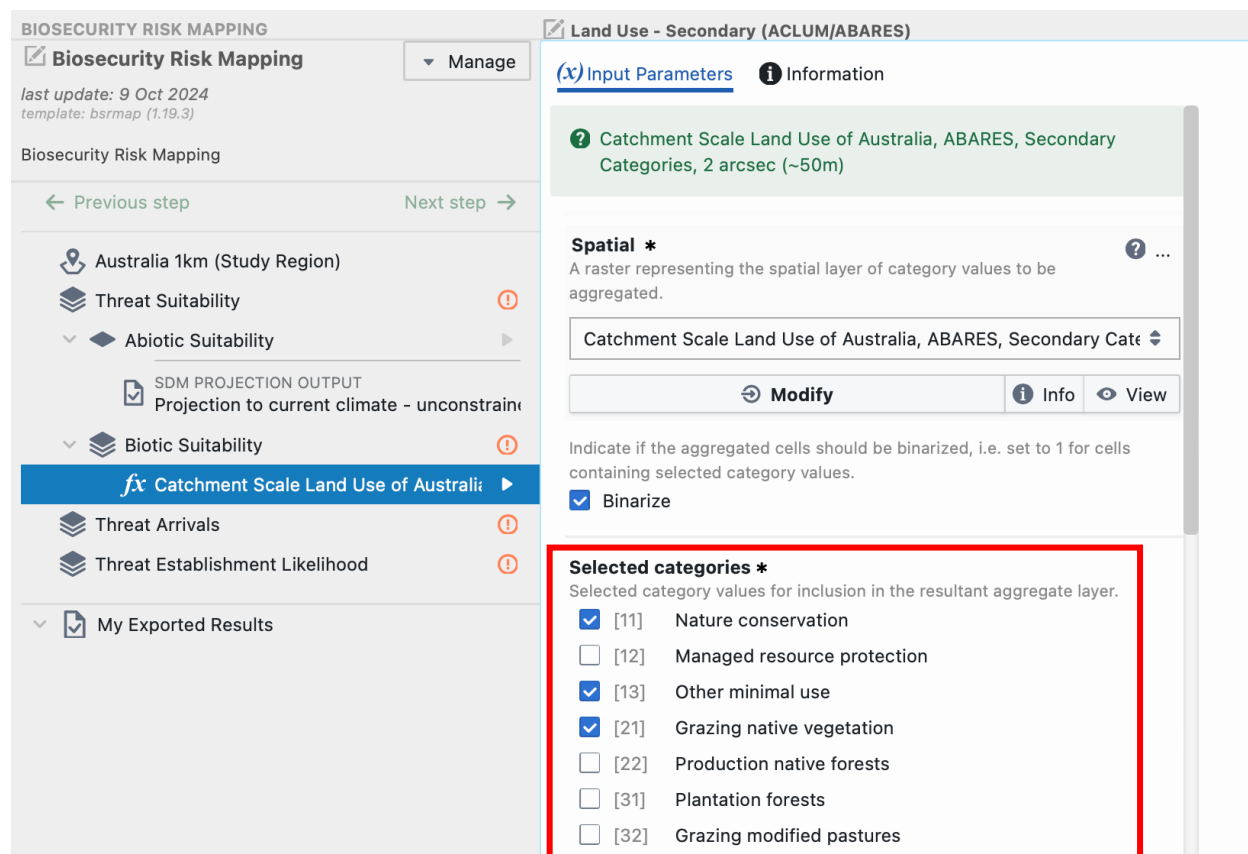
 **Import / upload data**
Import data from third-party or upload your own

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

Users can select one or more of these, explore datasets in either “My Results” or “Curated Datasets” or import a new dataset in the same way as is described above and is commonly done elsewhere on the platform.

The key distinction with biotic suitability is that it allows users to easily convert one or more multi-class rasters into a raster that can be used to inform biotic suitability.

For example, if a user selects “Land Use – Secondary (ACLUM/ABARES)” as an input, they will then be prompted to select suitable classes (see below).



BIOSECURITY RISK MAPPING

Biosecurity Risk Mapping Manage

last update: 9 Oct 2024
template: bsrmap (1.19.3)

Biosecurity Risk Mapping

← Previous step Next step →

- Australia 1km (Study Region)
- Threat Suitability
- Abiotic Suitability
 - SDM PROJECTION OUTPUT
Projection to current climate - unconstrained
- Catchment Scale Land Use of Australia**
- Threat Arrivals
- Threat Establishment Likelihood
- My Exported Results

Land Use - Secondary (ACLUM/ABARES)

(x) Input Parameters Information

Catchment Scale Land Use of Australia, ABARES, Secondary Categories, 2 arcsec (~50m)

Spatial *
A raster representing the spatial layer of category values to be aggregated.

Catchment Scale Land Use of Australia, ABARES, Secondary Cate

Modify Info View

Indicate if the aggregated cells should be binarized, i.e. set to 1 for cells containing selected category values.

Binarize

Selected categories *
Selected category values for inclusion in the resultant aggregate layer.

- [11] Nature conservation
- [12] Managed resource protection
- [13] Other minimal use
- [21] Grazing native vegetation
- [22] Production native forests
- [31] Plantation forests
- [32] Grazing modified pastures

In addition to checking the categories that are deemed suitable for the threat, users can also define whether they want to create a binary (i.e. suitable versus unsuitable) raster or calculate the proportion of area containing suitable land classes at the defined Study Region resolution.

Checking the Binarize tick-box will convert all selected classes to 1, and all non-selected classes to 0 in the grid cells of the map. If Binarize is not selected it will calculate the proportional area containing suitable land use types (in this case the fraction of each 1km² cell that is comprised of suitable 50m² cells, since the land use raster has 50m² resolution and the study region has 1km² resolution).

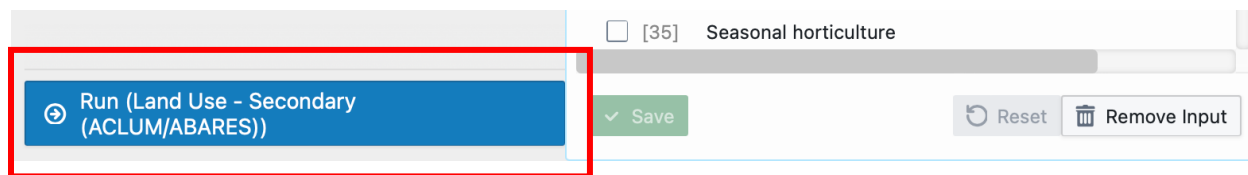
NOTE: If users are constructing a biotic suitability layer as a function of multiple input rasters, they should carefully inspect the “Use function” argument, which defines how multiple objects will be combined.

Currently three options are available:

- Prod – Multiply the layers together (Most commonly used option)
- Sum – Sum the layers together
- Union – Calculate the union via $1 - \text{prod}(1 - x)$. This is mostly used for probability layers where one is interested in calculating the likelihood of one or more layers being suitable.

If users wish for the combined output to be binary, they can select “Binarize”. This will binarize across layers and assign 1 to any non-zero/non-NA cell value.

Once the biotic suitability layer has been defined, click Save and then click Run.



When the function has run successfully, the orange exclamation mark next to your layer in the tree will turn into a green tick.

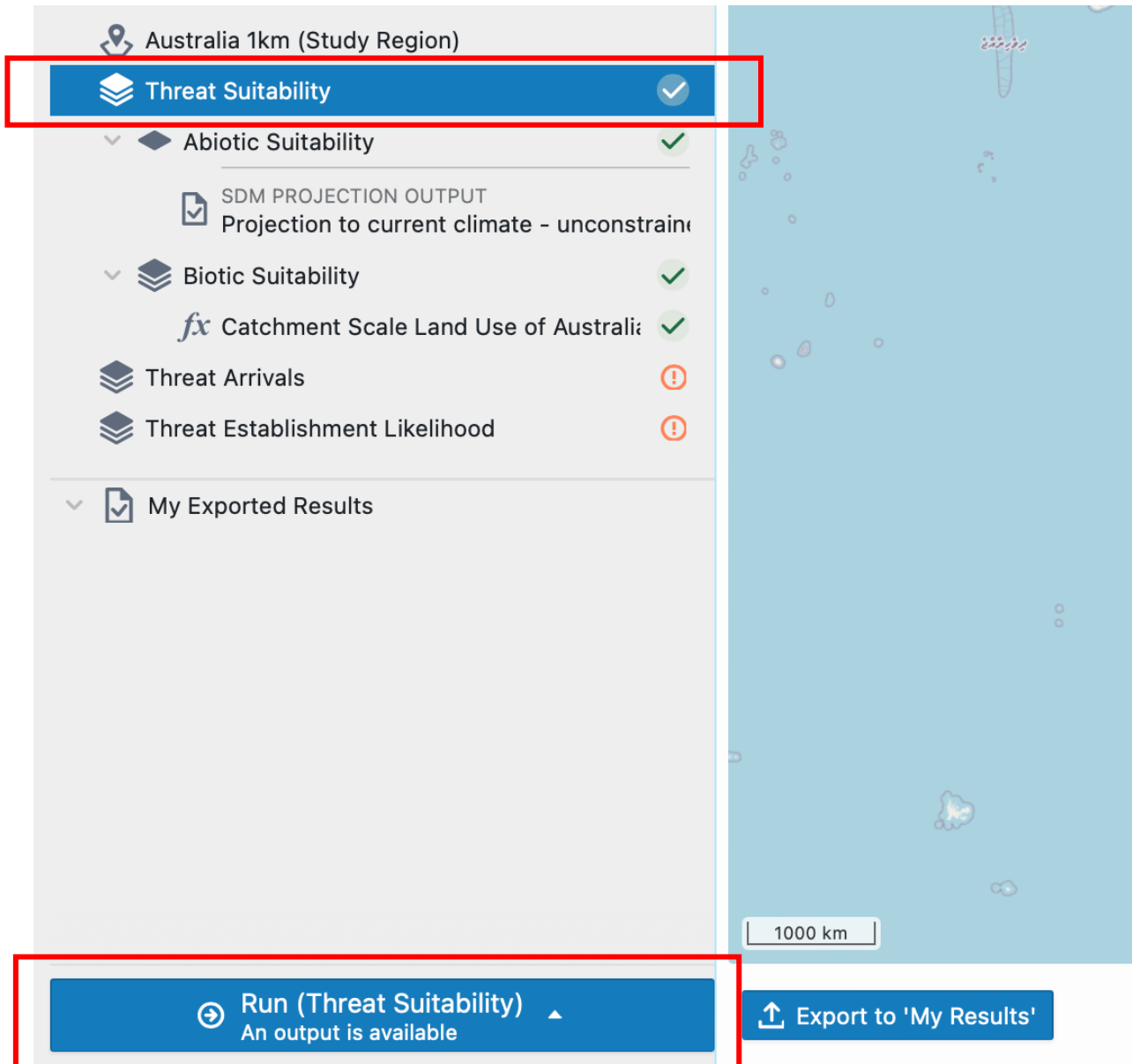
You can also click the “Export to ‘My Results’” button, which will appear next to the Run button after the layer has run successfully.

This allows users to add this layer to the “My results” section of their dashboard. From this section users may download this layer, make it available for use in other workflows, or share it with other registered users of Biosecurity Commons. Users can also view or download the R script used to generate the layer, the log file, the metadata, or the input parameters json file.

Finally, click on the Biotic Suitability step in the tree and select the blue “Run” button to complete this step.

3. Threat Suitability

Once the mandatory abiotic and biotic suitability functions have run successfully (green tick), or have been removed (if not required), select “Threat Suitability” in the tree and run the function to complete this stage (see screenshot below).



The screenshot displays the Biosecurity Commons interface. On the left, a sidebar menu shows a tree view of the workflow. The 'Threat Suitability' function is highlighted with a red box. Below it, 'Abiotic Suitability' and 'Biotic Suitability' are shown with green checkmarks, indicating successful completion. Under 'Abiotic Suitability', there is a sub-item 'SDM PROJECTION OUTPUT' with a sub-label 'Projection to current climate - unconstrained'. Under 'Biotic Suitability', there is a sub-item 'Catchment Scale Land Use of Australia' with a green checkmark. Below these, 'Threat Arrivals' and 'Threat Establishment Likelihood' are shown with red exclamation marks, indicating they are not yet completed. At the bottom of the sidebar, 'My Exported Results' is visible. On the right, a map of Australia is shown with a 1000 km scale bar. At the bottom of the interface, a blue button labeled 'Run (Threat Suitability)' with a play icon and the text 'An output is available' is highlighted with a red box. To its right is another blue button labeled 'Export to 'My Results'' with an upload icon.

Step 4. Threat Arrivals

The fourth step involves approximating the likelihood of an arrival event in each location (i.e. the propagule pressure).

While this component is included by default, users may remove this input the same way as they can remove the abiotic or biotic component, by simply selecting the branch (i.e. Threat Arrivals) and then selecting “Remove input”.









However, if users wish to account for likelihood of arrival, they can add relative weighting layers for one or more pathways of entry.

Simply click “Add New Input” to add one or more threat arrival layers, representing the different modes of entry into Australia. Users will then see the menu in the screenshot below which provides the option of adding predefined curated functions for pest arrivals. These predefined options are derived directly from Camac et al. 2021 (see below).



⊕ Add a new input for 'Threat Arrivals - pathway_likelihood_layers'

1 Select Input Type

From Workflow

-  **Generic Pathway**
User defined Threat Pathway
-  **Human Pathway**
Distribute risk by human population
-  **Tourists Pathway**
Tourist arrivals are distributed across an accommodation layer weighted by airport distance
-  **Torres Strait Arrivals Pathway**
Torres strait arrivals are distributed across human density weighted by Cairns airport distance
-  **Vessels Pathway**
Vessels are distributed across a layer weighted by sea port distance
-  **Containers Pathway**
Containers are distributed across container postcode distribution layers
-  **Agriculture Pathway**
Agricultural products distributed as a function of NRM fertiliser usage statistics
-  **Wind Pathway**
Wind pathways are constructed via speed-based wind band layers for winds coming from the north, the Pacific ocean, and from New Zealand. They can optionally be distance weighted using distance from the coast (a pre-curated layer)

Data Inputs

-  **Choose from My Results**
Browse results from previous workflow experiments
-  **Explore My Datasets**

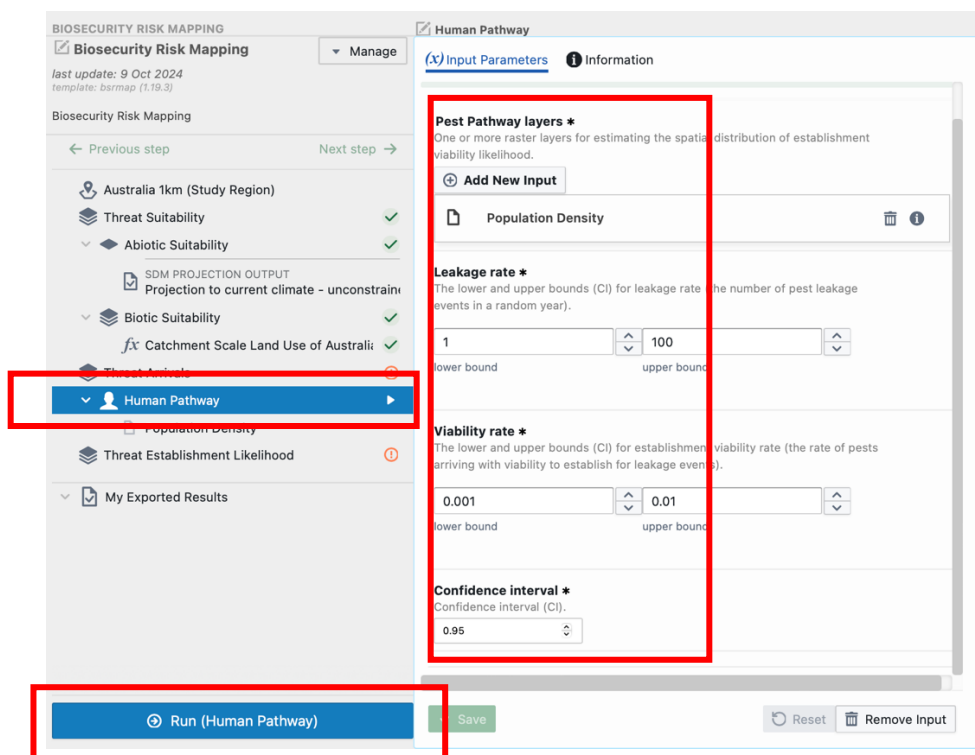
Custom label

Users can also create their own custom raster for distributing pathway risk by selecting Generic Pathway, which will prompt the user to specify one or more weighting rasters.

In the example below (see screenshot), the Human Pathway layer is selected, and a new step appears in the tree. The user can modify the following:

- Pest Pathway layers: A proportional weighting raster for distributing arrivals. In the example below the proportion of human population density is used
- Leakage rate: The lower and upper confidence limits of the expected number of contaminated events per time period (e.g. year) that pass pre-border and border inspection procedures
- Viability rate: The lower and upper confidence limits of the probability that a contaminated item that passes border inspection procedures is viable for potential establishment (prior to considering abiotic and biotic suitability of the arrival destination)
- Confidence interval: the confidence level associated with the lower and upper confidence limits provided above (default 0.95)

For more details about these parameters, please consult the [risk mapping support material](#).



After updating the parameters, click “Save” and then “Run” the function to generate the result. If successful, the Human Pathway layer will show a green tick.

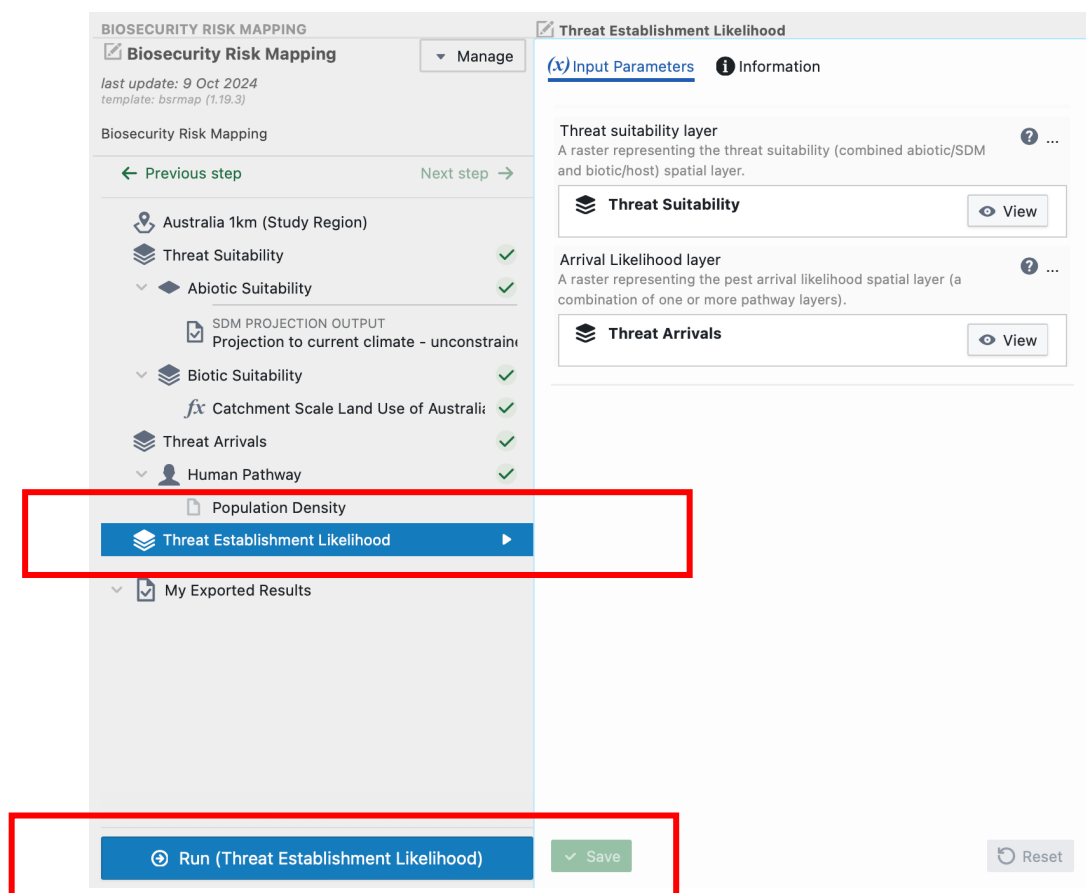
This step can be repeated for any of the other pathway options available.

Finally, to complete this section of the tree click on “Threat Arrivals” and then click on the blue “Run” button to turn the exclamation mark to a green tick.

Step 5. Threat Establishment Likelihood

Once the Threat Suitability and Threat Arrivals functions have been successfully run you will be able to run the overall Threat Establishment Likelihood function (see screenshot below).

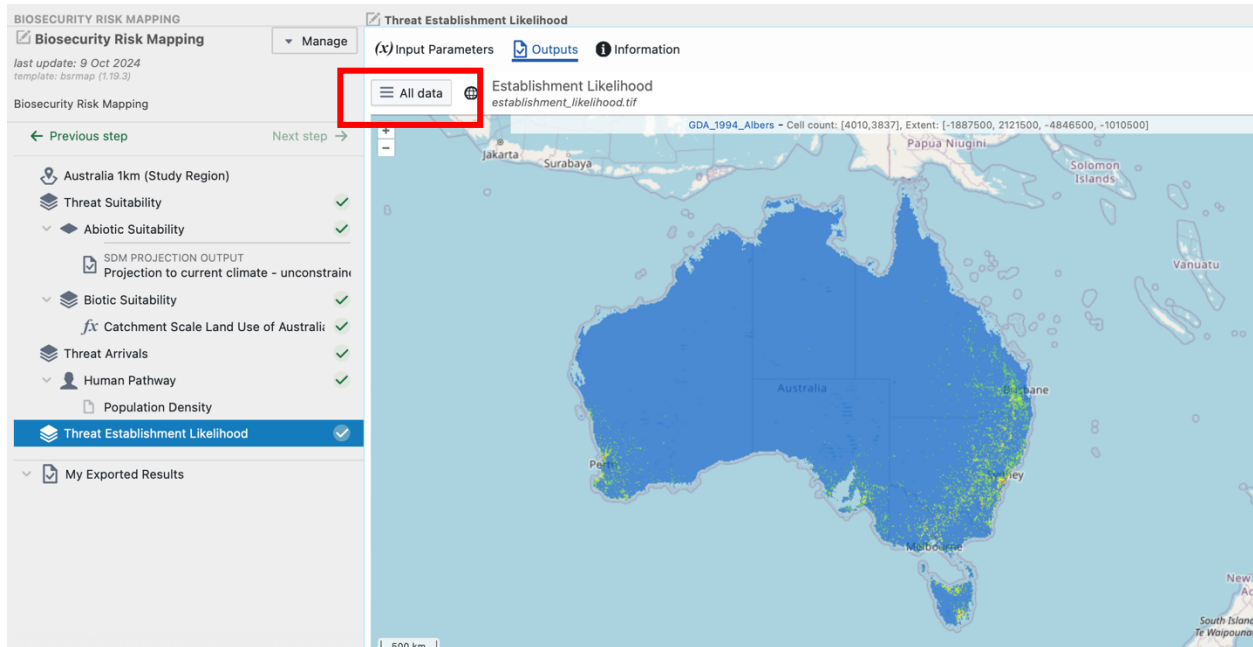
Click the blue ‘Run’ button in the bottom left to run your project. The output page will be updated as the job progresses from “Created”, “Submitted”, “Started” and “Success”.



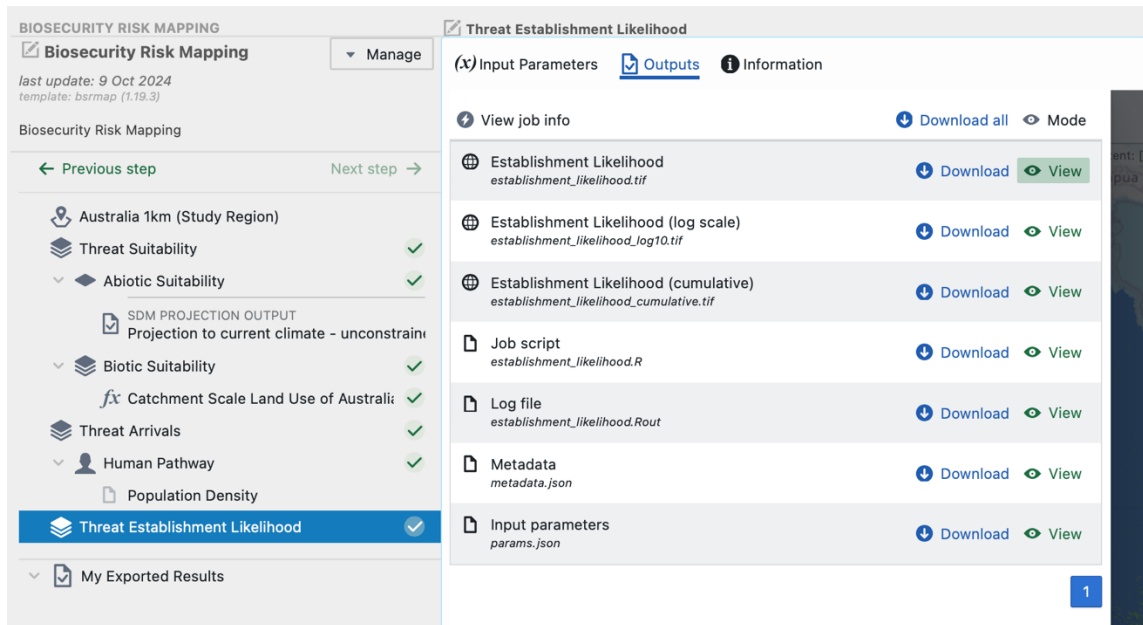
The screenshot displays the 'BIOSECURITY RISK MAPPING' interface. On the left, a tree view shows the workflow steps: 'Australia 1km (Study Region)', 'Threat Suitability' (with a green checkmark), 'Abiotic Suitability' (with a green checkmark), 'SDM PROJECTION OUTPUT Projection to current climate - unconstrained', 'Biotic Suitability' (with a green checkmark), 'Catchment Scale Land Use of Australia' (with a green checkmark), 'Threat Arrivals' (with a green checkmark), 'Human Pathway' (with a green checkmark), 'Population Density', 'Threat Establishment Likelihood' (highlighted with a red box and a right-pointing arrow), and 'My Exported Results'. On the right, the 'Threat Establishment Likelihood' configuration panel is shown, featuring 'Input Parameters' and 'Information' tabs. It includes two layers: 'Threat suitability layer' (described as a raster representing threat suitability) and 'Arrival Likelihood layer' (described as a raster representing pest arrival likelihood). Each layer has a 'View' button. At the bottom of the interface, a blue 'Run (Threat Establishment Likelihood)' button and a green 'Save' button are highlighted with red boxes, along with a grey 'Reset' button.

Once it has finished, a green tick will appear next to Threat Establishment Likelihood.

The model output will automatically be displayed as a viewable risk map in the interactive map pane (screenshot below). Users can zoom in or out of regions of interest. Interactive maps also allow users to change the type of legend displayed.



Clicking on the “All data” button allows users to view and download all the outputs.



These outputs include:

- **Establishment Likelihood:** The relative likelihood of establishment conditioned on threat suitability and/or Threat arrivals
- **Establishment Likelihood (log scale):** The relative likelihood on the log10 scale. Useful for viewing exceedingly small probabilities
- **Establishment Likelihood (cumulative):** Calculated by ranking raster cells based on their establishment likelihood and then computing the cumulative sum so that each cell's value represents the likelihood of threat establishment in that cell or any cell with a higher likelihood. Useful for highlighting locations with highest risk of establishment
- **Job script:** A copy of the R script used to build the risk map
- **Log file:** A text file containing processes, messages, and other details associated with model runs
- **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

Step 6. 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 “Export to My Results” in the bottom left corner of the interactive map.

This output will now be discoverable in the user's “My results” database, which in turn makes the layer available for use in other workflows.