**Note of information**

The repertory you can download contains two sub-repertories. The first one, called “scripts” contains all scripts you can use at will to test surrogacy analysis. The second one, called ‘input” contains all input data and functions necessary to make the scripts running. A short description of each file and its content is given in table 1.

**How to use our surrogacy analysis algorithms**

In the sub-directory “scripts”, you can find all scenarios tested. You can test surrogacy for diversity, richness, or rarity indices, for taxonomic data or functional data, or you can evaluate robustness of surrogacy analysis by successively reducing the initial dataset (27 stations) to a fewer number of stations (22 to 26 stations).

When you open with Tinn-R a particular script to run (i.e. a particular analysis to do), you must, first of all, indicate the “input” directory each time the input directory is defined in the script:

* open the directory “surrogacy.analysis” you downloaded
* copy the repertory path (by right click, copy)
* open the script you want to run
* click on: search/replace/
  + in ‘find for’, enter: "C:/Documents and Settings/vanw/Bureau/R"
  + in ‘Replace with’, click right, paste. Make sure to have a path composed by ‘/’ instead of ‘\’
  + click ok for all findings.

Then, you can connect Tinn-r with R (R/start Rterm) and run the analysis by “R:send file”.

**Results obtained**

At the end of the run, you obtain a matrix such as the one exposed in table 2. This matrix summarize all SAI calculated.

Note that the basic script of surrogacy analysis can take from 1 to 2 hours depending on computer rapidity. Analysis of robustness consist in 99 random suppressions of stations, and can therefore take several days.

**Tables**

Table 1 : Content of files you can find in ‘input’ directory

|  |  |
| --- | --- |
| File name | Content |
| Fish data |  |
| REQ\_site\_fonction.IRD | Functional groups observed at each sampling site |
| REQ\_site\_poisson.IRD | Species observed at each sampling site |
| abondance.midif\_sim\_output | Occurrence of functional class attributes at each sampling site |
| abondance\_taxo\_IRD | Occurrence of species observed at each sampling site |
| Habitat data |  |
|  |  |
| fc3\_intersect\_geo1 | Polygons of habitats based on coarse geomorphology present in the neighborhood of stations. Each line corresponds to a polygon. Colons give sampling site, neighborhood distance, and habitat surface associated |
| fc3\_intersect\_geo2 | Polygons of habitats based on medium geomorphology present in the neighborhood of stations. Each line corresponds to a polygon. Colons give sampling site, neighborhood distance, and habitat surface associated |
| fc3\_intersect\_geo3 | Polygons of habitats based on detailed geomorphology present in the neighborhood of stations. Each line corresponds to a polygon. Colons give sampling site, neighborhood distance, and habitat surface associated |
| fc3\_intersect\_bent1 | Polygons of topography based habitats present in the neighborhood of stations. Each line corresponds to a polygon. Colons give sampling site, neighborhood distance, and habitat surface associated |
| fc3\_intersect\_bent2 | Polygons of habitats based on coral cover present in the neighborhood of stations. Each line corresponds to a polygon. Colons give sampling site, neighborhood distance, and habitat surface associated |
| fc3\_intersect\_bent3 | Polygons of habitats based on overall benthic cover present in the neighborhood of stations. Each line corresponds to a polygon. Colons give sampling site, neighborhood distance, and habitat surface associated |
| fc3\_intersect\_geo1\_geo2 | Polygons of habitats based on the combination of coarse and medium geomorphology present in the neighborhood of stations. Each line corresponds to a polygon. Colons give sampling site, neighborhood distance, and habitat surface associated |
| fc3\_intersect\_geo1\_geo2\_geo3 | Polygons of habitats based on the combination of all three geomorphologic characterizations present in the neighborhood of stations. Each line corresponds to a polygon. Colons give sampling site, neighborhood distance, and habitat surface associated |
| fc3\_intersect\_g1\_g2\_g3\_b1 | Polygons of habitats based on the combination of geomorphology and topography, present in the neighborhood of stations. Each line corresponds to a polygon. Colons give sampling site, neighborhood distance, and habitat surface associated |
| fc3\_intersect\_g1\_g2\_g3\_b1\_b2 | Polygons of habitats based on the combination of geomorphology, topography, and coral cover, present in the neighborhood of stations. Each line corresponds to a polygon. Colons give sampling site, neighborhood distance, and habitat surface associated |
| fc3\_intersect\_g1\_g2\_g3\_b1\_b2\_b3 | Polygons of habitats based on all geomorphologic characterizations and all benthic characterizations, present in the neighborhood of stations. Each line corresponds to a polygon. Colons give sampling site, neighborhood distance, and habitat surface associated |
| R Scripts |  |
|  |  |
| Selecting sites |  |
| script.aleatoire.r | R script which select successively sampling sites, randomly |
| script.richesse.complementarite.r | R script which select successively sampling sites, on the bases of their fish or habitat richness |
| script.rarete.complementarite.r | R script which select successively sampling sites, on the bases of their fish or habitat rarity index |
| script.shannon.r | R script which select successively sampling sites, on the bases of their habitat diversity |
| script.shannon.poissons.r | R script which select successively sampling sites, on the bases of their fish diversity |
|  |  |
| Calculate fish characteristics in selected sites network | |
| script.diversite.selectionnee.r | R script which give fish species richness index of a given network of stations |
| script.diversite.selectionnee.fonction.r | R script which give fish functional richness of a given network of stations |
| script.diversite.rarete.selectionnee.r | R script which give fish rarity index of a given network of stations |
| script.diversite.shannon.selectionnee.fonction.r | R script which give fish functional diversity index of a given network of stations |
| script.diversite.shannon.selectionnee.r | R script which give fish species diversity index of a given network of stations |
| Assessing SAI index |  |
| script.sai.r | R script which calculate SAI index given i) the optimal accumulation curve, the tested accumulation curve, and the random accumulation curve. |

Table 2 : General configuration of the matrix summarizing SAI results for all habitats characterizations and all neighborhood distances tested. Geo1: Corase geomorphology; geo2: medium geomorphology; geo3: detailed geomorphology; bent1: topography ; bent2: coral cover; bent3: prevailing benthic cover.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Habitat/distance | All stations | 1st random run of suppressions of X stations | 2nd random run of suppressions of X stations | Etc… |
| Geo1/30m | SAI | SAI | SAI | SAI |
| Geo1/60m | SAI | SAI | Etc… |  |
| Geo1/100m |  |  |  |  |
| Geo1/250m |  |  |  |  |
| Geo1/500m |  |  |  |  |
| Geo1/750m |  |  |  |  |
| Geo1/1000m |  |  |  |  |
| Geo1/3000m |  |  |  |  |
| Geo1/5000m |  |  |  |  |
| Geo2/30m |  |  |  |  |
| Geo2/60m |  |  |  |  |
| Geo2/100m |  |  |  |  |
| Geo2/250m |  |  |  |  |
| Geo2/500m |  |  |  |  |
| Geo2/750m |  |  |  |  |
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| Geo3/100m |  |  |  |  |
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| Geo3/1000m |  |  |  |  |
| Geo3/3000m |  |  |  |  |
| Geo3/5000m |  |  |  |  |
| Bent1/30m |  |  |  |  |
| Bent1/60m |  |  |  |  |
| Bent1/100m |  |  |  |  |
| Bent1/250m |  |  |  |  |
| Bent1/500m |  |  |  |  |
| Bent1/750m |  |  |  |  |
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| Bent1/3000m |  |  |  |  |
| Bent1/5000m |  |  |  |  |
| Bent2/30m |  |  |  |  |
| Bent2/60m |  |  |  |  |
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| Bent3/30m |  |  |  |  |
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| Bent3/5000m |  |  |  |  |
| Geo1.geo2/30m |  |  |  |  |
| Geo1.geo2/60m |  |  |  |  |
| Geo1.geo2/100m |  |  |  |  |
| Geo1.geo2/250m |  |  |  |  |
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| Geo1.geo2/750m |  |  |  |  |
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| Geo1.geo2/3000m |  |  |  |  |
| Geo1.geo2/5000m |  |  |  |  |
| Geo1.geo2.geo3/30m |  |  |  |  |
| Geo1.geo2.geo3/60m |  |  |  |  |
| Geo1.geo2.geo3/100m |  |  |  |  |
| Geo1.geo2.geo3/250m |  |  |  |  |
| Geo1.geo2.geo3/500m |  |  |  |  |
| Geo1.geo2.geo3/750m |  |  |  |  |
| Geo1.geo2.geo3/1000m |  |  |  |  |
| Geo1.geo2.geo3/3000m |  |  |  |  |
| Geo1.geo2.geo3/5000m |  |  |  |  |
| Geo1.geo2.geo3.bent1/30m |  |  |  |  |
| Geo1.geo2.geo3.bent1/60m |  |  |  |  |
| Geo1.geo2.geo3.bent1/100m |  |  |  |  |
| Geo1.geo2.geo3.bent1/250m |  |  |  |  |
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| Geo1.geo2.geo3.bent1.bent2/60m |  |  |  |  |
| Geo1.geo2.geo3.bent1.bent2/100m |  |  |  |  |
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