

## Using raster file

This is a basic example which shows you how to run sensitivity analysis on pre-loaded parameters. As a pre-requisite, install package using

```
devtools::install_github("GarrettLab/CroplandConnectivity", subdir = "geohabnet",  
auth_token = "your PAT")
```

Package offers 2 ways to use custom raster file - using `parameters.yaml` and `sa_onrasters` which is also used internally to create raster object using the provided source.

Loading package

```
library(geohabnet)
```

```
get_parameters()
```

Set the `file` parameter under `Hosts` to the absolute path of `raster` file -

Hosts:

```
monfreda: ["avocado"]  
spam:  
  file: "full-path-to-tif/avocado_HarvestedAreaFraction.tif"
```

Feed the updated parameters to package -

```
set_parameters("parameters.yaml")
```

Raster files ends with extension `.tif`. Since, the internal workflow only uses harvested fractional area of a cropland, we recommend using raster files as specified in this dataset. For this particular example, we will use `spam2017V2r1_SSA_H_BEAN_A.tif` from the **monfreda**.

```
# Generate raster object  
# replace the tif file with actual path after download  
> rr <- get_crop_raster_fromtif("spam2017V2r1_SSA_H_BEAN_A.tif")  
> rr  
class      : RasterLayer  
dimensions : 2160, 4320, 9331200  (nrow, ncol, ncell)  
resolution : 0.083333, 0.083333  (x, y)  
extent     : -180, 179.9986, -89.99928, 90  (xmin, xmax, ymin, ymax)  
crs       : +proj=longlat +datum=WGS84 +no_defs  
source    : spam2017V2r1_SSA_H_BEAN_A.tif  
names     : spam2017V2r1_SSA_H_BEAN_A
```

To ensure we have the correct raster,

```
raster::plot(rr)
```

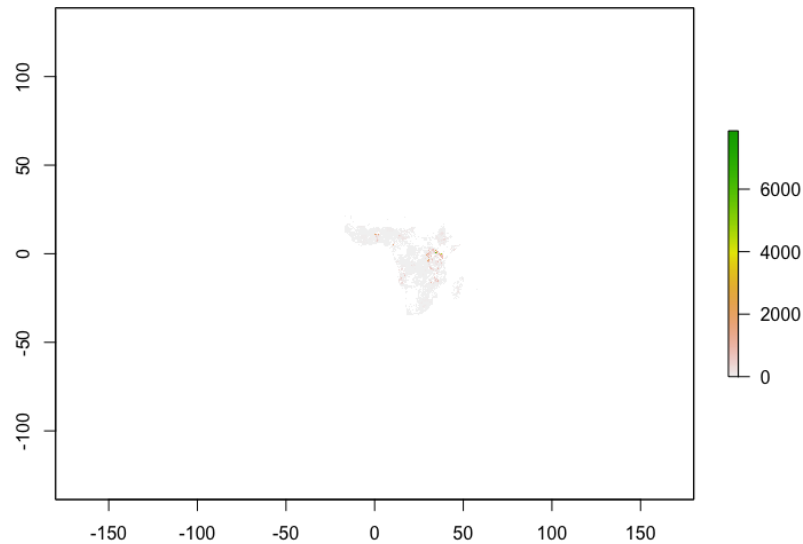


Figure 1: Raster plot for Beans

Next, once you have all the values ready, run risk analysis with `geohabnet::sa_onrasters()`

```
geohabnet::sa_onrasters(cropharvest_raster = rr,  
                        geo_scales = list(c(-50, 50, -50, 50)),  
                        link_thresholds = c(0),  
                        host_density_thresholds = c(0.0000015),  
                        resolution = 24)
```

On successful analysis, function will produce output maps. See example below.

If the extent is incorrect and no valid cells can be discovered based threshold, then analysis will be interrupted and error will be thrown -

```
Error in .extract_cropland_density(the$cropharvest_aggtm_crop, host_density_threshold) :  
  host density threshold: 0.00015 is greater than the max value: -Inf of aggregate raster
```

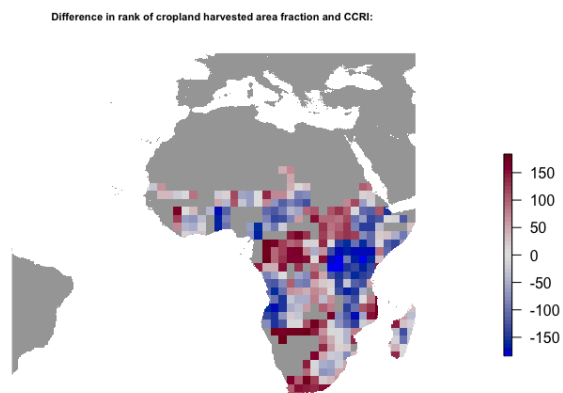


Figure 2: Difference map