The R function to get the python input is currently the following:

GetPythonIn(coordinates, polygon, sampletable, speciestable)

coordinates = a table of the input point coordinates, with 3 columns in the following order: identifier (character), YCOOR (numeric), XCOOR (numeric)

polygon = a table of the input points for the polygons with three columns in the following order: identifier (polygonname, character), XCOOR (numeric), YCOOR (numeric))

sampletable = a table with 2 columns, in the following order, with the following haeders: identifier(sample name, character), homepolygon (name of the polygon the sample was classified to, character)

speciestable = a table with ncol = n Polygons and nrow = number species; summarizing the number of occurences per species per polygon

The easiest way to produce the graphical output from python is:

Copy the R library to your working directory

Start R

>setwd(“path\_of\_your\_working\_directory”)

>source(“SpecieGeoCodeR.R”)

>dummy <- GetPythonIn(coordinates, polygon, sampletable, speciestable)

>WriteTablesSpGeo(dummy)

>PlotOutSpGeo(dummy)

Close R. The files should now be in the working directory.