# Little Handbook of RPPA analysis in R

1. You need to install the R scripts for RPPA analysis:

install.packages(file.choose(), type="source", repos=NULL)

S:\CI\ci-mo\Mollenhauer Group\RPPA\R scripts\rppa.zip

1. You can initialize any library with the command  
   library(packageName), e.g. library(rppa)
2. You can install additional packages that are required through  
   install.packages(“packageName”), you’ll need  
   1. ggplot2
   2. reshape
   3. plyr
   4. manipulate
   5. gridExtra
   6. grid
   7. tcltk2

# Method overview:

spots always refers to a slide data frame that has been imported from CSV. Remember that changes are only persisted if the user does so actively, e.g. ab7792 <- rppa.set.title(ab7792, “fancy title”)

**Get and set title:**

rppa.set.title(spots, title)

rppa.get.title(spots)

**Get and set blocks per row (for heatmap):**

rppa.set.blocksPerRow(spots, 12)

rppa.get.blocksPerRow(spots)

**Correct horizontal and vertical shifts (through columns hshift and vshift in the input data)**

rppa.vshift(spots)

rppa.hshift(spots)

**Compare raw data through box plots:**

rppa.boxPlotComparison(spots)

**Heatmap:**

rppa.heatmap(spots)

rppa.compare.heatmap(spotsA, spotsB)

**Reorder sample names:**

rppa.reorderFactors(spots)

**Plot raw data:**

rppa.slide.plot(spots)

**Make concentrations Plot:**

rppa.slide.concentration.plot

**Serial Dilution Curve algorithm:**

Single slide convenience plot (can be manipulated):

rppa.serialDilution(spots)

Single slide manual plot with returned results:

rppa.serialDilution.factor(spots)

The layout of the plot can be manipulated for example through:

* normalize.depositions = T/F
* unify.depositions = T/F
* normalize.each.cellLine =T/F
* plot.serial.dilution = T/F

Whole slide normalization (using estimated protein amounts):

rppa.serialDilution(spots, normalizationSpots)

Single dilution normalization, e.g. for Sypro Ruby:

rppa.serialDilution(spots, normalizationSpots, 0.25)

In order to compare several slides under the serial dilution curve algorithm use in similar fashion:

rppa.compare.serialDilution(list(spotsA, spotsB), …)

and

rppa.compare.serialDilution.factor(list(spotsA, spotsB), …)