

The pepStat user guide

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A step-by-step guide in the analysis of peptide microarray antibody binding

Contents

1	Introduction	2
2	Generating a peptideSet	2
3	Normalizing the peptideSet	2
4	Making calls	2

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1 Introduction

As with any R package, it should first be loaded in the session.

```
> library(pepStat)
```

2 Generating a peptideSet

The reading function takes a path as its argument and parse all the files in the given directory.

```
> mapFile <- system.file("extdata/mapping.csv", package = "pepStat")
> dirToParse <- system.file("extdata/RVV", package = "pepStat")
> pSet <- makePeptideSet(files = NULL, path = dirToParse, mapping.file = mapFile,
+   rm.control.list = c("empty", "none", "JPT-", "Ig", "Cy",
+   "landmark"), log = TRUE)
```

A new object of class `peptideSet`. It contains only the sequence of the peptides and the intensities measured. Any additional information must be passed using a known collection of peptides. In this example, we use `pep_hxb2` available in the `PEP.db` package.

```
> library(PEP.db)
> data(pep_hxb2)
> psSet <- summarizePeptides(pSet, summary = "mean", position = pep_hxb2)
```

`pep_hxb2` gives information regarding the position of each peptide, their z-scores, the clades they belong to and the alignment with the reference sequence HXB2.

3 Normalizing the peptideSet

```
> pnSet <- NormalizeArray(psSet)
```

4 Making calls

```
> Vsum <- subset(psSet, treatment != "PLACEBO")
> Vnorm <- subset(pnSet, treatment != "PLACEBO")
> V_smooth <- slidingMean(Vnorm, width = 9)
> cutoff <- 1.1
> V_calls <- makeCalls(V_smooth, cutoff = cutoff, method = "absolute")
```