

Statistical analysis code for analysis of CASTxB6 F2 mouse cross

3. Preservation of liver modules in adipose expression data

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1 Setting up the R session and loading of data

In this document we detail the calculation of network preservation statistics between liver and adipose expression data of the CASTxB6 cross. We use the WGCNA package [1] to calculate the network preservation statistics. The first step of the analysis is to set the working directory. We recommend to use a subdirectory (folder) within the directory in which the network calculations (part 2) were performed.

```
# Set working directory. This step is necessary if your data is saved in a directory other than the current
directory. Replace the path name below with the directory where the data is stored on your drive.
# setwd("Z:/home/plangfelder/Work/Mouse-ReciprocalCXB/CxBOnly/NetworkAnalysis/Preservation-LiverInAdipose");
# Load the WGCNA library
library(WGCNA)
# This setting is important, do not leave out
options(stringsAsFactors = FALSE);
options(width = 109)
set.seed(1); #needed for .Random.seed to be defined
```

We now set up a few basic variables and load the preprocessed expression data as well as module labels. Liver and adipose will be indexed 1 and 2, respectively. The files necessary for this step have been generated in parts 1 and 2 of the analysis. Adjust file paths below to point correctly to the necessary files.

```
tissueLabels = c("Liver", "Adipose");
nTissues = length(tissueLabels);
# Load expression data. Change file names (paths) if necessary.
files = c("../CxBOnly-Liver-outliersRemoved-exprFemaOR-pValFemaOR.RData",
          "../CxBOnly-Adipose-outliersRemoved-exprFemaOR-pValFemaOR.RData");
express = list();
for (tis in 1:nTissues)
{
  x = load(file = files[tis]);
  express[[tis]] = list(data = exprFemaOR);
}
expr = express;
rm(express);
collectGarbage();
# Load module labels
load(file = "../Female-LA-labels-MEs-ordMEs-afterCleaning.RData");
colors = lapply(labels, labels2colors)
```

```
# Assign necessary names
names(labels) = tissueLabels;
names(expr) = tissueLabels;
collectGarbage()
```

Next we call the module preservation function. This calculation can take several hours. It may be best to run it overnight. At the end we save the results so they can be re-used in future runs.

```
mp = modulePreservation(expr,
                        labels,
                        randomSeed = 948521,
                        referenceNetworks = c(1:2),
                        nPermutations = 100,
                        networkType = "signed hybrid",
                        corFnc = "bicor",
                        quickCor = 0,
                        greyName = 0,
                        verbose = 3);
save(mp, file = "modulePreservation-mp.RData");
```

We continue this analysis in Part 4, after calculating the preservation in male data and in other crosses.

References

- [1] Peter Langfelder and Steve Horvath. WGCNA: an R package for weighted correlation network analysis. *BMC Bioinformatics*, 9(1):559, 2008.