

Analysis of Pixel-Wise Correlations

So far we've only looked at the mean stain levels between different patients. However, this ignores any spatial processes that might play a role. In order to start gaining a first insight into what spatial processes might play a role we'll here analyse the pixel-wise correlation matrices for the cores from different patients. This will for example highlight the presence/absence of specific cell types/meta-phenotypes.

1 A First Look at the Data

I compute the correlation matrices using python and save the lower triangular parts of these matrices to file. In order to adjust for the different scales of the stains I calculate the standardised correlations using the `np.corrcoef()` function.

Let's load in the results and label the columns with the correlation they measure:

```
corrArr = read.csv("pixelcorrelations.csv",header=F)
dim(corrArr)

## [1] 121 668

# Label the columns
labelArr = c("CoreId", "PtSnty")
markerLabelsVec = c('SrBCK', 'RR101', 'RR102', 'AvantiLipid', 'XeBCK', 'CD196', 'CD19', 'Vimentin',
                    'CD163', 'CD20', 'CD16', 'CD25', 'p53', 'CD134', 'CD45', 'CD44s', 'CD14', 'FoxP3',
                    'CD4', 'E-cadherin', 'p21', 'CD152', 'CD8a', 'CD11b', 'Beta-catenin', 'B7-H4', '
                    'CollagenI', 'CD3', 'CD68', 'PD-L2', 'B7-H3', 'HLA-DR', 'pS6', 'HistoneH3', 'DNA
                    'DNA193')

for (i in seq(2,37)) {
  for (j in seq(i-1)) {
    labelArr = c(labelArr, paste0(markerLabelsVec[i], ":", markerLabelsVec[j]))
  }
}
names(corrArr) = labelArr
```

Let's compute the difference in the mean matrix of the responders and the non-responders and visualise it to see if there are any obvious differences

```
library(ggplot2)
library(reshape2)
corrArr = corrArr[with(corrArr, order(PtSnty)), ]
corrArr = data.frame(corrArr, LinId=seq(nrow(corrArr)))
corrArr_reshaped = melt(corrArr[, -1], id.vars=c("LinId"))
ggplot(corrArr_reshaped, aes(variable, LinId)) +
  geom_tile(aes(fill = value), colour="white") +
  scale_fill_gradient(low="white", high="steelblue") +
  theme_bw() +
  labs(x="", y="Core") +
  theme(axis.text.x = element_text(angle=90, hjust=1))
```

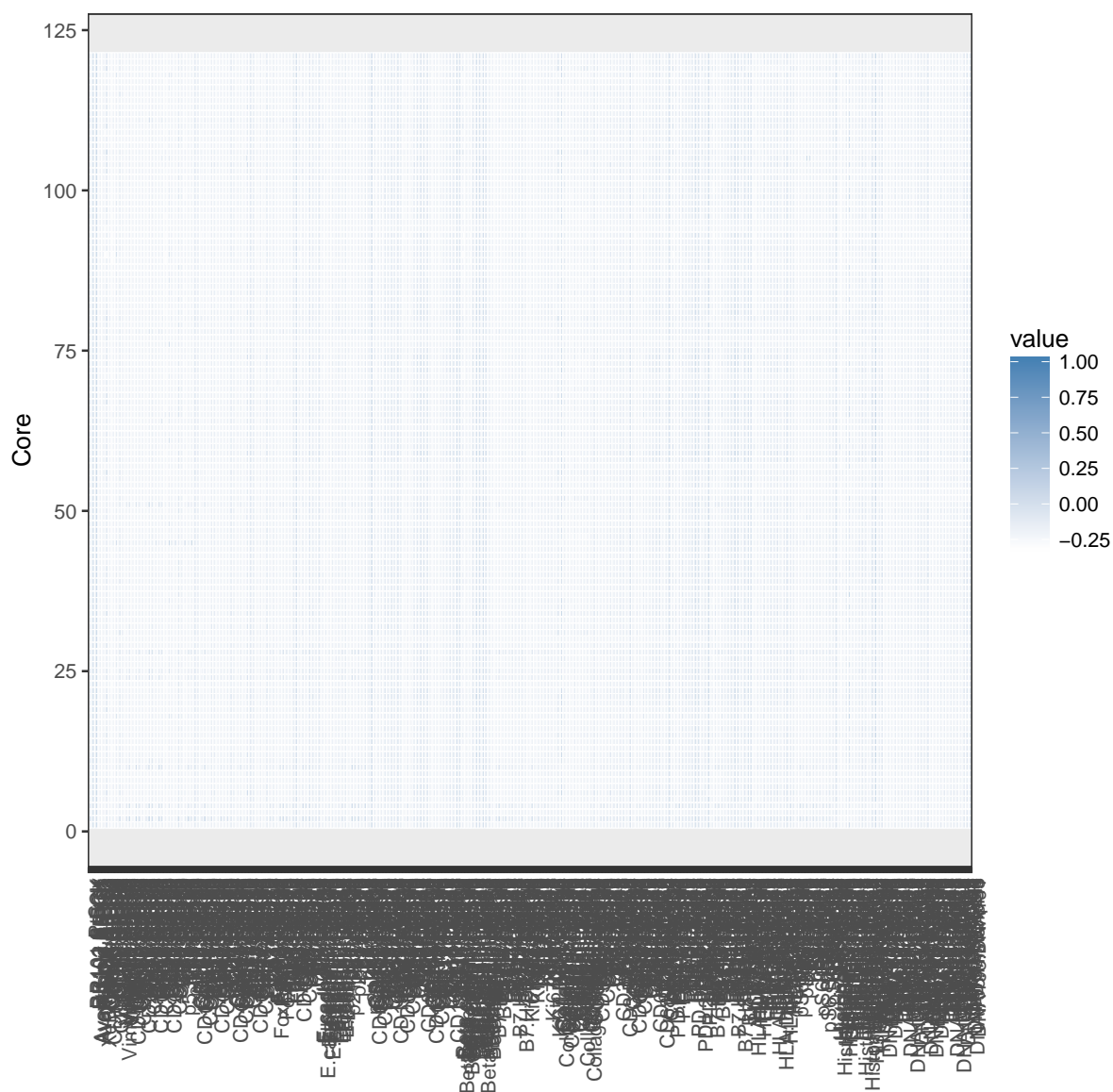


Figure 1: Pixel-wise correlation of the different stains for responders (top-half) and non-responders (bottom-half).