

Integration of copy number and transcriptomics provides risk stratification in prostate cancer: A discovery and validation cohort study Ross-Adams et al. (2015) doi:10.1016/j.ebiom.2015.07.017

In this document, I describe how the GEO data entry for the Stockholm (validation) cohort of Ross-Adams et al (2015) data was processed and saved into an object for analysis in Bioconductor. First of all load the relevant libraries for grabbing and manipulating the data

```
> library(GEOquery)
```

Now use the `getGEO` function with the correct ID. If the series matrix file has already been downloaded, don't bother to download again.

```
> url <- "ftp://ftp.ncbi.nlm.nih.gov/geo/series/GSE70nnn/GSE70769/matrix/"
> destfile <- "GSE70769_series_matrix.txt.gz"
> if(!file.exists(destfile)){
+   download.file(paste(url,destfile,sep=""),destfile=destfile)
+ }
> geoData <- getGEO(filename=destfile)
```

We tidy up the data from GEO; creating a new data frame of just the clinical characteristics of interest. Make sure that only NA is used for missing values.

The pheno data also contains the five `iCluster` groups which were determined by integrative clustering.

```
> pd <- pData(geoData)
> pd2 <- data.frame("geo_accession" = pd$geo_accession,
+   Sample = gsub("tumour tissue_robotic radical prostatetctomy_", "", pd$title),
+   Gleason = gsub("tumour gleason: ", "", pd$characteristics_ch1),
+   ECE = gsub("extra capsular extension (ece): ", "", pd$characteristics_ch1.2, fixed=TRUE),
+   PSM = gsub("positive surgical margins (psm): ", "", pd$characteristics_ch1.3, fixed=TRUE),
+   BCR = gsub("biochemical relapse (bcr): ", "", pd$characteristics_ch1.4, fixed=TRUE),
+   Time = gsub("time to bcr (months): ", "", pd$characteristics_ch1.5, fixed=TRUE),
+   iCluster = gsub("derived data (iclusterplus group): ", "", pd$characteristics_ch1.6, fixed=TRUE),
+   PSA = gsub("psa at diag: ", "", pd$characteristics_ch1.7, fixed=TRUE),
+   ClinicalStage = gsub("clinical stage: ", "", pd$characteristics_ch1.8, fixed=TRUE),
+   PathStage = gsub("pathology stage: ", "", pd$characteristics_ch1.9, fixed=TRUE),
+   FollowUpTime = gsub("total follow up (months): ", "", pd$characteristics_ch1.10, fixed=TRUE),
+   pd2$iCluster <- gsub("NA", NA, pd2$iCluster)
+   pd2$Gleason <- gsub("N/A", NA, pd2$Gleason)
+   pd2$Gleason <- gsub("unknown", NA, pd2$Gleason)
+   pd2$ECE <- gsub("UNKNOWN", NA, pd2$ECE)
+   pd2$ECE[which(pd2$ECE == "")] <- NA
+   pd2$PSM <- gsub("UNKNOWN", NA, pd2$PSM)
+   pd2$PSM[which(pd2$PSM == "")] <- NA
+   pd2$BCR <- gsub("N/A", NA, pd2$BCR)
+   pd2$BCR[which(pd2$BCR == "")] <- NA
```

```

> pd2$Time <- gsub("N/A", NA, pd2$Time)
> pd2$Time <- gsub("UNKNOWN",NA,pd2$Time)
> pd2$Time[which(pd2$Time == "")] <- NA
> pd2$FollowUpTime <- gsub("N/A", NA, pd2$FollowUpTime)
> pd2$FollowUpTime <- gsub("UNKNOWN",NA,pd2$FollowUpTime)
> pd2$FollowUpTime[which(pd2$FollowUpTime == "")] <- NA
> rownames(pd2) <- pd2$geo_accession
> pData(geoData) <- pd2
> stockholm <- geoData
> save(stockholm, file="data/stockholm.rda",compress="xz")

```