# Hiiragi Dataset

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### Gene expression in mammalian embryonic tissues.

The following RMarkdown document explores the data from "Cell-to-cell expression variability followed by signal reinforcement progressively segregates early mouse lineages" (Ohnishi et al. 2014).

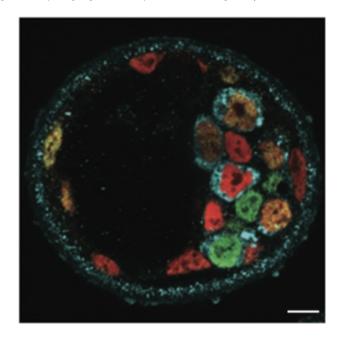
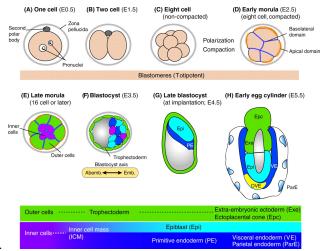


Figure 1: Heterogeneity in protein expression level of the EPI and PrE markers Serpinh1 (blue), Gata6 (red), Nanog (green)



The following graphic is from (Rossant and Tam 2009).

### Modern Statistics for Modern Biology

This dataset is explored in the book Modern Statistics for Modern Biology.

#### Chapter 3 - High quality graphics

```
http://web.stanford.edu/class/bios221/book/Chap-Graphics.html#rgraphics:sec:exampledata
```

```
## Loading required package: affy
## Loading required package: BiocGenerics
## Loading required package: parallel
##
## Attaching package: 'BiocGenerics'
##
  The following objects are masked from 'package:parallel':
##
       clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##
##
       clusterExport, clusterMap, parApply, parCapply, parLapply,
       parLapplyLB, parRapply, parSapply, parSapplyLB
##
## The following objects are masked from 'package:stats':
##
##
       IQR, mad, sd, var, xtabs
## The following objects are masked from 'package:base':
##
##
       anyDuplicated, append, as.data.frame, basename, cbind, colnames,
       dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,
##
##
       grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,
##
       order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
##
       rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,
##
       union, unique, unsplit, which, which.max, which.min
## Loading required package: Biobase
## Welcome to Bioconductor
##
##
       Vignettes contain introductory material; view with
##
       'browseVignettes()'. To cite Bioconductor, see
       'citation("Biobase")', and for packages 'citation("pkgname")'.
##
```

```
## Loading required package: boot
## Loading required package: clue
## Warning: package 'clue' was built under R version 4.0.2
## Loading required package: cluster
## Loading required package: genefilter
## Loading required package: geneplotter
## Loading required package: lattice
##
## Attaching package: 'lattice'
## The following object is masked from 'package:boot':
##
##
       melanoma
## Loading required package: annotate
## Loading required package: AnnotationDbi
## Loading required package: stats4
## Loading required package: IRanges
## Loading required package: S4Vectors
##
## Attaching package: 'S4Vectors'
## The following object is masked from 'package:base':
##
##
       expand.grid
## Loading required package: XML
## Loading required package: gplots
##
## Attaching package: 'gplots'
## The following object is masked from 'package: IRanges':
##
##
       space
## The following object is masked from 'package:S4Vectors':
##
##
       space
## The following object is masked from 'package:stats':
##
##
       lowess
## Loading required package: gtools
## Attaching package: 'gtools'
## The following objects are masked from 'package:boot':
##
##
       inv.logit, logit
```

```
## Loading required package: KEGGREST
## Loading required package: MASS
##
## Attaching package: 'MASS'
## The following object is masked from 'package: AnnotationDbi':
##
##
       select
## The following object is masked from 'package:genefilter':
##
##
## Loading required package: mouse4302.db
## Loading required package: org.Mm.eg.db
##
##
## Loading required package: RColorBrewer
## Loading required package: xtable
           File.name Embryonic.day Total.number.of.cells lineage genotype
## 1 E3.25 1 C32 IN
                             E3.25
                                                       32
## 2 E3.25 2 C32 IN
                             E3.25
                                                       32
                                                                         WT
## 3 E3.25 3 C32 IN
                             E3.25
                                                       32
                                                                         WT
## 4 E3.25 4_C32_IN
                             E3.25
                                                       32
                                                                         WT
## 5 E3.25 5_C32_IN
                             E3.25
                                                       32
                                                                         WT
## 6 E3.25 6_C32_IN
                             E3.25
                                                       32
                                                                         WT
             ScanDate sampleGroup sampleColour
## 1 E3.25 2011-03-16
                            E3.25
                                        #CAB2D6
## 2 E3.25 2011-03-16
                            E3.25
                                        #CAB2D6
## 3 E3.25 2011-03-16
                            E3.25
                                        #CAB2D6
## 4 E3.25 2011-03-16
                            E3.25
                                        #CAB2D6
## 5 E3.25 2011-03-16
                            E3.25
                                        #CAB2D6
## 6 E3.25 2011-03-16
                            E3.25
                                        #CAB2D6
##
## Attaching package: 'dplyr'
## The following object is masked from 'package:MASS':
##
##
       select
## The following object is masked from 'package:AnnotationDbi':
##
##
## The following objects are masked from 'package: IRanges':
##
       collapse, desc, intersect, setdiff, slice, union
##
## The following objects are masked from 'package:S4Vectors':
##
       first, intersect, rename, setdiff, setequal, union
##
## The following object is masked from 'package:Biobase':
```

```
##
##
       combine
## The following objects are masked from 'package:BiocGenerics':
##
       combine, intersect, setdiff, union
##
## The following objects are masked from 'package:stats':
##
##
       filter, lag
## The following objects are masked from 'package:base':
##
       intersect, setdiff, setequal, union
##
## `summarise()` ungrouping output (override with `.groups` argument)
## # A tibble: 8 x 3
##
     sampleGroup
                          n color
##
     <chr>
                      <int> <chr>
## 1 E3.25
                         36 #CAB2D6
## 2 E3.25 (FGF4-KO)
                         17 #FDBF6F
## 3 E3.5 (EPI)
                         11 #A6CEE3
## 4 E3.5 (FGF4-KO)
                          8 #FF7F00
## 5 E3.5 (PE)
                         11 #B2DF8A
## 6 E4.5 (EPI)
                          4 #1F78B4
## 7 E4.5 (FGF4-KO)
                         10 #E31A1C
## 8 E4.5 (PE)
                          4 #33A02C
                                                                         Groups
   30 -
                                                                              E3.25
                                                                              E3.25 (FGF4-KO)
                                                                              E3.5 (EPI)
   20 -
                                                                              E3.5 (FGF4-KO)
 \subseteq
                                                                              E3.5 (PE)
                                                                              E4.5 (EPI)
   10-
                                                                              E4.5 (FGF4-KO)
                                                                              E4.5 (PE)
```

E4.5 (EPI)

E3.5 (PE)

E3.5 (FGF4-KO) <sup>7</sup>

sampleGroup

E3.5 (EPI)

E3.25 (FGF4-KO) 7

E4.5 (PE) <sup>7</sup>

E4.5 (FGF4-KO) 7

## **Bibliography**

The bibliography is autogenerated and appears at the end of the document.

Ohnishi, Yusuke, Wolfgang Huber, Akiko Tsumura, Minjung Kang, Panagiotis Xenopoulos, Kazuki Kurimoto, Andrzej K. Oleå, et al. 2014. "Cell-to-cell expression variability followed by signal reinforcement progressively segregates early mouse lineages." Nature Cell Biology 16 (1): 27–37. https://doi.org/10.1038/ncb2881.

Rossant, Janet, and Patrick P. L. Tam. 2009. "Blastocyst lineage formation, early embryonic asymmetries and axis patterning in the mouse." *Development* 136 (5): 701–13. https://doi.org/10.1242/dev.017178.