

Visualize Properties of ROC's Posterior Estimates of Phi

Michael A. Gilchrist

22 Jul 2020

Preliminary Information

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

ESS Commands

See (~/Software/R/r.notes.Rmd) for more details

Load Packages and Data

```
##library(Biostrings) ## process first to avoid conflicts
library(tidyr)
library(tibble)
library(readr)
library(dplyr)

##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##     filter, lag
## The following objects are masked from 'package:base':
##     intersect, setdiff, setequal, union

library(stringr)
library(forcats)
library(ggplot2)
library(knitr)
library(ggpubr)
library(ggpmisc)
library(gridExtra)

##
## Attaching package: 'gridExtra'
```

```

## The following object is masked from 'package:dplyr':
##
##      combine

library(purrr)
library(eivtools)

## Loading required package: R2jags
## Loading required package: rjags
## Loading required package: coda
## Linked to JAGS 4.3.0
## Loaded modules: basemod,bugs
##
## Attaching package: 'R2jags'

## The following object is masked from 'package:coda':
##
##      traceplot

creationInfo <- paste0("\tDate: ", date(), "\n\tLocation: ", sub("../AcrossTissue", "AcrossTissue", get

exportPlots=TRUE ## Flag for exporting plots

```

C. elegans

Should do a similar analysis of yeast genome. Since there is isoform/gene, yeast analysis will be at the ‘gene level’.

```

## Load Data
## load objects: summaryStatsPhiData, seqData, phiData
load(file="Input/processed.ROC.data-NCBI.Rdata")

```

Examine Data

```

str(formals(qplot))

## Dotted pair list of 16
## $ x      : symbol
## $ y      : symbol
## $ ...    : symbol
## $ data   : symbol
## $ facets : NULL
## $ margins: logi FALSE
## $ geom   : chr "auto"
## $ xlim   : language c(NA, NA)
## $ ylim   : language c(NA, NA)
## $ log    : chr ""
## $ main   : NULL
## $ xlab   : NULL
## $ ylab   : NULL
## $ asp    : logi NA

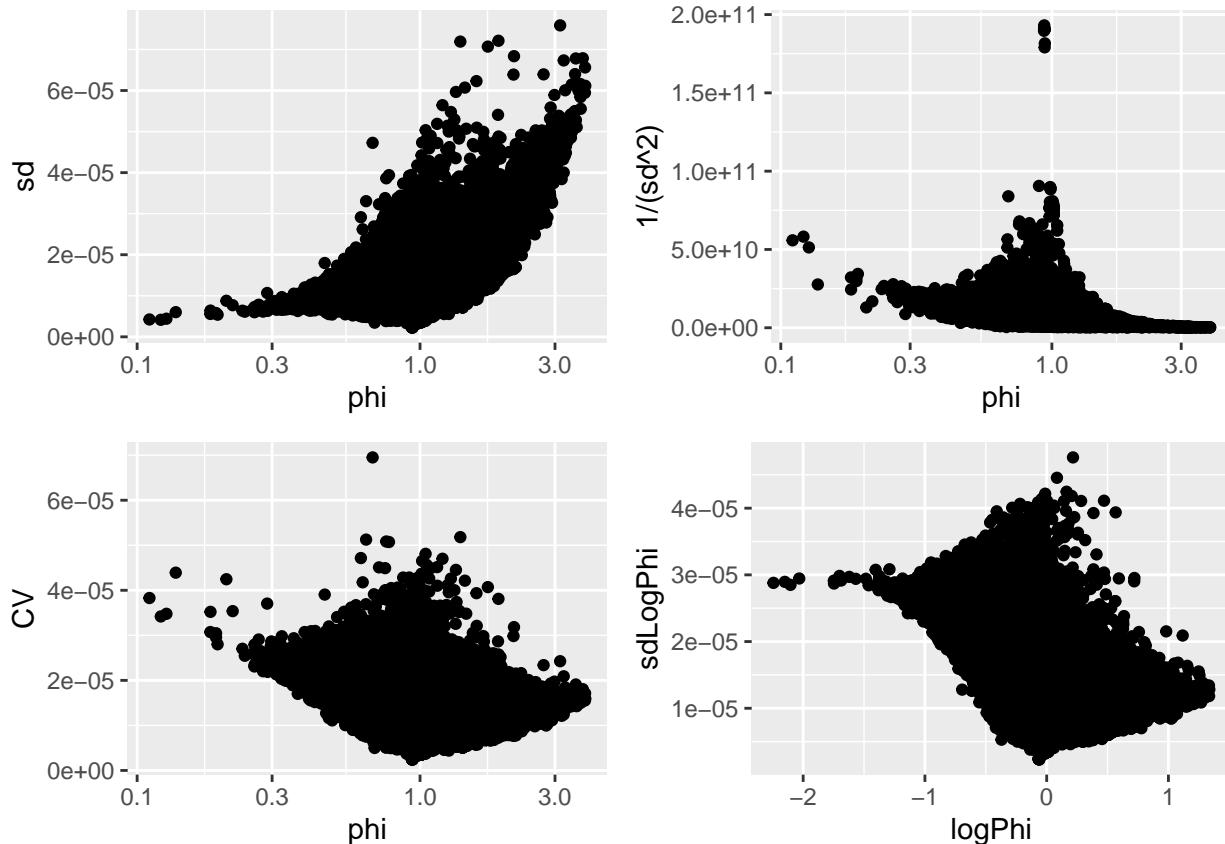
```

```

## $ stat      : NULL
## $ position: NULL
## Isoform Scale
myPlots <-
  list(
    qplot(x = phi, y=sd, log = c("x", "y"), data=phiData),
    qplot(x = phi, y=1/(sd^2), log = c("x", "y"), data=phiData),
    qplot(x = phi, y=sd/phi, ylab="CV", log = c("x", "y"), data=phiData),
    qplot(x = logPhi, y=sdLogPhi, data=phiData)
  )
)

do.call(grid.arrange, myPlots)

```



```

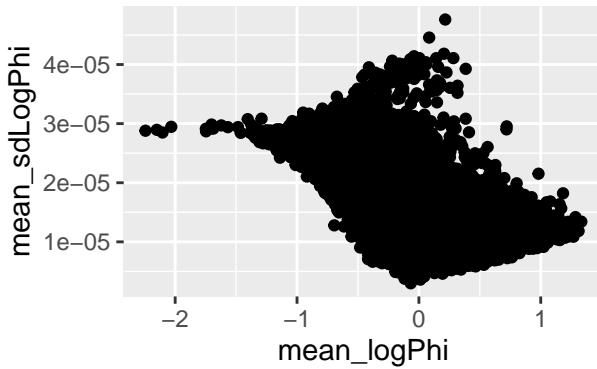
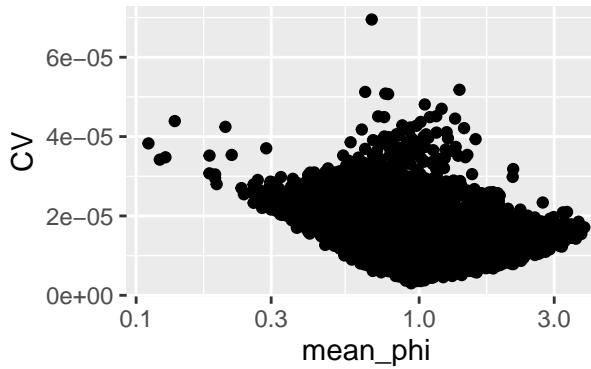
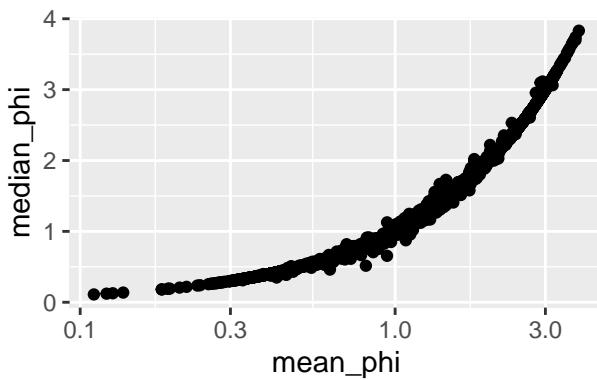
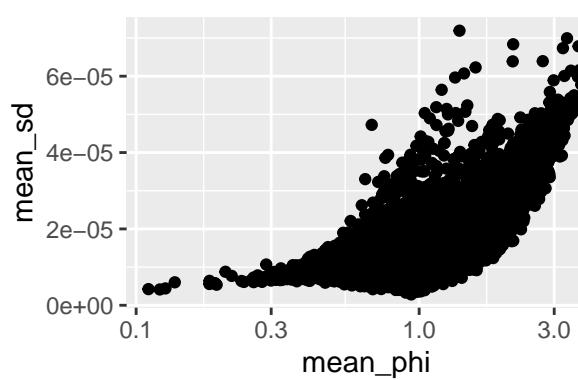
## Gene Scale
myPlots <-
  list(
    qplot(x = mean_phi, y=mean_sd, log = c("x", "y"), data=summaryStatsPhiData),
    qplot(x = mean_phi, y=median_phi, log = c("x", "y"), data=summaryStatsPhiData),
    qplot(x = mean_phi, y=mean_sd/mean_phi, ylab="CV", log = c("x", "y"), data=summaryStatsPhiData),
    qplot(x = mean_logPhi, y=mean_sdLogPhi, data=summaryStatsPhiData)
  )

do.call(grid.arrange,
  list(
    grobs = myPlots,
    top = "Gene Level",
    bottom = "Merging Information Across Isoforms"
  )
)

```

```
)  
)
```

Gene Level



Merging Information Across Isoforms

```
## Gene Scale: Median  
myPlots <-  
  list(  
    qplot(x = median_phi, y=median_sd, log = c("x", "y"), data=summaryStatsPhiData),  
    qplot(x = mean_sd, y=median_sd, log = c("x", "y"), data=summaryStatsPhiData),  
    qplot(x = median_phi, y=median_sd/median_phi, ylab="CV", log = c("x", "y"), data=summaryStatsPhiData),  
    qplot(x = median_logPhi, y=median_sdLogPhi, data=summaryStatsPhiData)  
)  
  
do.call(grid.arrange,  
  list(  
    grobs = myPlots,  
    top = "Gene Level",  
    bottom = "Median of Isoforms"  
)  
)
```

Gene Level

