Plot Moments of Fine Scale Embryo Data

Michael A. Gilchrist

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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.

Evaluate Chunks

M-n v * - v polymode-eval-region-or-chunk - b polymode-eval-buffer - u or ↑ polymode-eval-buffer-from-beg-to-point - d or ↓ polymode-eval-buffer-from-point-to-end

M-n e : Evaluate buffer # Load Libraries

```
library(tidyr)
library(tibble)
library(readr)
library(dplyr)
library(stringr)
library(forcats)
library(ggplot2)
library(ggpubr)
library(ggpmisc)
library(optimx)
library(gridExtra) ## supplies plotting on grid function marrangegrob
```

Plot Hermaphrodite Embryo Data

- Embryonic data from various development points. Data processed in `../21_Processed.Published.Means/load.and.pr`
- Use this data to
  - Examine how the variation in the measurements increases with its value.
  - It clearly increase linearly on a log scale. Increasing the order of the polynomial helps some.
  - Model error seems a bit off at higher values. Perhaps it's the error in the x variable tempering things?
  - Note 832 points are excluded due to 0 values.

```
## To place 'items' in the ggplot pipeline, you need to use lists.
myFits <- function(i){
    list(geom_smooth(method = "lm", formula = y ~ poly(x, i, raw = TRUE), color = myColors[i]),
         stat_poly_eq(
             aes(label =  paste(..eq.label.., ..rr.label.., ..AIC.label.., sep = "~~")),
             formula = y ~ poly(x, i, raw = TRUE),
```

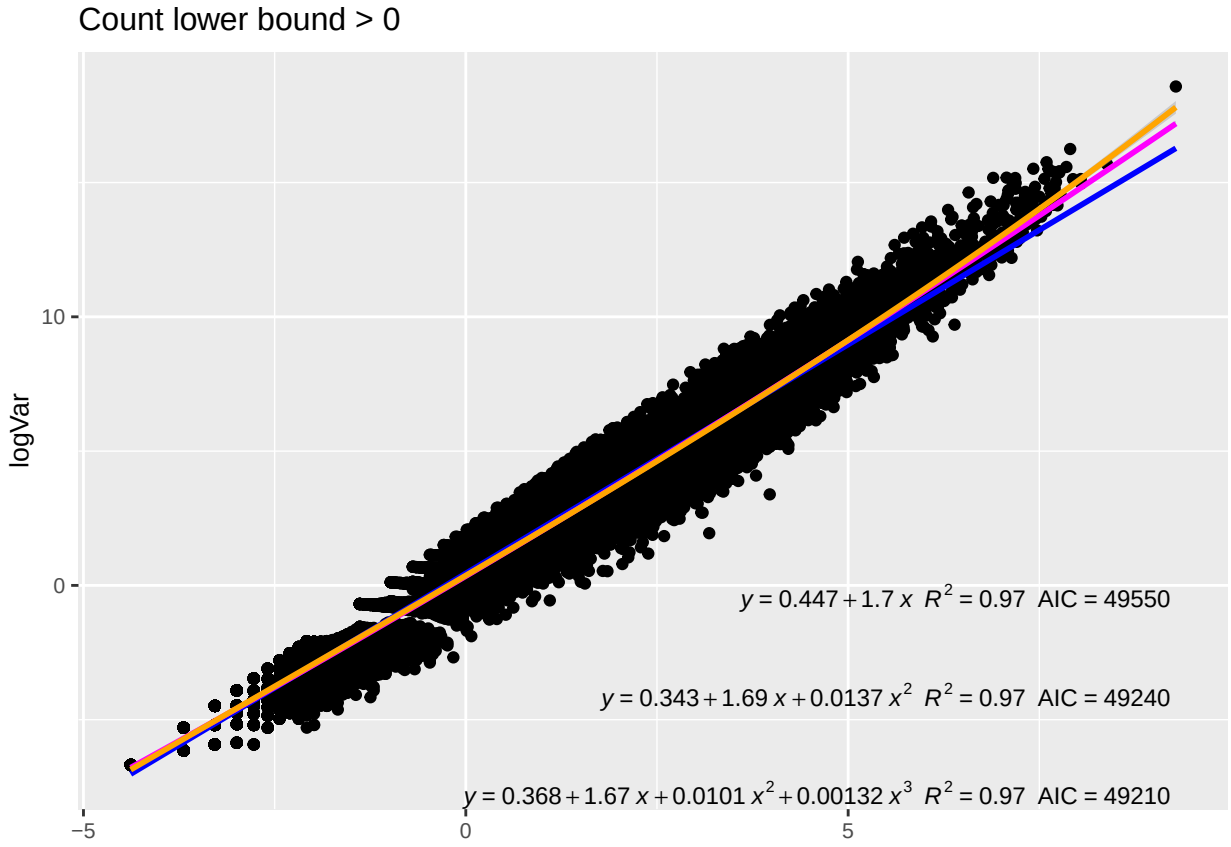
```
            size = 3,
            label.x = "right",
            label.y= 0.39-i*0.13,
            parse = TRUE
        )
        )
}

pl <- lapply(c(0, 1, 10, 100), function(lowerBound){
    tmpData <- embryoStageCountMoments %>% filter(logMean > log(lowerBound) )
    ggplot(tmpData, aes(logMean, logVar)) +
        geom_point() +
        ggtitle(paste0("Count lower bound > ", lowerBound)) +
        lapply(1:3, myFits) +
        theme(text = element_text(size=10))+
        labs(x=switch(lowerBound==100, "logMean")) ## switch will return NULL except when condition is
    ## Vectorized nature of ifelse prevents it from working with NULL
}
)
```

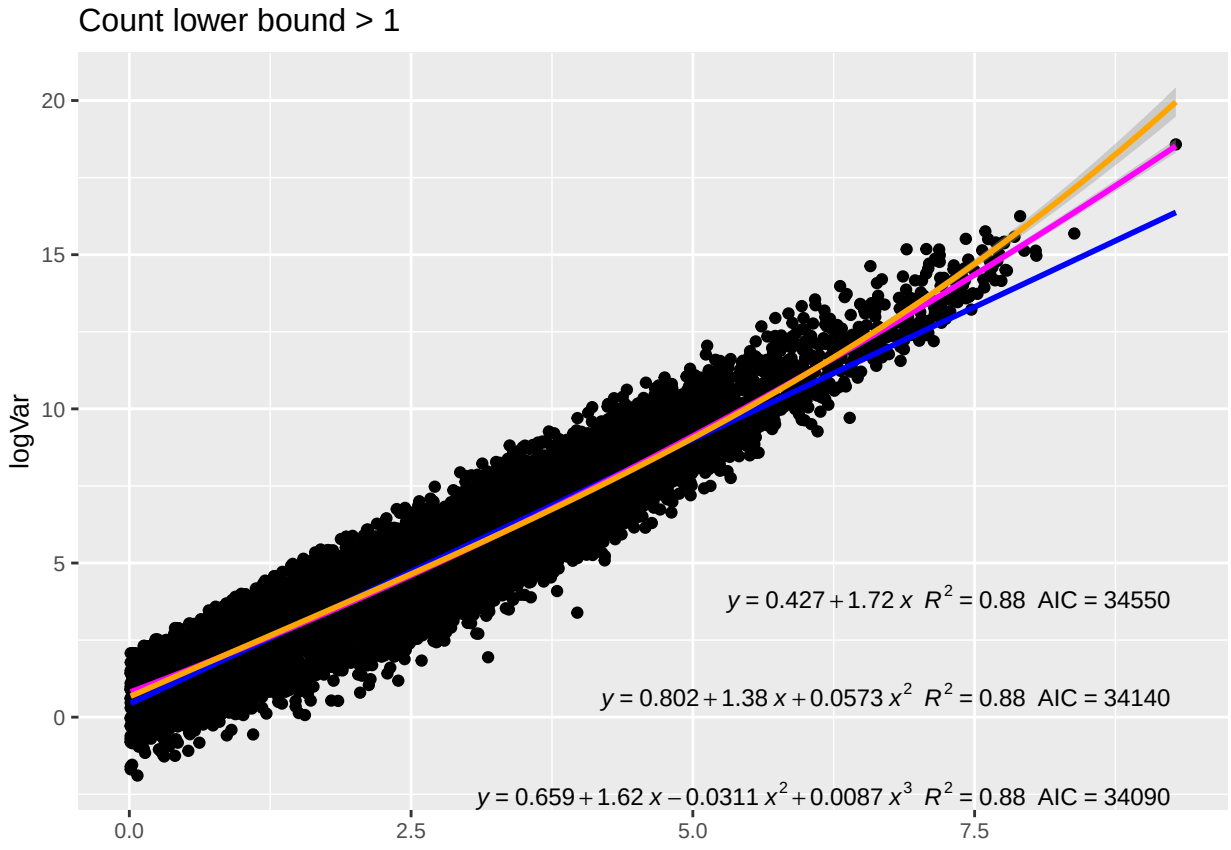
```
#knitr::opts_chunk$set(out.height = "\\textheight",  out.width = "\\textwidth")
                                        #marrangeGrob(pl, nrow=4, ncol=1, aes(logMean, logVar), heights=
```

```
pl
```

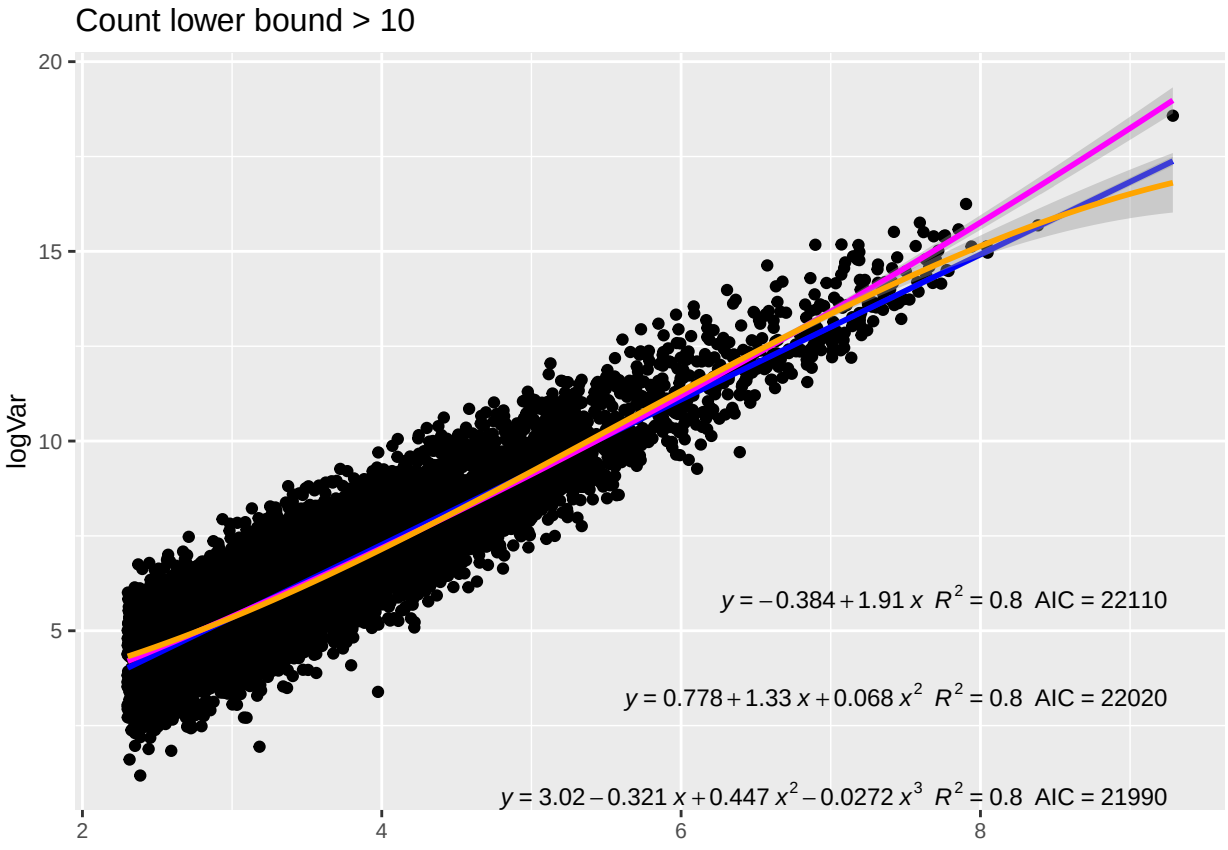
```
## [[1]]
```



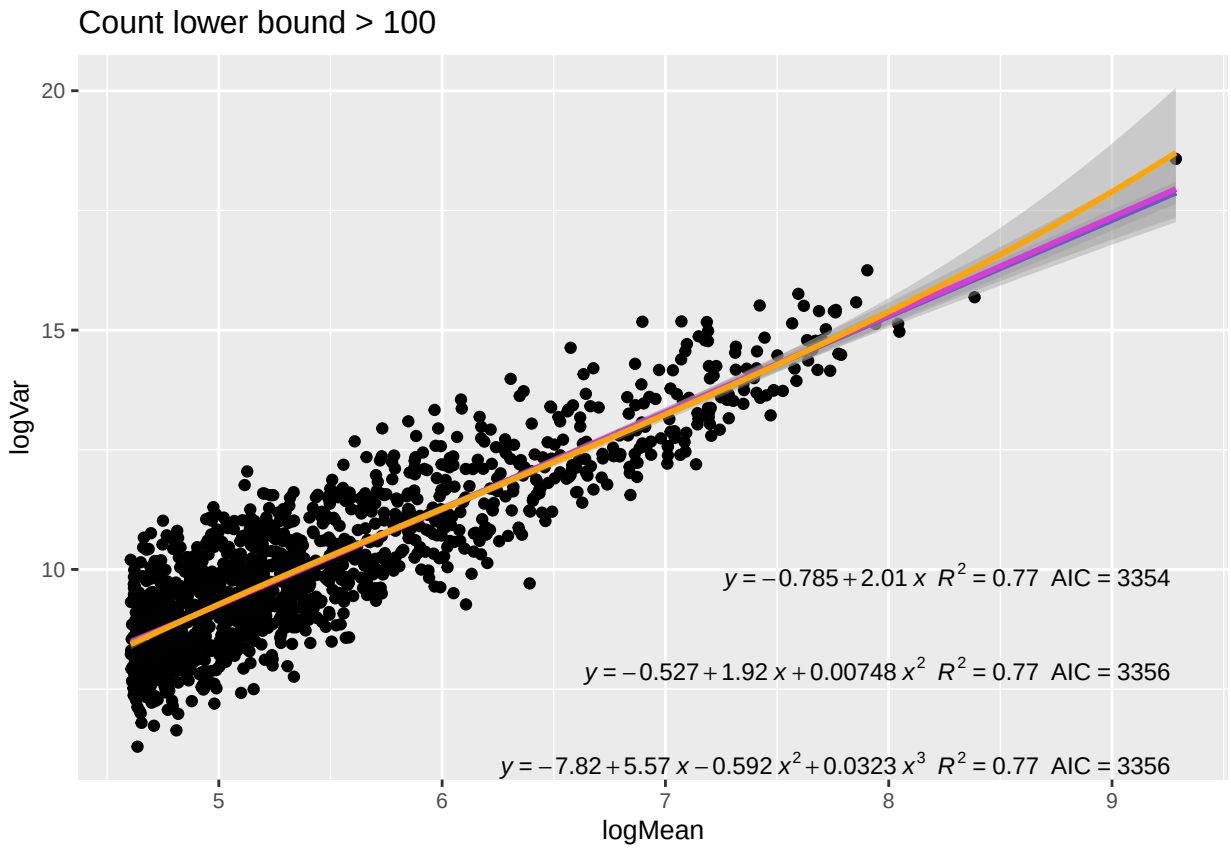

```
##
## [[2]]
```


Count lower bound > 1
logVar
20
15
10
5
0
0.0
2.5
5.0
7.5
y = 0.427 + 1.72 x R² = 0.88 AIC = 34550
y = 0.802 + 1.38 x + 0.0573 x² R² = 0.88 AIC = 34140
y = 0.659 + 1.62 x − 0.0311 x² + 0.0087 x³ R² = 0.88 AIC = 34090

```
##
## [[3]]
```


Count lower bound > 10
logVar
20
15
10
5
2
4
6
8
y = −0.384 + 1.91 x R² = 0.8 AIC = 22110
y = 0.778 + 1.33 x + 0.068 x² R² = 0.8 AIC = 22020
y = 3.02 − 0.321 x + 0.447 x² − 0.0272 x³ R² = 0.8 AIC = 21990

```
##
## [[4]]
```


Count lower bound > 100
20
15
10
logVar
5
6
7
8
9
logMean
y = −0.785 + 2.01 x R2 = 0.77 AIC = 3354
y = −0.527 + 1.92 x + 0.00748 x2 R2 = 0.77 AIC = 3356
y = −7.82 + 5.57 x − 0.592 x2 + 0.0323 x3 R2 = 0.77 AIC = 3356