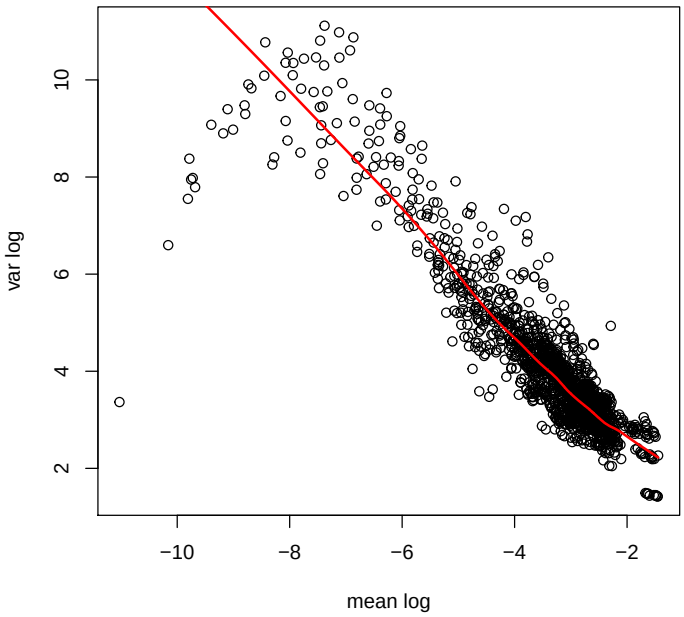
```
> library(knitr)
> opts_chunk$set(
+ concordance=TRUE
+ )

> library(RERconverge)
>
```

Read in some the tree data. This function puts trees with different number of present sepcies into a unified format and therefor takes some time.

```
> treefile=system.file("extdata", "mammal_62_aa_sub.tre", package = "RERconverge")
> show(treefile)

[1] "/home/mchikina/R/x86_64-pc-linux-gnu-library/3.4/RERconverge/extdata/mammal_62_aa_sub.t

> mamTrees=readTrees(treefile,max.read = 200)
>
```



This generates the mean variance plot for log transformed measurements and the corresponding weights fit. The plot can also be used to define a reasonable cutoff for the residual calculation based on the region of low values where the variance starts to decrease. Here around exp(-8). We set the cutoff to be exp(-7) (approximately 0.001) to be slightly more conservative.

Next we calculate the relative evolutionary rate (RER).

This is the basic method that performs a simple regression on the original CODEML output values. This takes some time as seperate the expected rates are calculated for every subset of species that is represented by a single tree.

```
> mamRER=getAllResiduals(mamTrees,transform = "none",weighted = F, cutoff=0.001)
```

We have found that scaling each branch generally improves results so we can generate a scaled version of the same RER data.

```
> mamRERs=scale(mamRER)
```

This method performs a weighted regression in log space and has been found to perform better in benchmarks

```
> mamRERlogW=getAllResiduals(mamTrees, transform = "log",weighted = T, cutoff=0.001)
```

These results can also be scaled, almost always improves results in our exprience

```
> mamRERlogWs=scale(mamRERlogW)
```