Burden

Partition enhancers based on distance to TSS based on strict overlap. Basically, her pipeline takes intersections between enhancers and distance ranges, and remove bases of enhancers that are not overlapped. ### NOTICE

```
getwd()
```

```
## [1] "/media/yuwen/F/ASD/analysis"
```

```
knitr::opts_chunk$set(warning=FALSE, message=FALSE)
```

read in data with predicted mutation count and observed mutation count

load in functions and datastes that make the functions work

Set the scaling factor for nonysn to 0.32 for now (which is actually used for Polyphen-2 Mis3 rate)

ASD manuscript data, stringent ASD genes

```
predicted
```

```
## [1] 3.26384
```

```
observed
```

```
## [1] 9
```

```
ppois(observed-1, predicted,lower.tail = FALSE)
```

```
## [1] 0.006458456
```

ASD manuscript data, relaxed ASD genes

```
predicted
```

```
## [1] 20.93894
```

```
observed
```

```
## [1] 64
```

```
ppois(observed-1, predicted,lower.tail = FALSE)
```

[1] 3.246687e-14

control_model_693_mutrate data, stringent ASD genes

```
predicted
```

[1] 5.474641

```
observed
```

[1] 11

```
ppois(observed-1, predicted,lower.tail = FALSE)
```

[1] 0.02453533

control_model_693_mutrate, relaxed ASD genes

```
predicted
```

[1] 35.07132

```
observed
```

[1] 88

```
ppois(observed-1, predicted,lower.tail = FALSE)
```

[1] 4.696851e-14