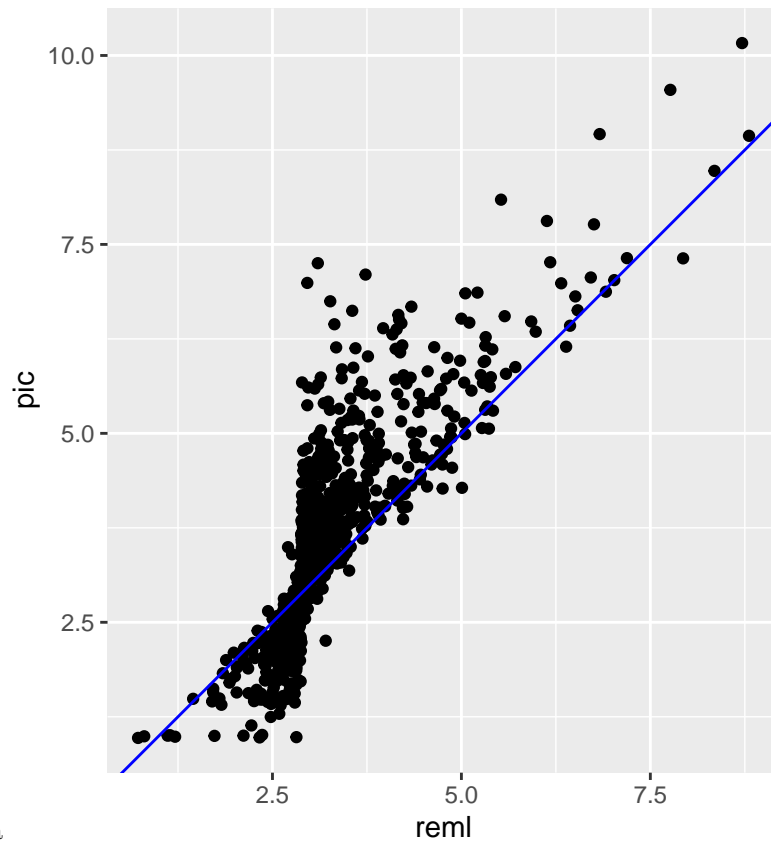


## ML\_only

```
## Warning in sqrt(diag(solve(h))): NaNs produced
```

```
## Warning in sqrt(1/out$hessian): NaNs produced
```



Plotting various data

```
{r, echo = FALSE} # # B_methods = data.frame( #   reml = litter_ancestral_ML$ace # ) # # # Add node numbers  
#   ml = litter_ancestral_ML$ace # ) # # # Add node numbers  
to the data frame # B_methods$node = seq(1:nrow(B_methods))  
+ n_tips # B_methods %>% #   ggplot(aes(x = reml,y = ml)) + #  
geom_point() + #   geom_abline(slope = 1, intercept = 0, color  
= "blue") + coord_equal(ratio = 1) # #
```