reconstruction methods

First we create a phylogeny

```r
s <- sim_phyl(seed=3)
s2 <- phylo2p(drop.fossil(s$newick))
ltt = NULL
nsim =10000
for(i in 1:nsim){
  s3 = p2phylo(rec_tree(wt = s2$wt,rec_method = 1))
  ltt[i] = ltt_stat(s3,s$newick)
}
```

```r
summary(ltt)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   12.59   43.68   55.89   58.62   70.95  164.50
```

```r
ltt2 = NULL
nsim =10000
for(i in 1:nsim){
  s3 = p2phylo(rec_tree(wt = s2$wt,rec_method = 2))
  ltt2[i] = ltt_stat(s3,s$newick)
}
```

```r
summary(ltt2)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   15.38   46.89   56.36   57.12   66.07  131.60
```
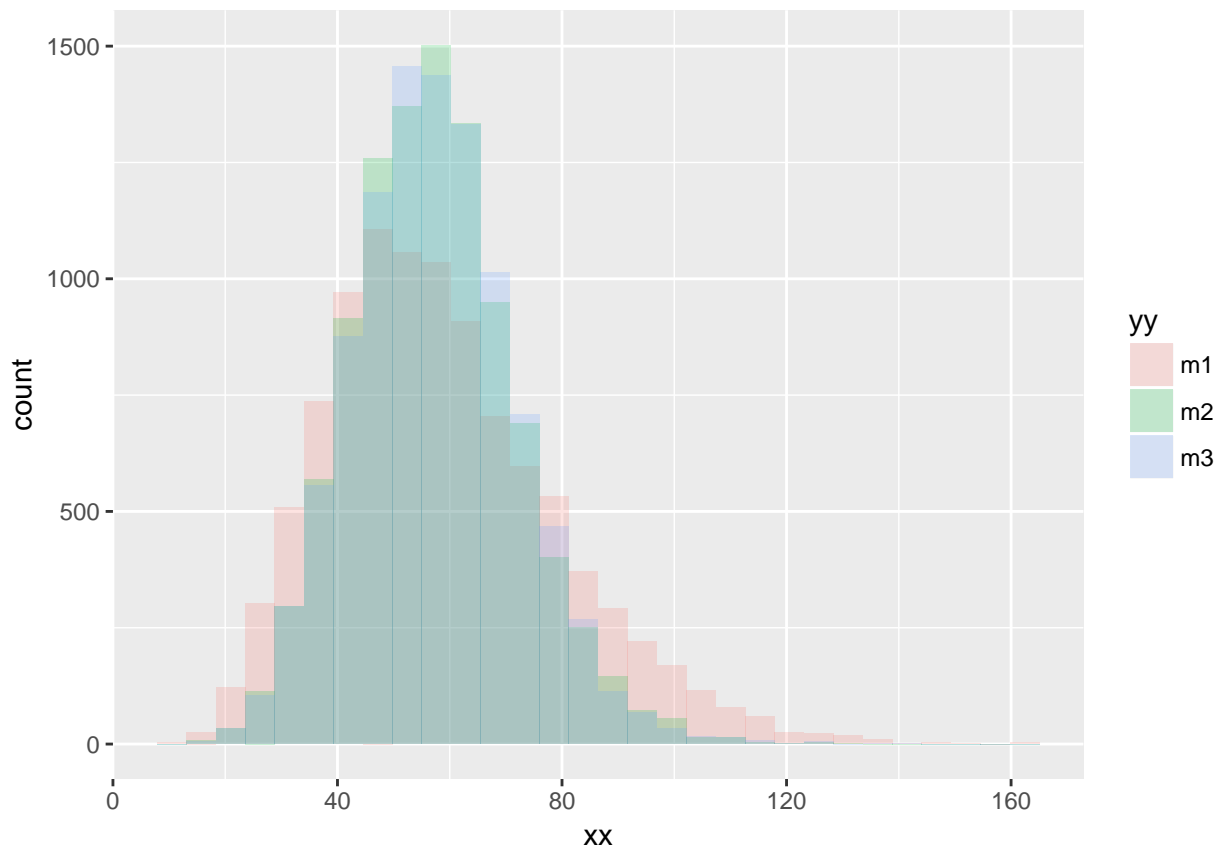
```r
ltt3 = NULL
nsim =10000
for(i in 1:nsim){
  s3 = p2phylo(rec_tree(wt = s2$wt,rec_method = 2))
  ltt3[i] = ltt_stat(s3,s$newick)
}
```

```r
summary(ltt3)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   14.28   47.50   56.66   57.38   66.35  143.30
```

```r
dat <- data.frame(xx = c(ltt,ltt2,ltt3),yy = rep(c('m1','m2','m3'),each = 10000))

ggplot(dat, aes(x=xx, fill=yy)) + geom_histogram(alpha=0.2, position="identity")
```

A new method?

```
pars = c(0.8,0.1,40)
obsPhylo = drop.fossil(s$newick)
f = cond_exp_ltt(obsPhylo,pars)
ltt_stat(s$newick,p2phylo(f))
```

```
## [1] 40.53075
```

Now for another phylogeny (seed 44)

```
s <- sim_phyl(seed=44)
s2 <- phylo2p(drop.fossil(s$newick))
ltt = NULL
nsim =10000
for(i in 1:nsim){
  s3 = p2phylo(rec_tree(wt = s2$wt,rec_method = 1))
  ltt[i] = ltt_stat(s3,s$newick)
}
```

```
summary(ltt)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   12.31   31.31   43.92   46.29   58.25  128.00
```

```
ltt2 = NULL
nsim =10000
for(i in 1:nsim){
  s3 = p2phylo(rec_tree(wt = s2$wt,rec_method = 2))
  ltt2[i] = ltt_stat(s3,s$newick)
```

2

```
}
```

```
summary(ltt2)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   12.09   26.87   34.18   36.52   43.73  104.80
```

```
ltt3 = NULL
nsim =10000
for(i in 1:nsim){
  s3 = p2phylo(rec_tree(wt = s2$wt,rec_method = 2))
  ltt3[i] = ltt_stat(s3,s$newick)
}
```
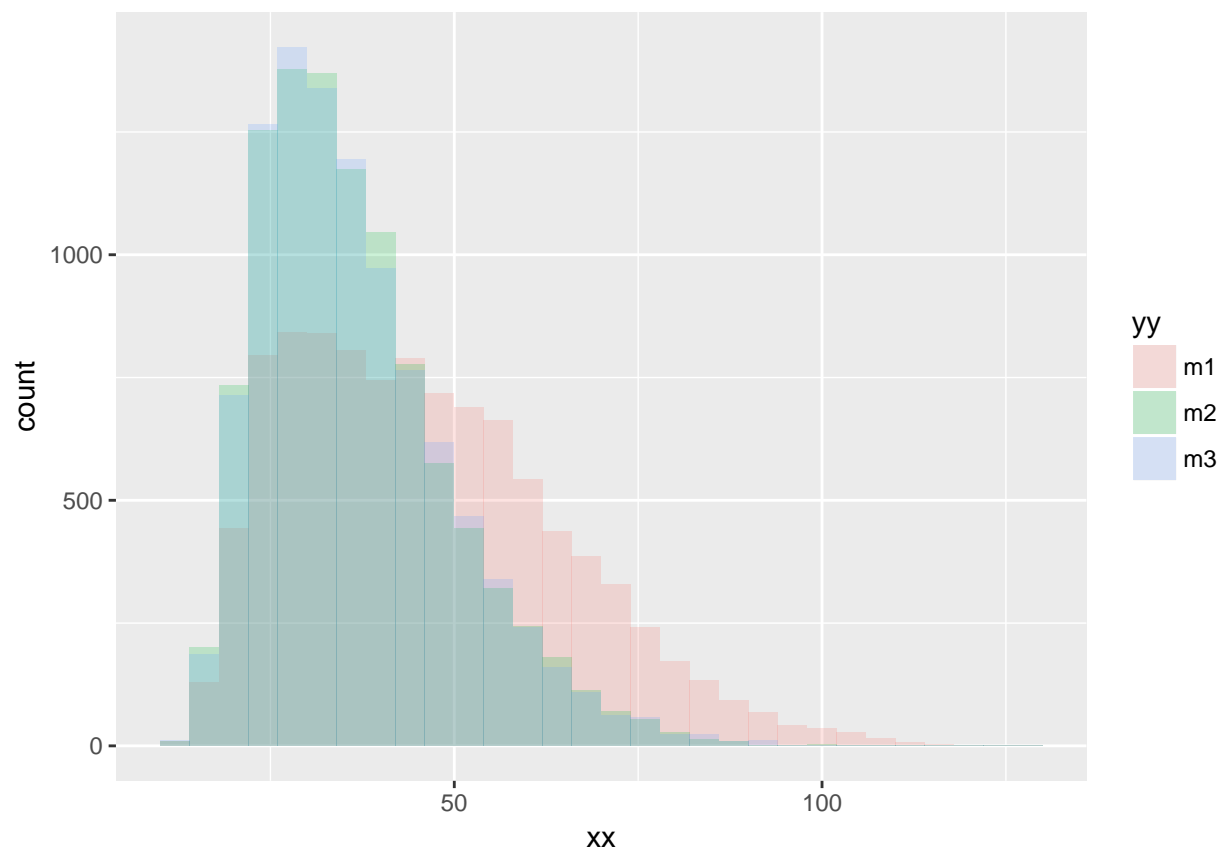
```
summary(ltt3)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   12.78   26.87   34.23   36.61   43.92  111.10
```

```
dat <- data.frame(xx = c(ltt,ltt2,ltt3),yy = rep(c('m1','m2','m3'),each = 10000))

ggplot(dat, aes(x=xx, fill=yy)) + geom_histogram(alpha=0.2, position="identity")
```


A new method?

```
pars = c(0.8,0.1,40)
obsPhylo = drop.fossil(s$newick)
f = cond_exp_ltt(obsPhylo,pars)
ltt_stat(s$newick,p2phylo(f))
```

```
## [1] 54.37765
```

Now for another phylogeny (seed 234)

```
s <- sim_phyl(seed=234)
s2 <- phylo2p(drop.fossil(s$newick))
ltt = NULL
nsim =10000
for(i in 1:nsim){
  s3 = p2phylo(rec_tree(wt = s2$wt,rec_method = 1))
  ltt[i] = ltt_stat(s3,s$newick)
}
```

```
summary(ltt)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   14.82   48.98   67.61   69.97   87.75  185.30
```

```
ltt2 = NULL
nsim =10000
for(i in 1:nsim){
  s3 = p2phylo(rec_tree(wt = s2$wt,rec_method = 2))
  ltt2[i] = ltt_stat(s3,s$newick)
}
```

```
summary(ltt2)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   13.12   36.04   44.99   47.24   55.70  136.90
```
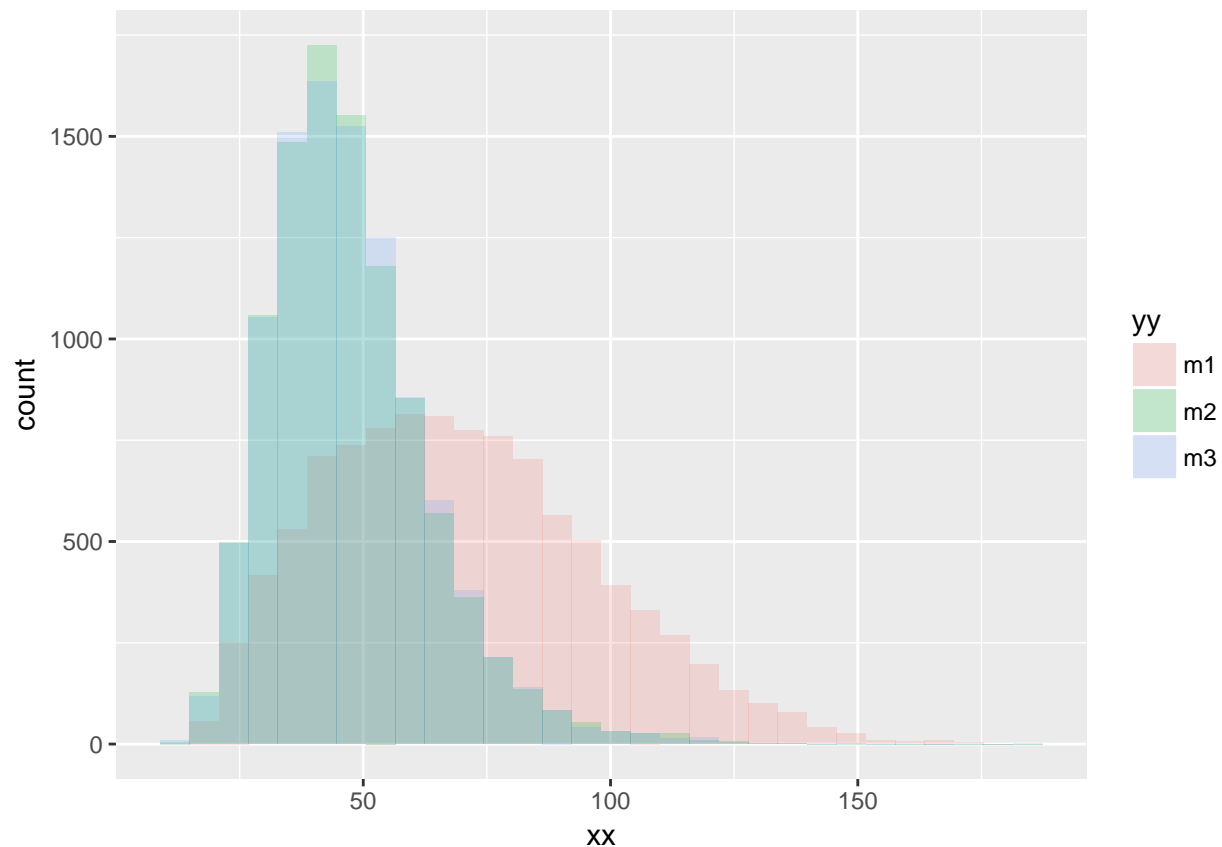
```
ltt3 = NULL
nsim =10000
for(i in 1:nsim){
  s3 = p2phylo(rec_tree(wt = s2$wt,rec_method = 2))
  ltt3[i] = ltt_stat(s3,s$newick)
}
```

```
summary(ltt3)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   12.81   36.18   45.25   47.35   56.01  145.80
```

```
dat <- data.frame(xx = c(ltt,ltt2,ltt3),yy = rep(c('m1','m2','m3'),each = 10000))

ggplot(dat, aes(x=xx, fill=yy)) + geom_histogram(alpha=0.2, position="identity")
```

A new method?

```
pars = c(0.8,0.1,40)
obsPhylo = drop.fossil(s$newick)
f = cond_exp_ltt(obsPhylo,pars)
ltt_stat(s$newick,p2phylo(f))
```

```
## [1] 39.22841
```

simulations?

```
pars = c(0.8,0.1,40)
obsPhylo = drop.fossil(s$newick)
f = cond_exp_ltt(obsPhylo,pars,n_it=1000)
ltt_stat(s$newick,p2phylo(f))
```

```
## [1] 50.56871
```

random?

```
pars = c(0.8,0.1,40)
obsPhylo = drop.fossil(s$newick)
f = cond_exp_ltt(obsPhylo,pars,n_it=100)
ltt_stat(s$newick,p2phylo(f))
```

```
## [1] 45.00384
```

more simulations?

```
ltt4 = NULL
pars = c(0.8,0.1,40)
```

```
obsPhylo = drop.fossil(s$newick)
for(j in 1:10){
  f = cond_exp_ltt(obsPhylo,pars,n_it=100)
  ltt4[j] = ltt_stat(s$newick,p2phylo(f))
}
ltt4
```

```
##  [1] 45.86833 45.86833 45.86833 45.86833 45.86833 45.86833 45.86833
##  [8] 45.86833 45.86833 45.86833
```