Test fitness distributions and S from example simulations

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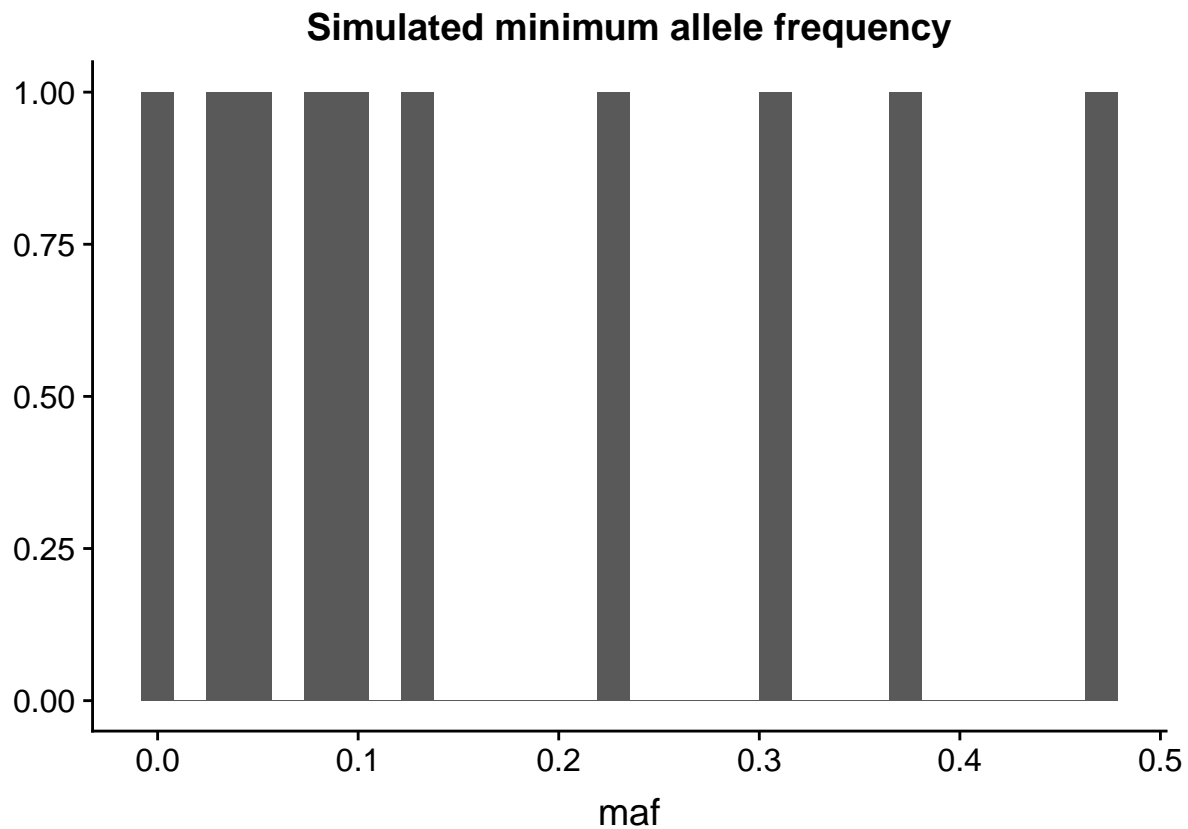
2019-04-04

```r
# Rcpp::sourceCpp('../MCMC.cpp')

svar=0.05
a=0.0
b=0.1
p=0
replicates=5
n=500
m=2
m=10

# Genome matrix
maf=mafsim(m)
qplot(x = maf) +labs(title="Simulated minimum allele frequency")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```
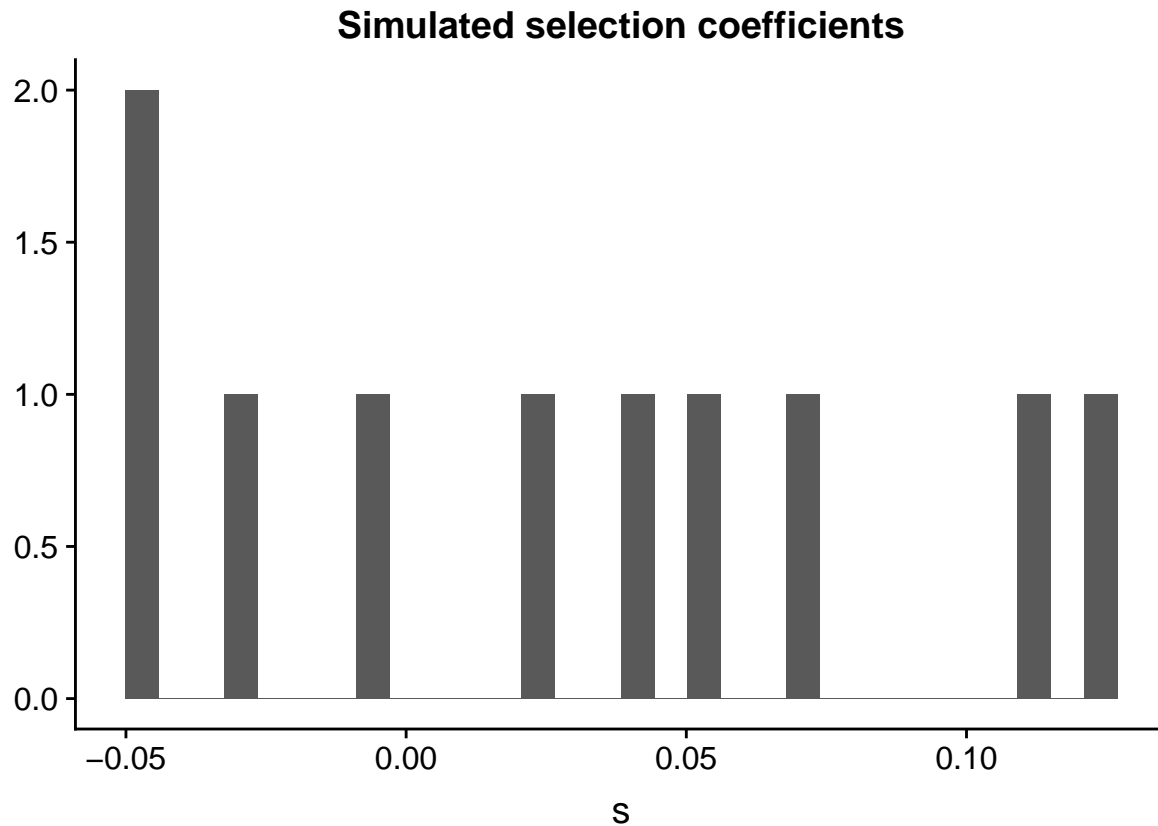


```r
X <- Xsim(n,m,maf)
```

```
# Selectionc oefficient
s= ssim(m,svar)
qplot(s) +labs(title="Simulated selection coefficients")
```

`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

Simulated selection coefficients


```
# Fitness
Ey1=wsim(X,s,mode=1)
Ey2=wsim(X,s,mode=2)
Ey3=wsim(X,s,mode=3)
Ey=wsim(X,s,mode=1)
plot_grid(
         (qplot(Ey) + labs(title="Simulated true fitness values") ),
         (qplot(y=Ey, x=1+(X %*% s)) + labs(title="Check simulated additive with C++ vs R")),
         ncol=2
         )
```
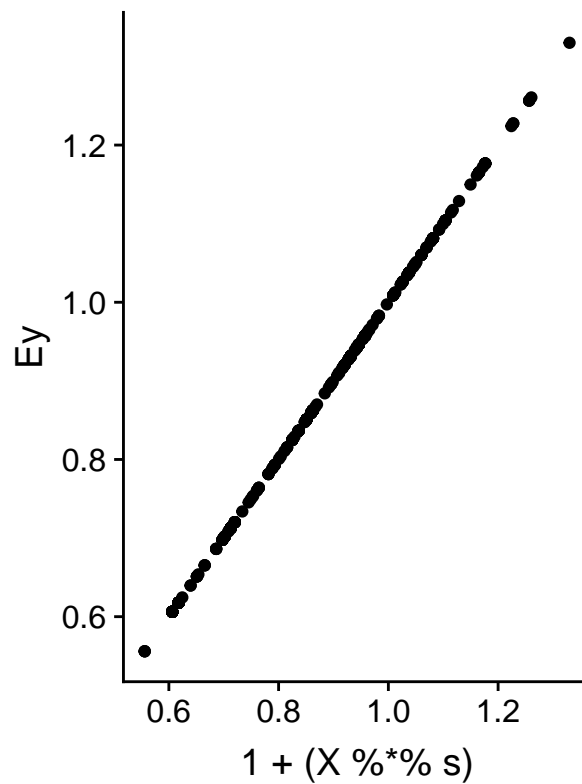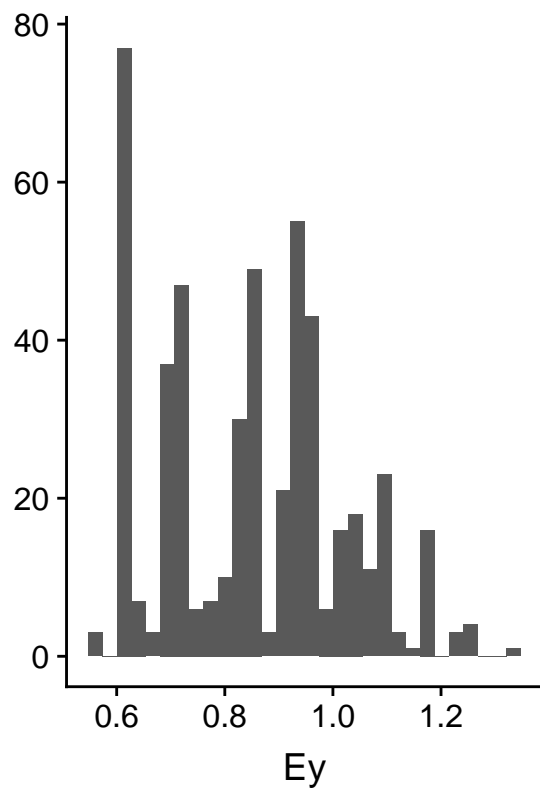
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.

Simulated true fitness values Check simulated additive with C++


```r
# Fitness samples
y=sampleW(Ey,a,b,p,rep = replicates)
h=sort(rep.int(1:n,replicates))

qplot(y=y,x=Ey[h]) + labs(title="Simulated true fitness vs fitness with sampling variance")
```

Simulated true fitness vs fitness with sampling variance