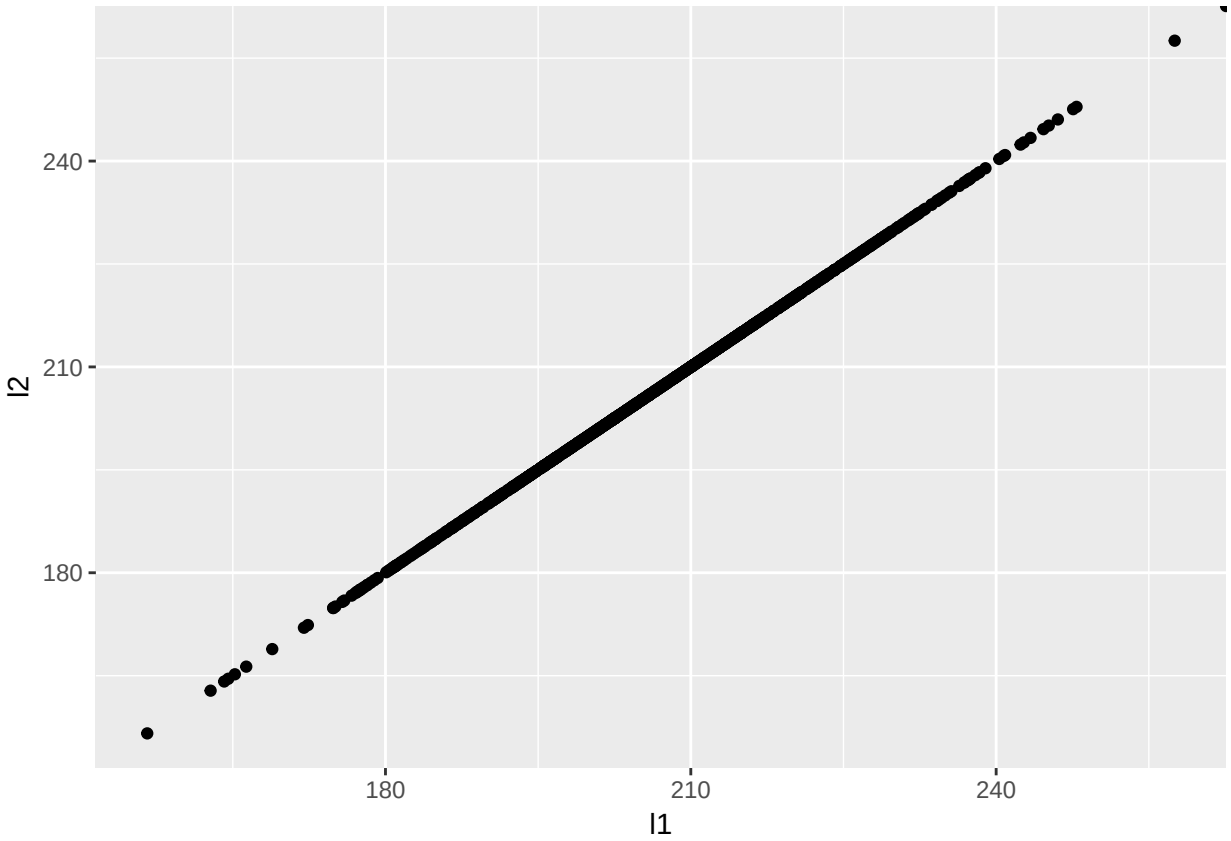
Tests

In order to search for possible bugs and test the package we have create alternative functions to the original ones which should be equivalent. There are a series of possible test to check that the package is doing the proper things to do

log-likelihood function

```
time = proc.time()
#dendroica
btdd = c(4.9999999998,4.806886544,4.70731246478,4.50735197578,4.37856240588,4.29594855558,4.19207515688
pars = c(3.2,0.3,40)
m = 1000
S = sim.sct(btdd,pars,m,print=FALSE)
l1 = vector(mode="numeric",length=m)
l2 = vector(mode="numeric",length=m)
for(i in 1:m){
  s = S$rec[[i]]
  l1[i] = nllik.tree(pars,s)
  l2[i] = nllik.tree2(pars,s)
}
qplot(l1,l2)
```



```
all.equal(l1,l2)
```

```
## [1] TRUE
```

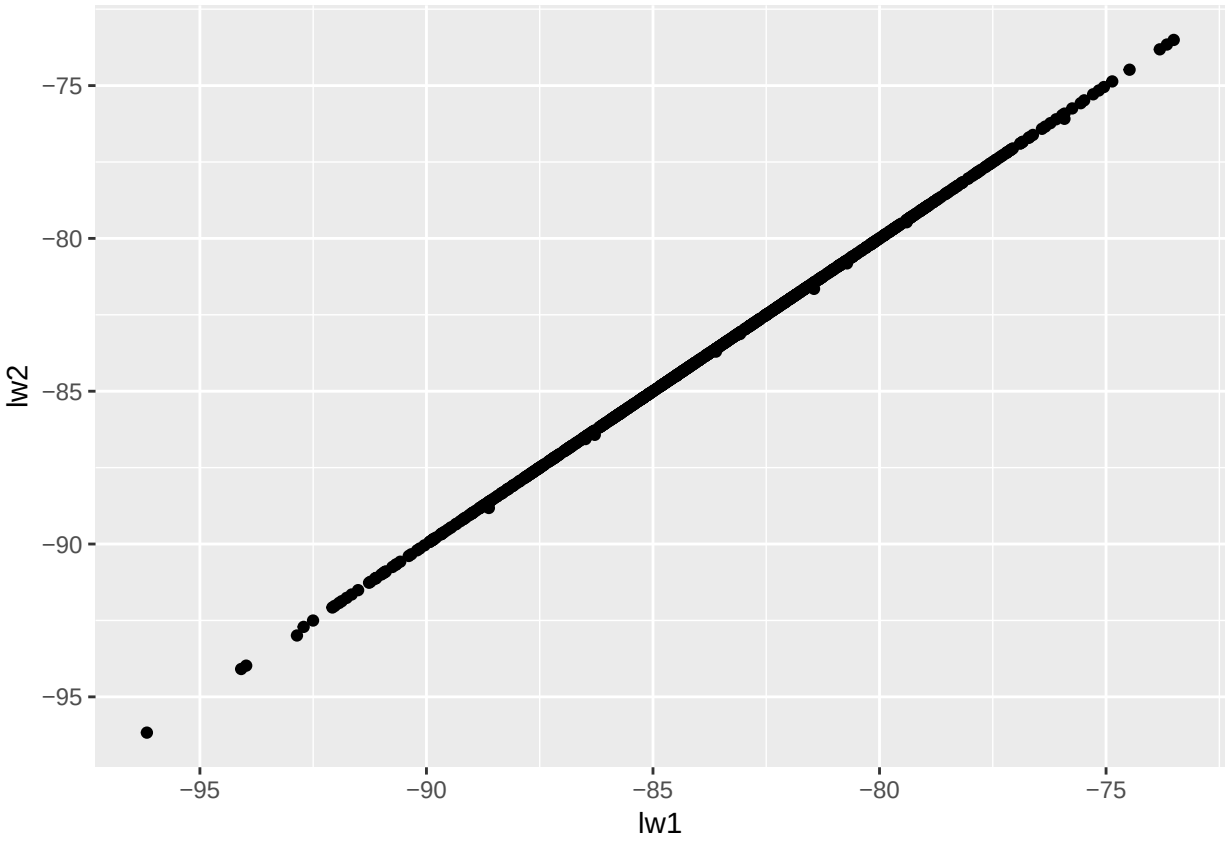
```
get.time(time)
```

```
## [1] 5.298
```

Importance sampling weights

To check if the importance sampling weights are well calculated we use the previous and the current method using the `sim.extinct_old` function.

```
lw1 = vector(mode="numeric",length=m)
lw2 = vector(mode="numeric",length=m)
w1 = vector(mode="numeric",length=m)
w2 = vector(mode="numeric",length=m)
for(i in 1:1000){
  si = sim.extinct_old(btdd,pars)
  w1[i] = si$weight
  w2[i] = si$weight2
  lw1[i] = si$logweight
  lw2[i] = si$logweight2
}
qplot(lw1,lw2)
```




```
all.equal(lw1,lw2)
```

```
## [1] "Mean relative difference: 2.491663e-05"
```

```
all.equal(w1,w2)
```

```
## [1] TRUE
```