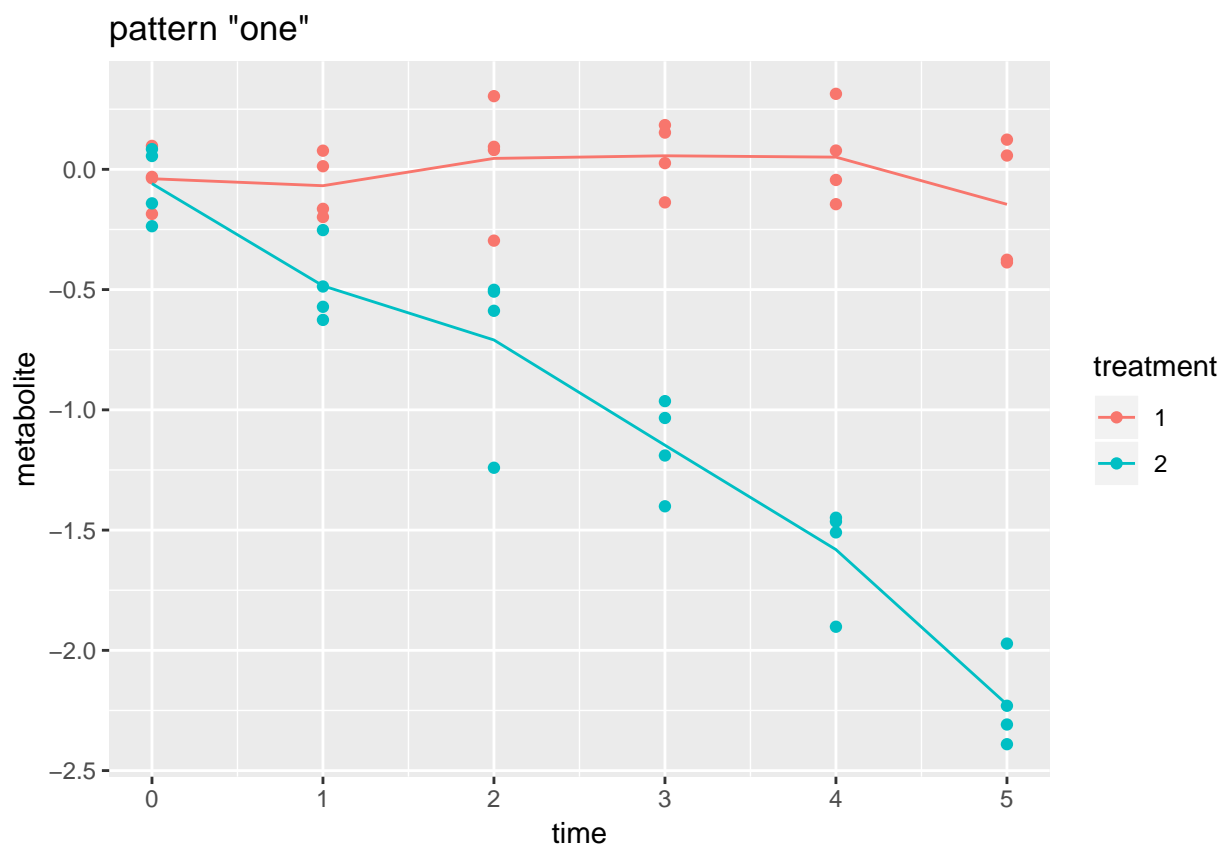


# sim\_favor\_masigpro

*zhu*

11/12/2018

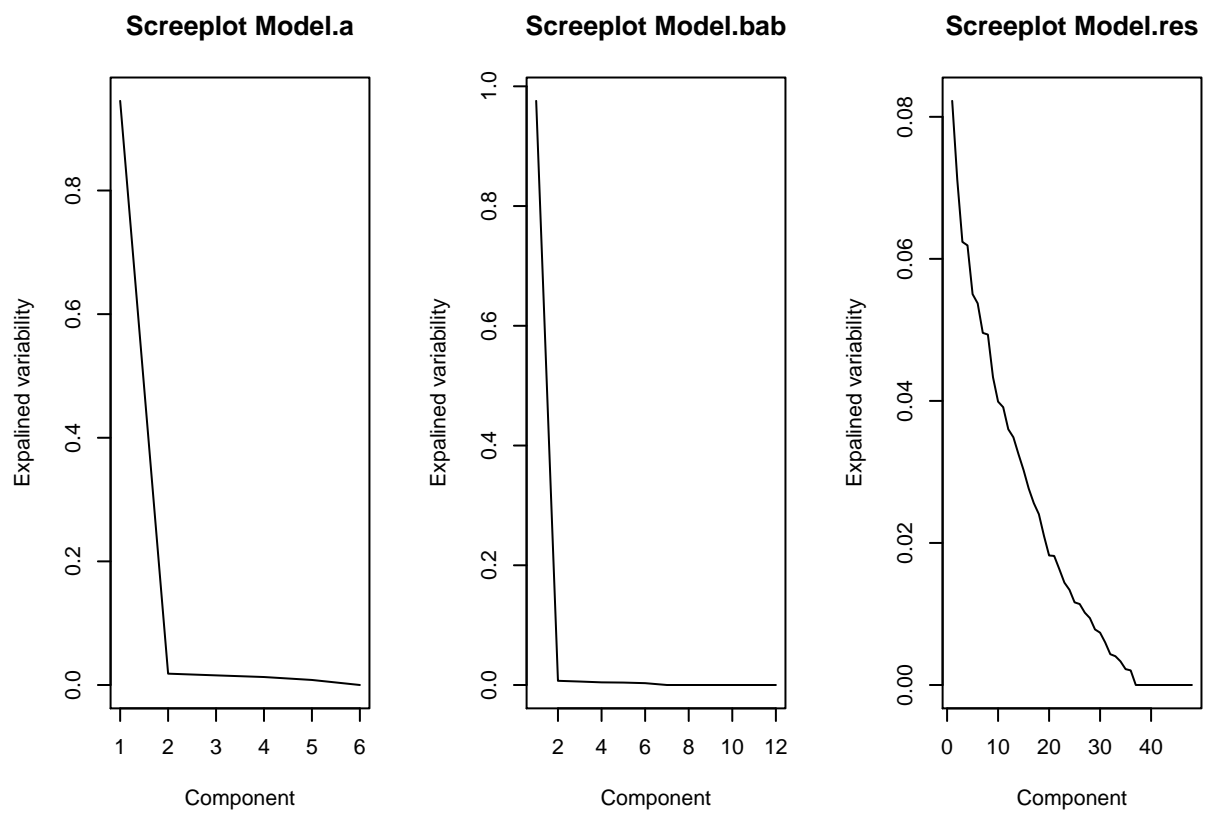


There are 31 metabolites with differential expressed metabolites. there are only 30 flat metabolites.

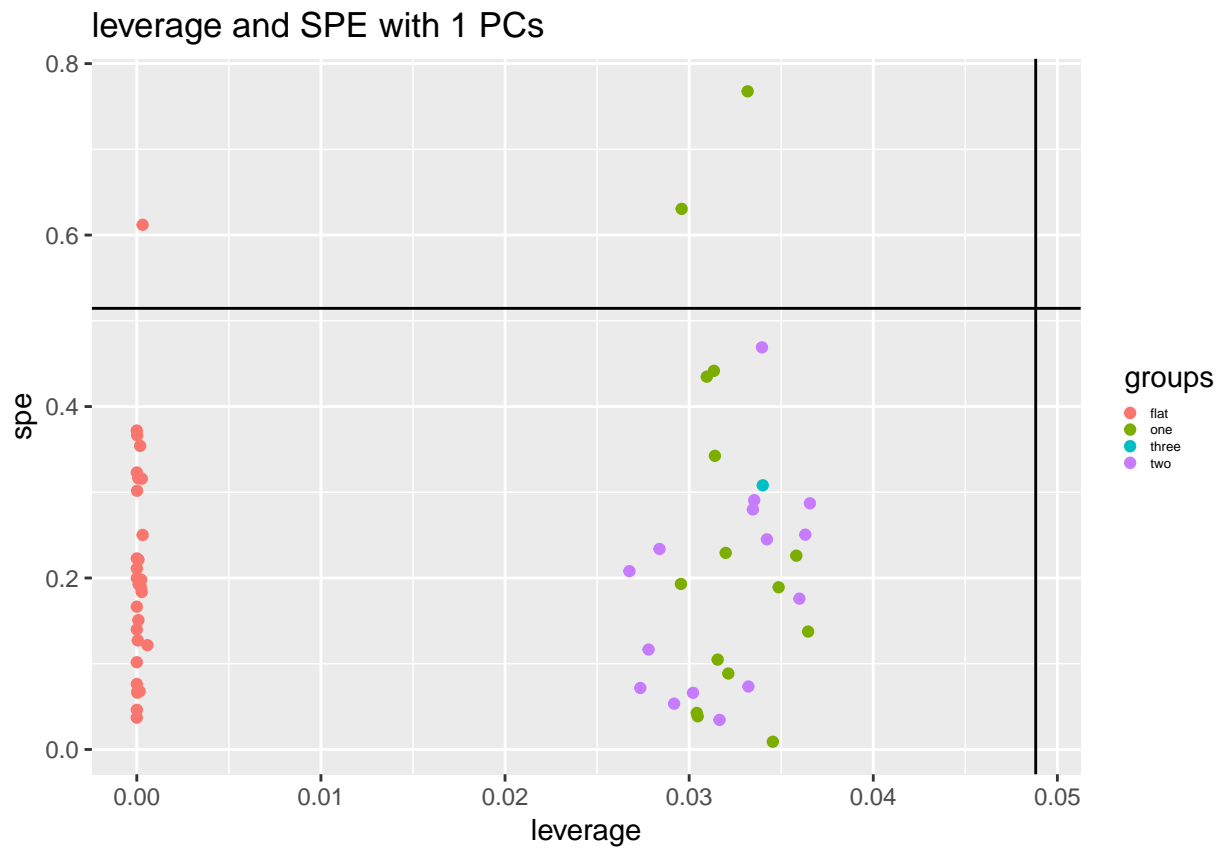
```
##      treatment1 treatment2vstreatment1
## 1         one 5          one 1
## 2         one 6          one 2
## 3         one 9          one 3
## 4         one 12         one 4
## 5         one 13         one 5
## 6         one 14         one 6
## 7         one 15         one 7
## 8         two 4          one 8
## 9         two 12         one 9
## 10        two 14         one 10
## 11        three 1        one 11
## 12                                     one 12
## 13                                     one 13
## 14                                     one 14
## 15                                     one 15
## 16                                     two 1
## 17                                     two 2
```

```
## 18      two 3
## 19      two 4
## 20      two 5
## 21      two 6
## 22      two 7
## 23      two 8
## 24      two 9
## 25      two 10
## 26      two 11
## 27      two 12
## 28      two 13
## 29      two 14
## 30      two 15
## 31      three 1
```

all the patterns are identified by masigpro.

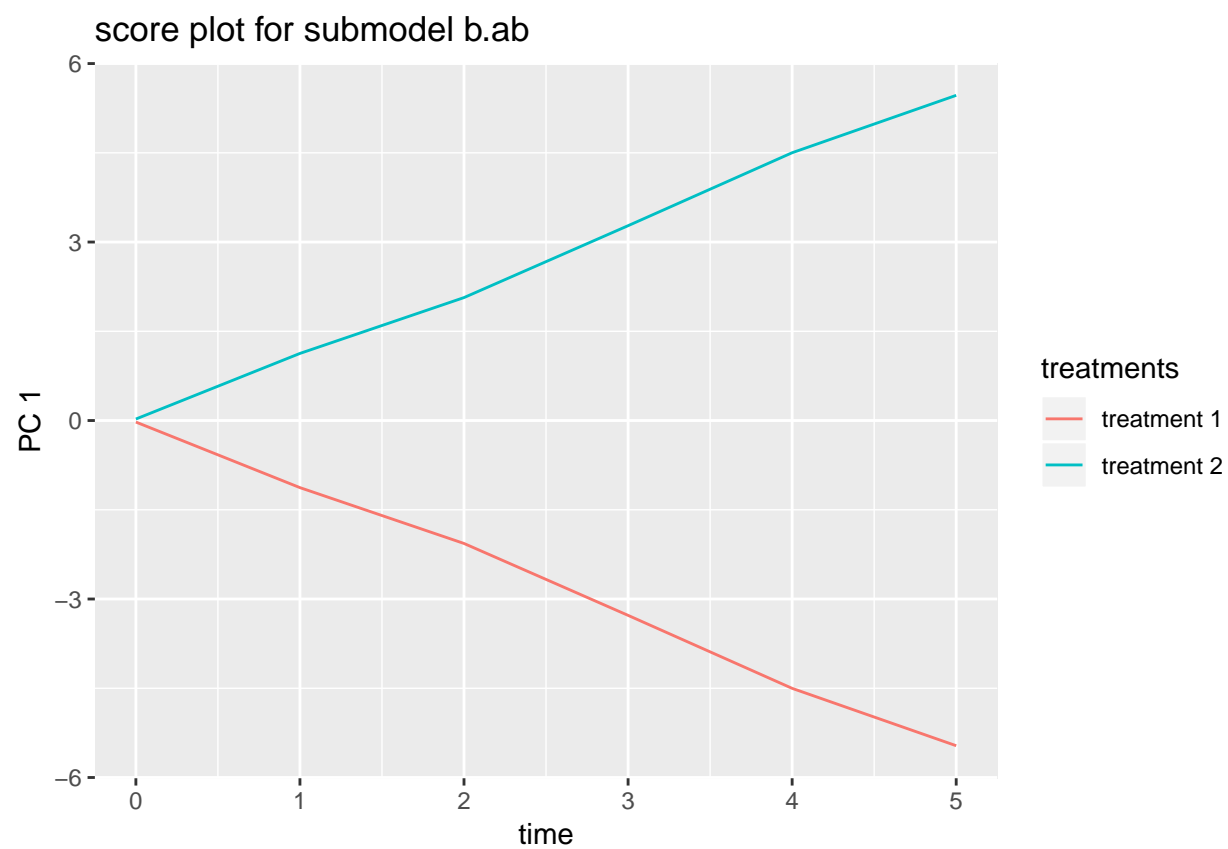


Screeplot shows that 1 PC to be included for submodel b.ab(treatment+interaction).



```
## character(0)
```

With 1 PCs selected, all the patterns are within the leverage limits.



score plot of submodel b.ab shows a clear separation between treatment1 and treatment2.

