

sim_favor_asca

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11/12/2018

```
####pipeline####
```

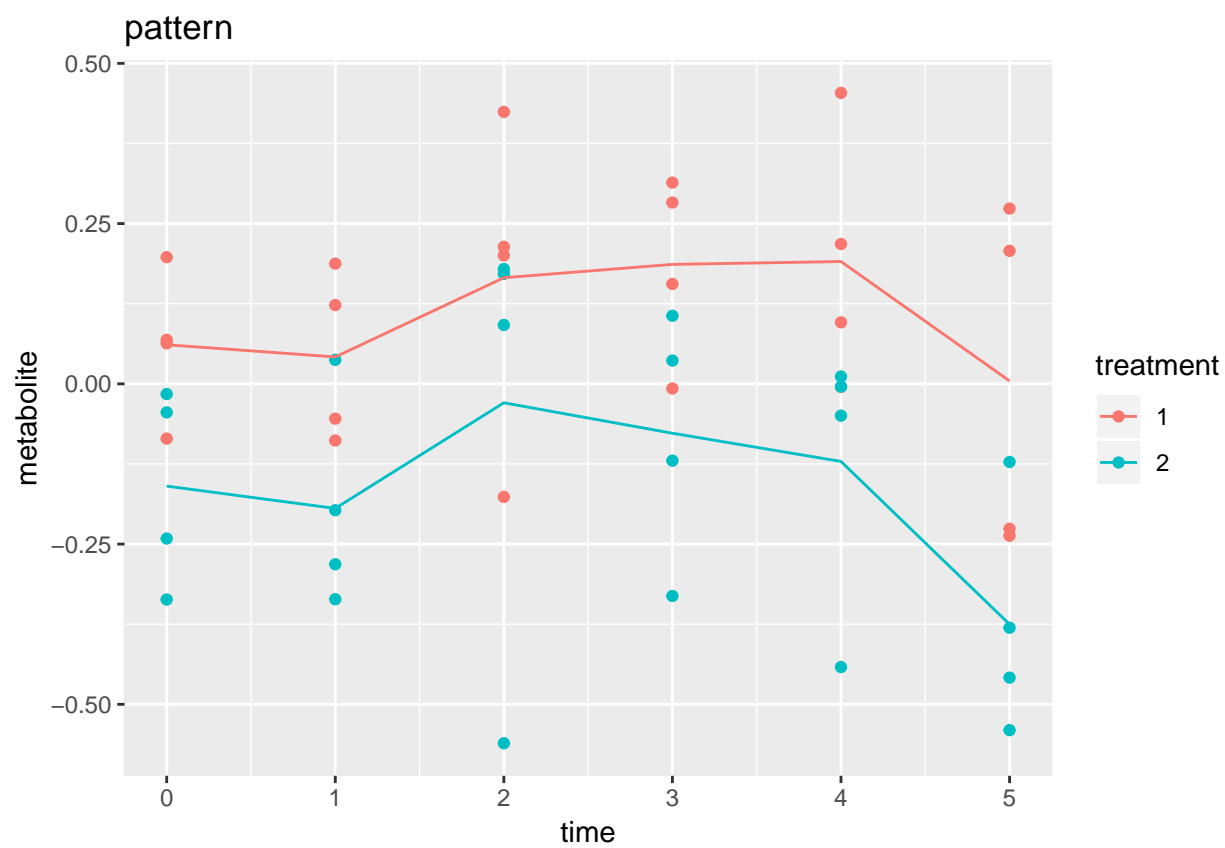
```
i=2#treatment
```

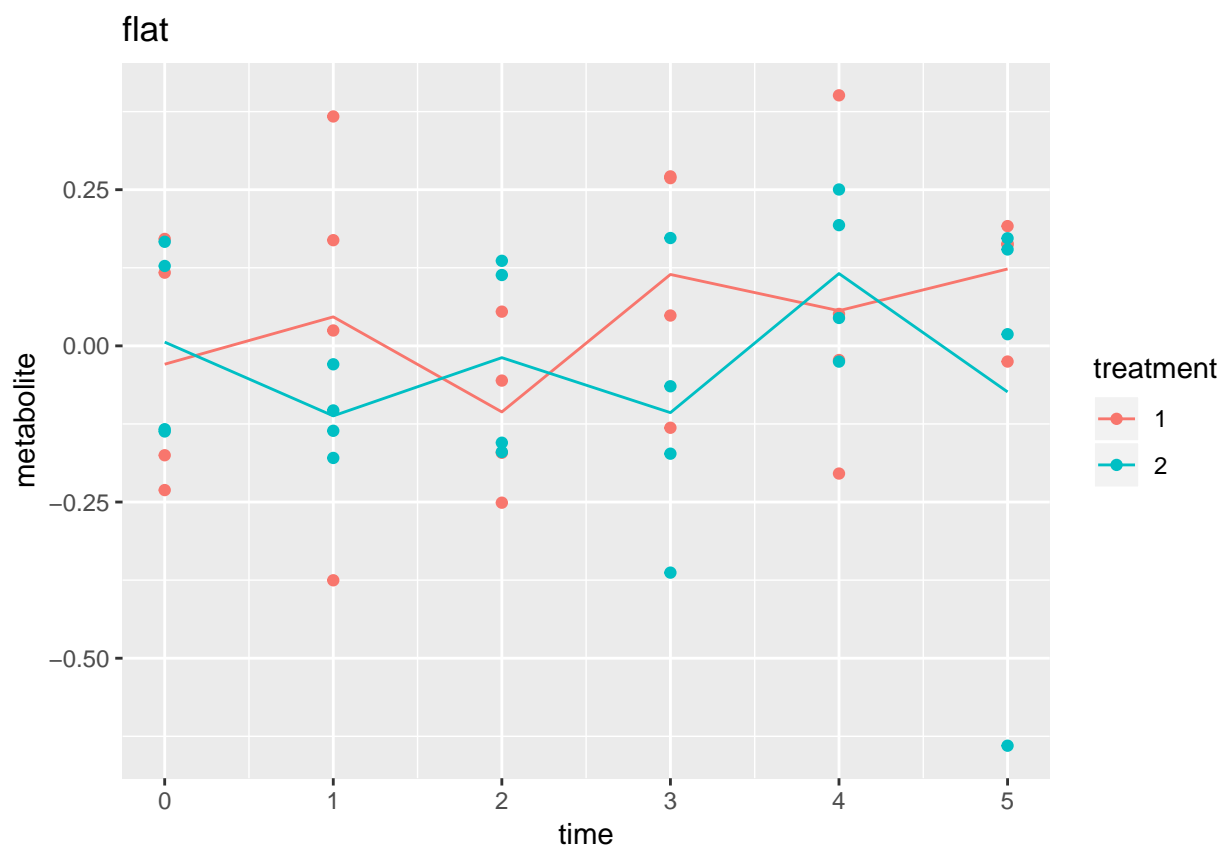
```
j=6#time
```

```
r=4#replicate
```

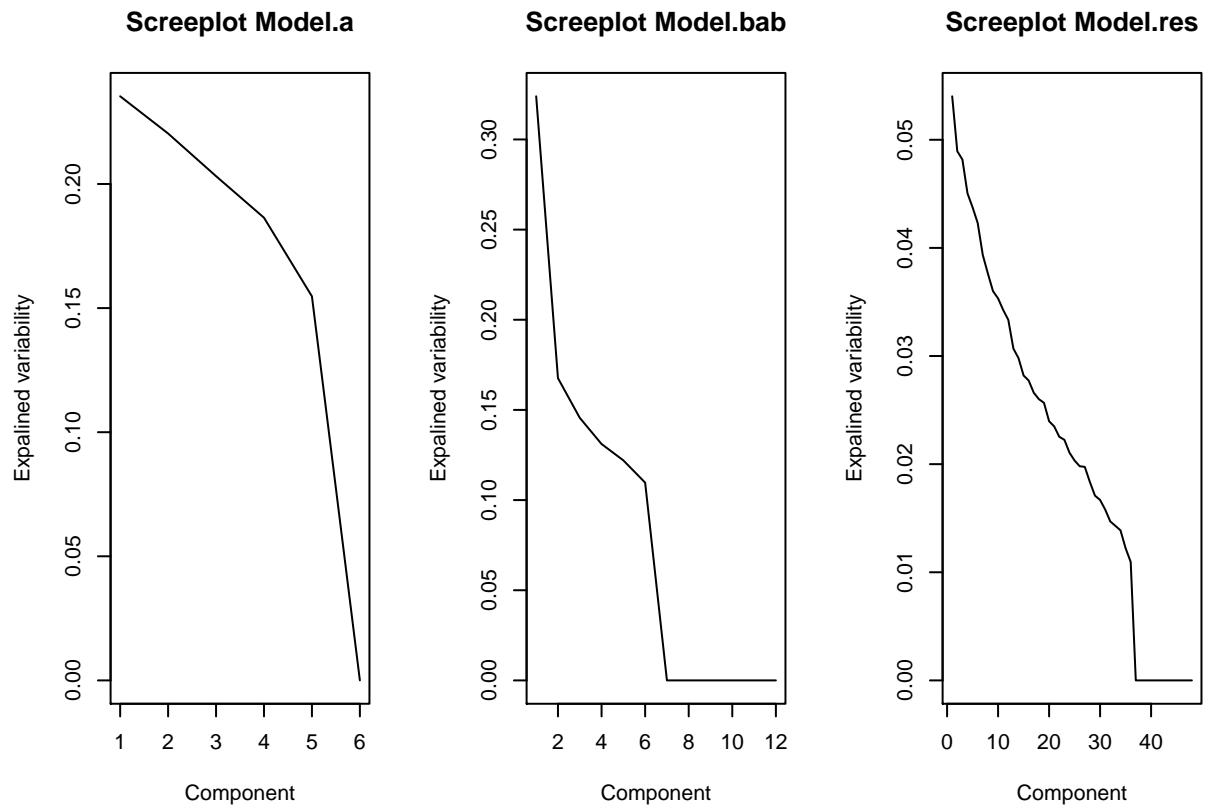
```
time=c(0,1,2,3,4,5)#time points
```

White noise is $N(0,0.2)$

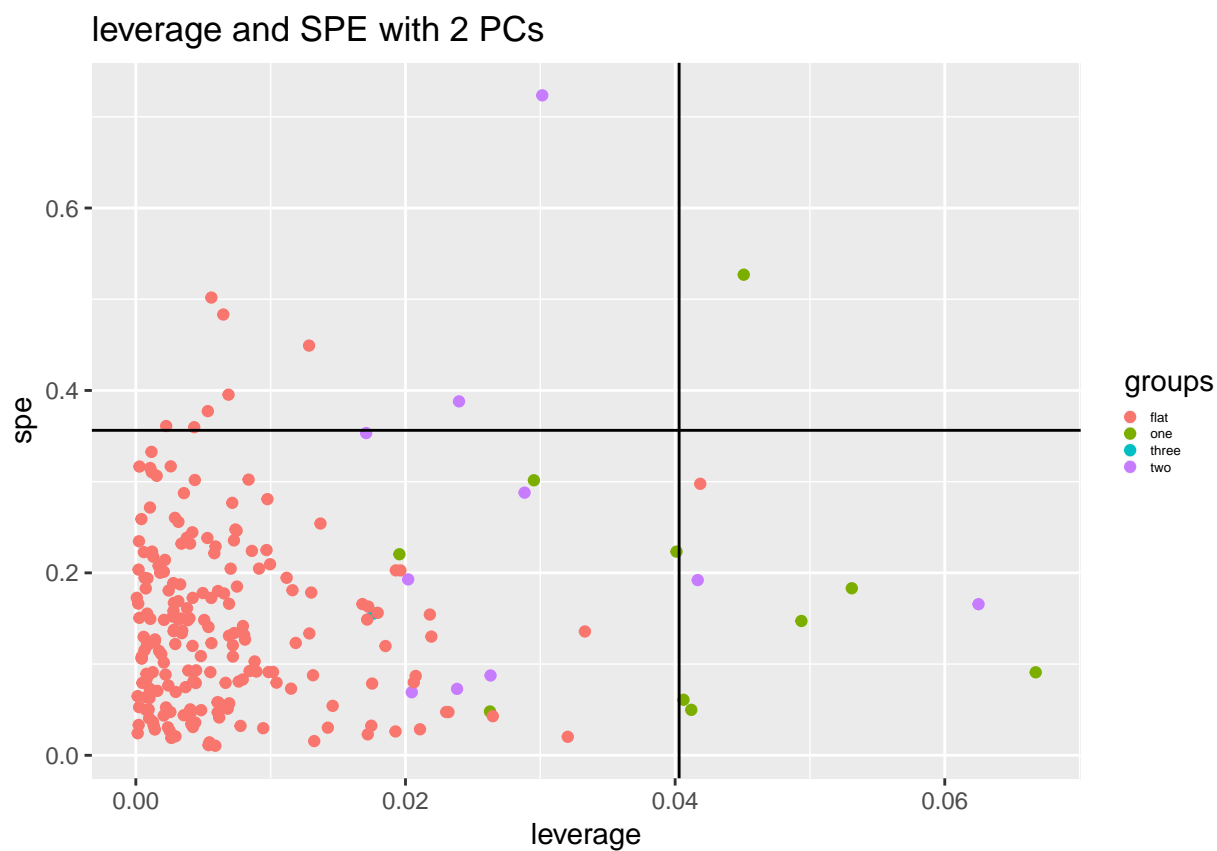




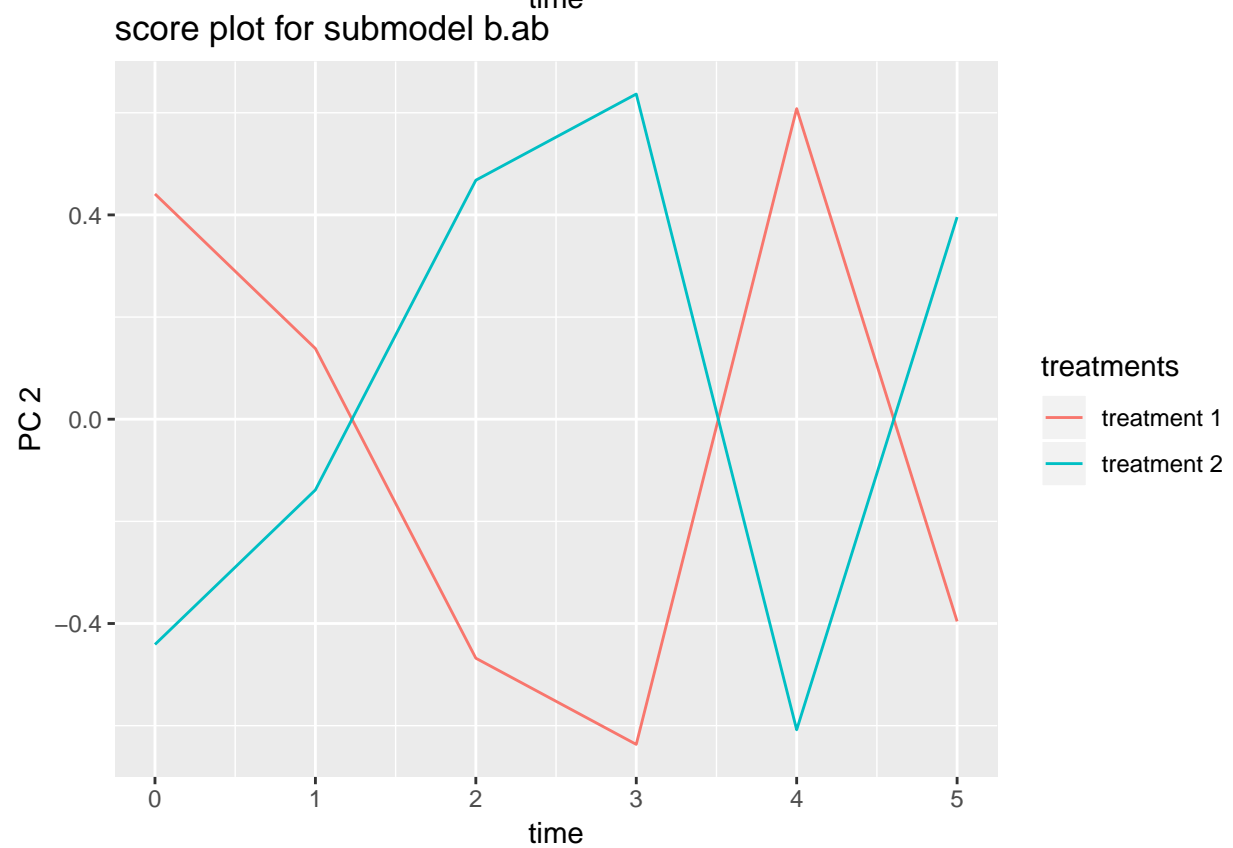
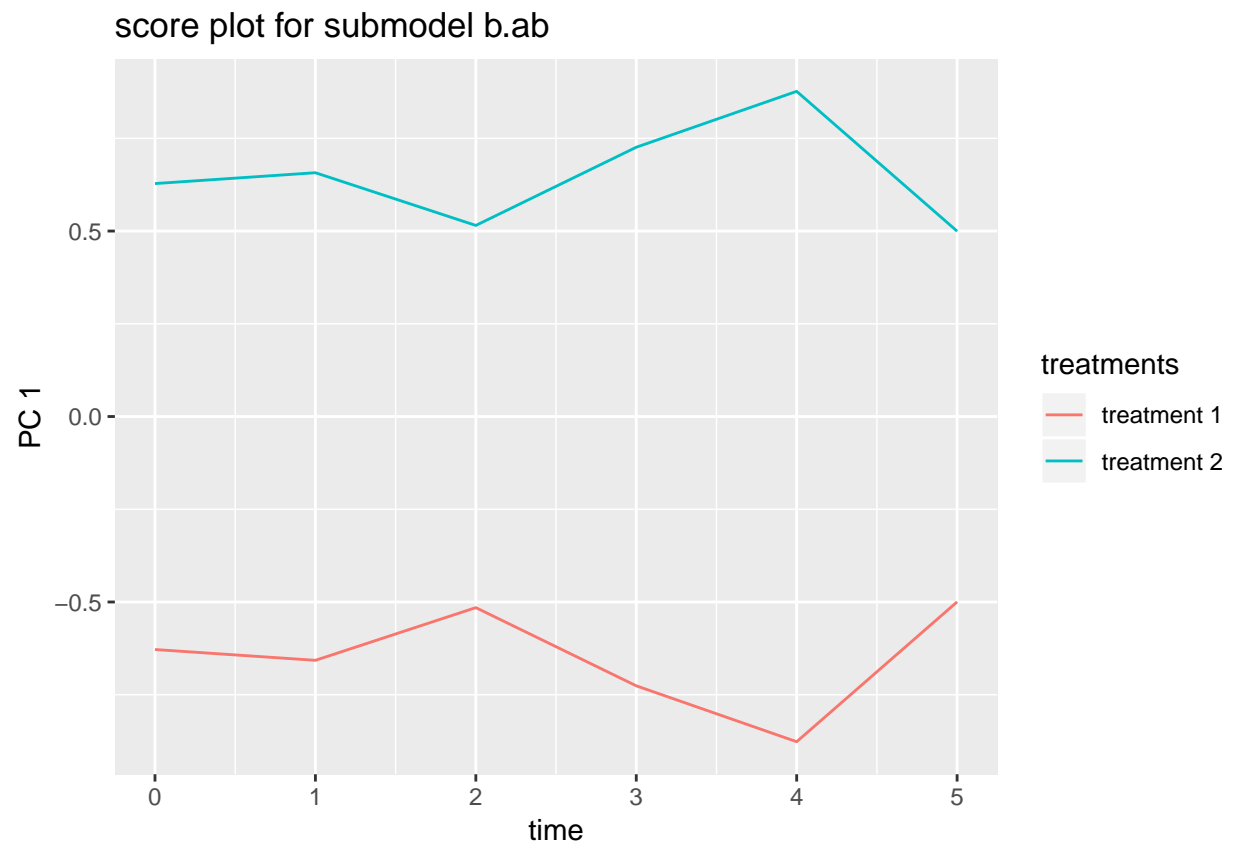
There are 21 metabolites with the differential expression shown in the above linear function and 200 metabolites with flat expression.



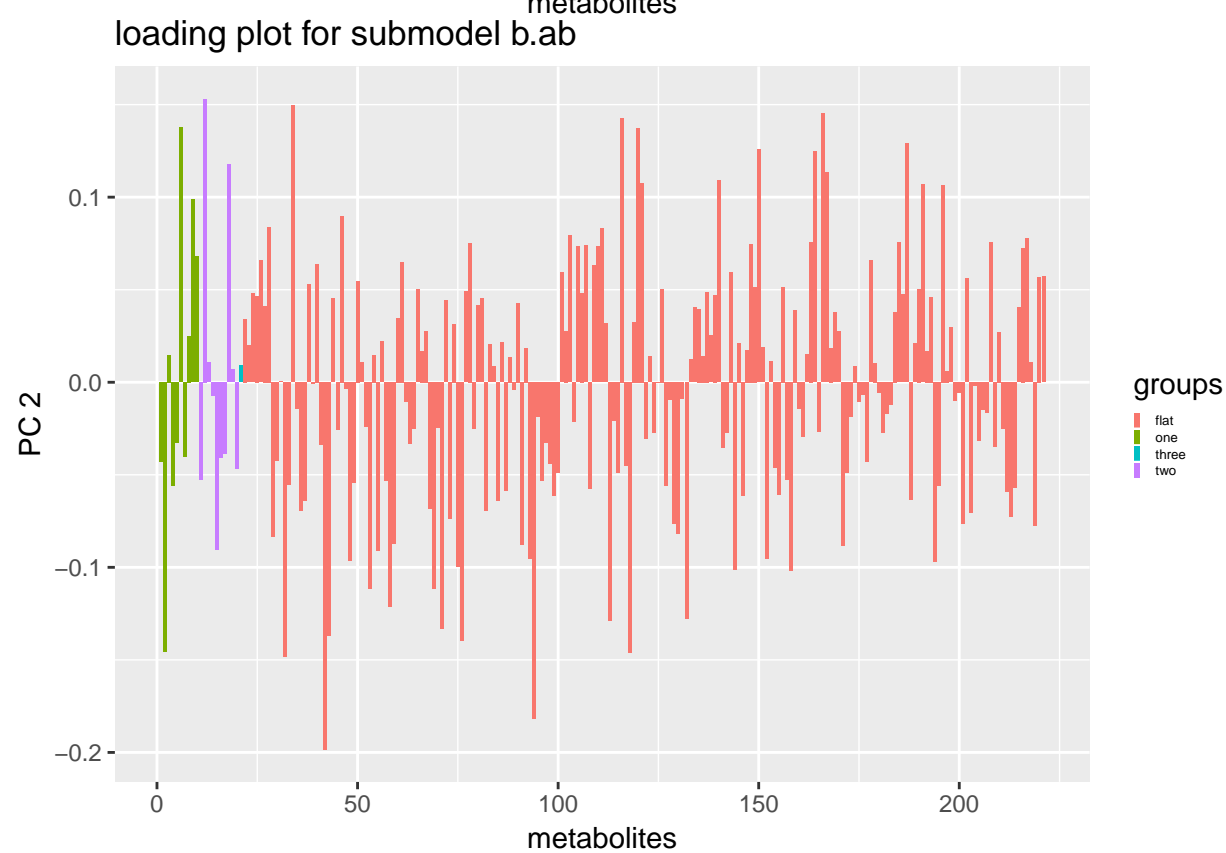
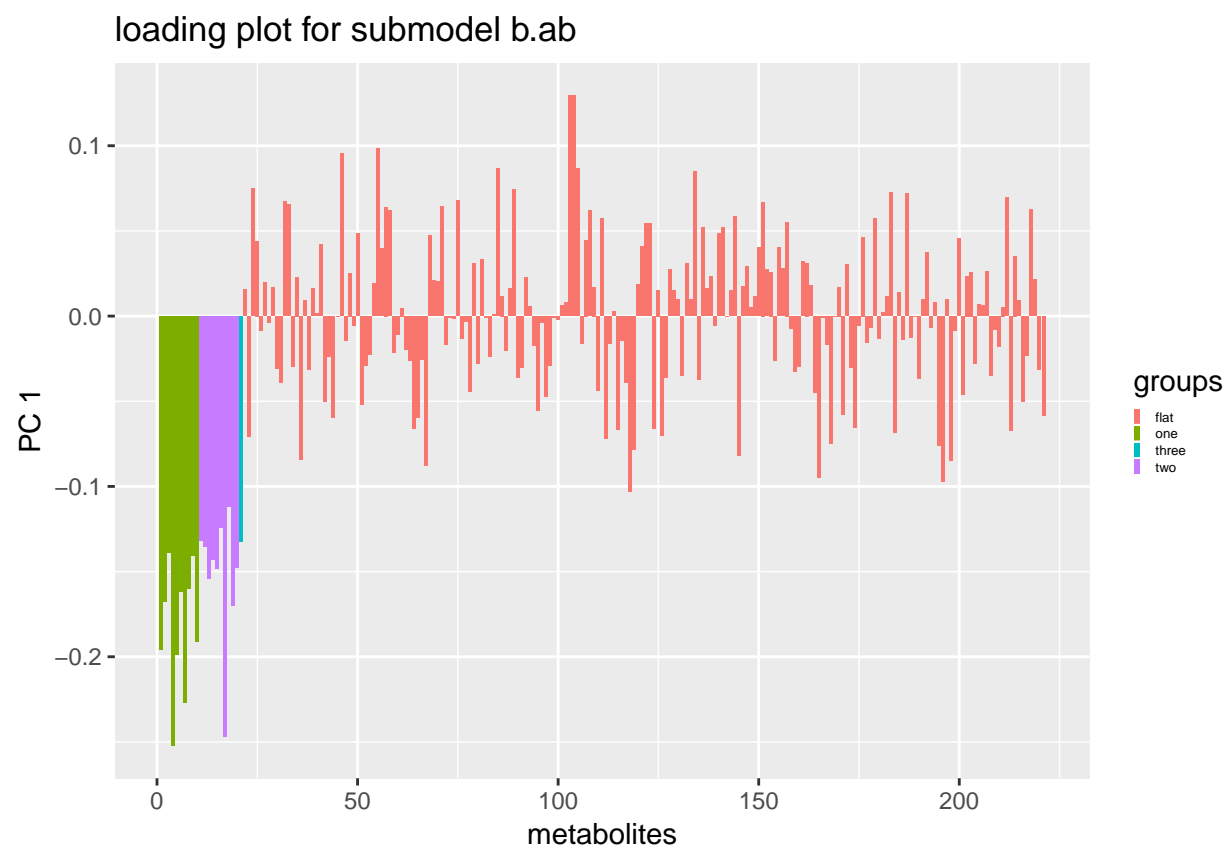
Screeplot shows that 1-2 PCs to be included for submodel b.ab(treatment+interaction). Here 2 pcs were selected



With 2 PCs selected, 10 out of 12 differential expressed metabolites corrected identified, fall into right-bottom quadrant.



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



loading plot shows differentially expressed metabolites making high contribution in this pc.

```
## [1] "running design"
## [1] "running p.vector"
## [1] "fitting gene 100 out of 221"
## [1] "fitting gene 200 out of 221"
## [1] "running T.fit"
## [1] "running get.siggenes"
## [1] "no significant genes"
## [1] "maSigPro halted at get.siggenes"
## [1] "no significant genes"
```

However, masigpro could not identify any significant abnormal metabolites.