

4. Compare DDEGs from same biological pathway but two different groups

```
library(TrendCatcher)
```

1. Load TrendCatcher R package.

```
severe.path<-system.file("extdata", "MasterListSevere.rda", package = "TrendCatcher")
load(severe.path)
moderate.path<-system.file("extdata", "MasterListModerate.rda", package = "TrendCatcher")
load(moderate.path)
ht.path<-system.file("extdata", "htSevere.rda", package = "TrendCatcher")
load(ht.path)
```

```
#head(ht.severe$GO.df)
head(ht.severe$GO.df)
```

2. Now read the two demo master.list objects.

	ID	Description	t.name	direction
## 1	G0:0006958	complement activation, classical pathway	0W-1W	Activation
## 2	G0:0006958	complement activation, classical pathway	1W-2W	Activation
## 3	G0:0006958	complement activation, classical pathway	2W-3W	Deactivation
## 4	G0:0006958	complement activation, classical pathway	3W-4W	Deactivation
## 5	G0:0006958	complement activation, classical pathway	4W-5W	Deactivation
## 6	G0:0006958	complement activation, classical pathway	5W-6W	Deactivation
##	Avg_log2FC	n_total	n_background	n_up n_down
## 1	2.1002689	77	141	77 0
## 2	0.6301674	32	141	32 0
## 3	-0.2587066	52	141	20 32
## 4	-0.3352649	62	141	16 46
## 5	-0.1453267	67	141	15 52
## 6	-0.5720138	68	141	0 68
##				
## 1	CLU/SERPING1/C1QB/CD55/CR1/IGKC/IGKV4-1/IGKV3D-20/IGKV3D-11/IGLV6-57/IGLV1-51/IGLV1-47/IGLV1-44/IGLV1-43/IGLV1-42/IGLV1-41/IGLV1-40/IGLV1-39/IGLV1-38/IGLV1-37/IGLV1-36/IGLV1-35/IGLV1-34/IGLV1-33/IGLV1-32/IGLV1-31/IGLV1-30/IGLV1-29/IGLV1-28/IGLV1-27/IGLV1-26/IGLV1-25/IGLV1-24/IGLV1-23/IGLV1-22/IGLV1-21/IGLV1-20/IGLV1-19/IGLV1-18/IGLV1-17/IGLV1-16/IGLV1-15/IGLV1-14/IGLV1-13/IGLV1-12/IGLV1-11/IGLV1-10/IGLV1-9/IGLV1-8/IGLV1-7/IGLV1-6/IGLV1-5/IGLV1-4/IGLV1-3/IGLV1-2/IGLV1-1/IGLV1-0			
## 2				
## 3				
## 4				
## 5				
## 6				
##				
## 1				
## 2				
## 3				
## 4				
## 5				

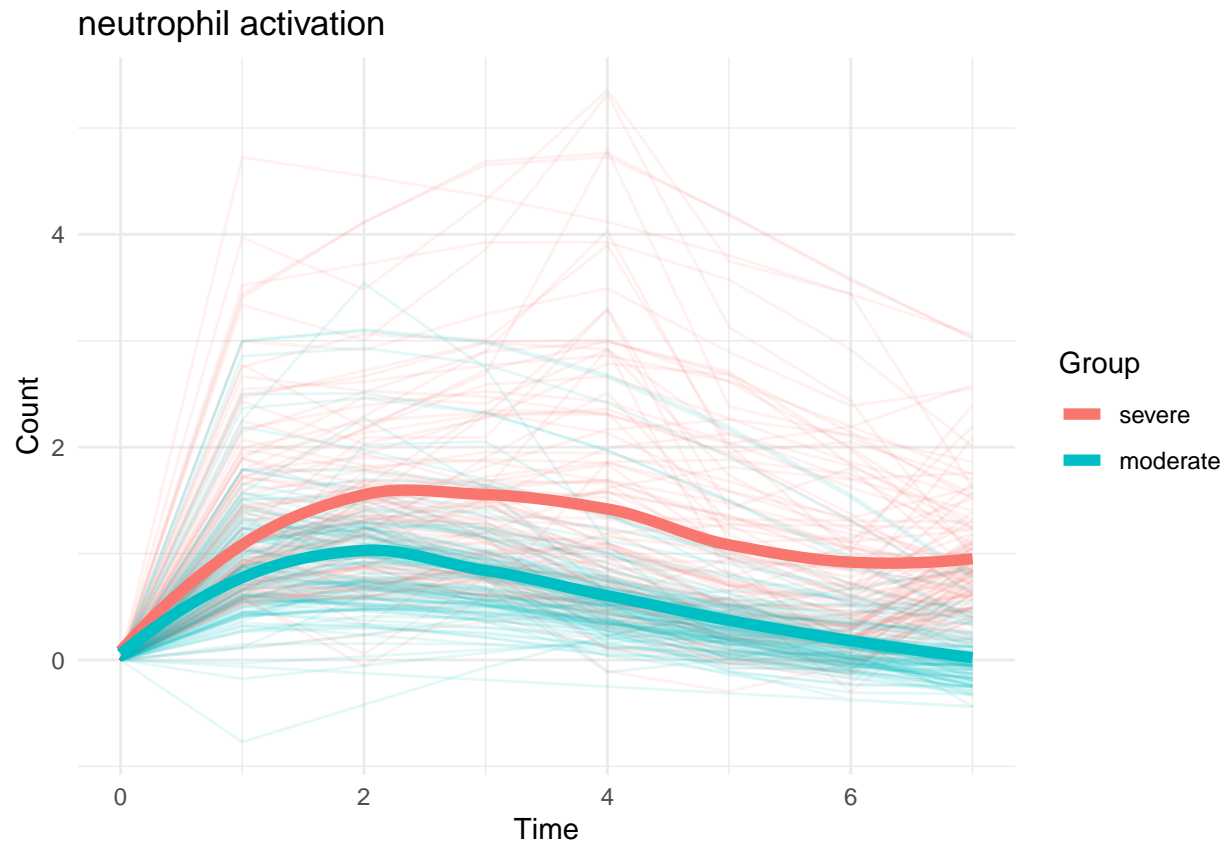
```
## 6 SERPING1/C1QB/CR1/IGKC/IGKV3D-20/IGKV3D-11/IGLV6-57/IGLV1-51/IGLV1-47/IGLV1-44/IGLV7-43/IGLV1-40/I
##           p.adjust.up           p.adjust.down
## 1 6.67222905253988e-72
## 2 2.19506922004502e-18
## 3 1.63402445206667e-08 9.9477266204752e-33
## 4 2.74522759489778e-05 7.55610755399035e-46
## 5 2.69045301915842e-05 3.3223517232817e-48
## 6                      6.7007249596023e-69
```

```
#### To compare DDEGs trajectories from a specific biological pathway
### In this example, we show DDEGs from "neutrophil activation", one of the top enriched timeheatmap bi
```

```
g<-draw_CurveComp(master.list.1 = master.list.severe, master.list.2 = master.list.moderate, ht.1 = ht.s
```

```
## Found 117 DDEGs from neutrophil activation
```

```
print(g)
```



```
#### Permutation to check which time interval two curves are significantly seperated
perm_output<-draw_CurveComp_Perm(master.list.1 = master.list.severe,
                                master.list.2 = master.list.moderate,
                                ht.1 = ht.severe,
                                pathway = "neutrophil activation",
                                group.1.name = "severe",
                                group.2.name = "moderate",
                                n.perm = 100,
                                parall = FALSE,
                                pvalue.threshold = 0.05)
```

```
## Found 117 DDEGs from neutrophil activation/nStart Permutation
## |
```

```
perm_output$plot
```

