

1. Read GWAS data

```
library(snpStats)  
gwas <- read.plink("bed_file")
```

2. Generate SNP network

```
gs <- get_GS_network(gwas) # OR  
gm <- get_GM_network(gwas) # OR  
gi <- get_GI_network(gwas)
```

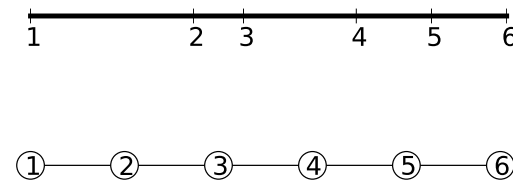
3. Search interconnected, associated SNPs

```
res <- scones.cv(gwas, gi) # OR  
res <- sigmod.cv(gwas, gi)
```

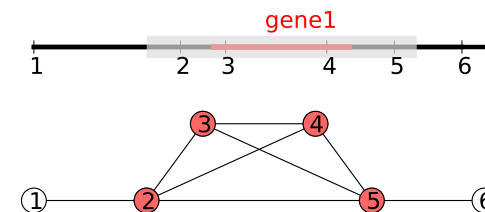
4. Visualize results

```
plot_ideogram(gwas, res)
```

GS



GM



GI

