

Rat Application

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We consider variables are divided into groups:

- Example p : SNPs grouped into K genes

$$\mathbf{X} = [\underbrace{SNP_1, \dots, SNP_k}_{gene_1} | \underbrace{SNP_{k+1}, SNP_{k+2}, \dots, SNP_h}_{gene_2} | \dots | \underbrace{SNP_{l+1}, \dots, SNP_p}_{gene_K}]$$

- Example p : genes grouped into K pathways/modules ($X_j = \text{gene}_j$)

$$\mathbf{X} = [\underbrace{X_1, X_2, \dots, X_k}_{M_1} | \underbrace{X_{k+1}, X_{k+2}, \dots, X_h}_{M_2} | \dots | \underbrace{X_{l+1}, X_{l+2}, \dots, X_p}_{M_K}]$$

```
load("RAT.RData")
X <- RAT$X
Y <- RAT$Y
MAP.file <- RAT$MAP.file
gsize <- RAT$gsize
dim(X)
```

```
## [1] 29 770
```

```
dim(Y)
```

```
## [1] 29 4
```