`optBiomarker`: **R package for estimating optimal number of biomarkers at a given error tolerance level for various classification rules**
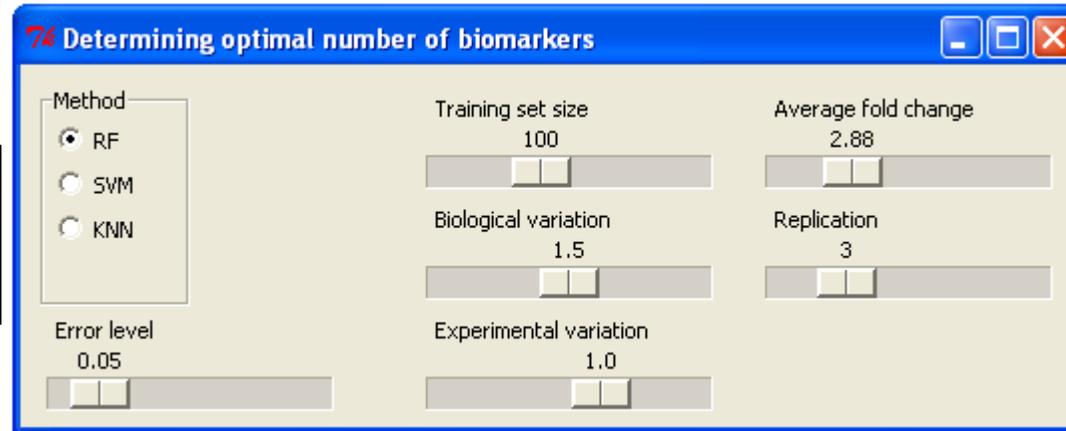
Example code:

```
data(errorDbase)
optimiseBiomarker(error=errorDbase)
```

Determining optimal number of biomarkers

Method
- ⦿ RF
- ○ SVM
- ○ KNN

Training set size
100

Average fold change
2.88

Biological variation
1.5

Replication
3

Error level
0.05

Experimental variation
1.0

Optimal number: 16

Error rate

Biological variation

No. of Biomarker