









































































Pre-process

```
graph TD; A[Pre-process] --> B[Reduce dimension]; B --> C[Cluster]; C --> D[Learn graph];
```

**Reduce
dimension**

Cluster

Learn graph





**Compare expression
between clusters**

Gene1



Gene2



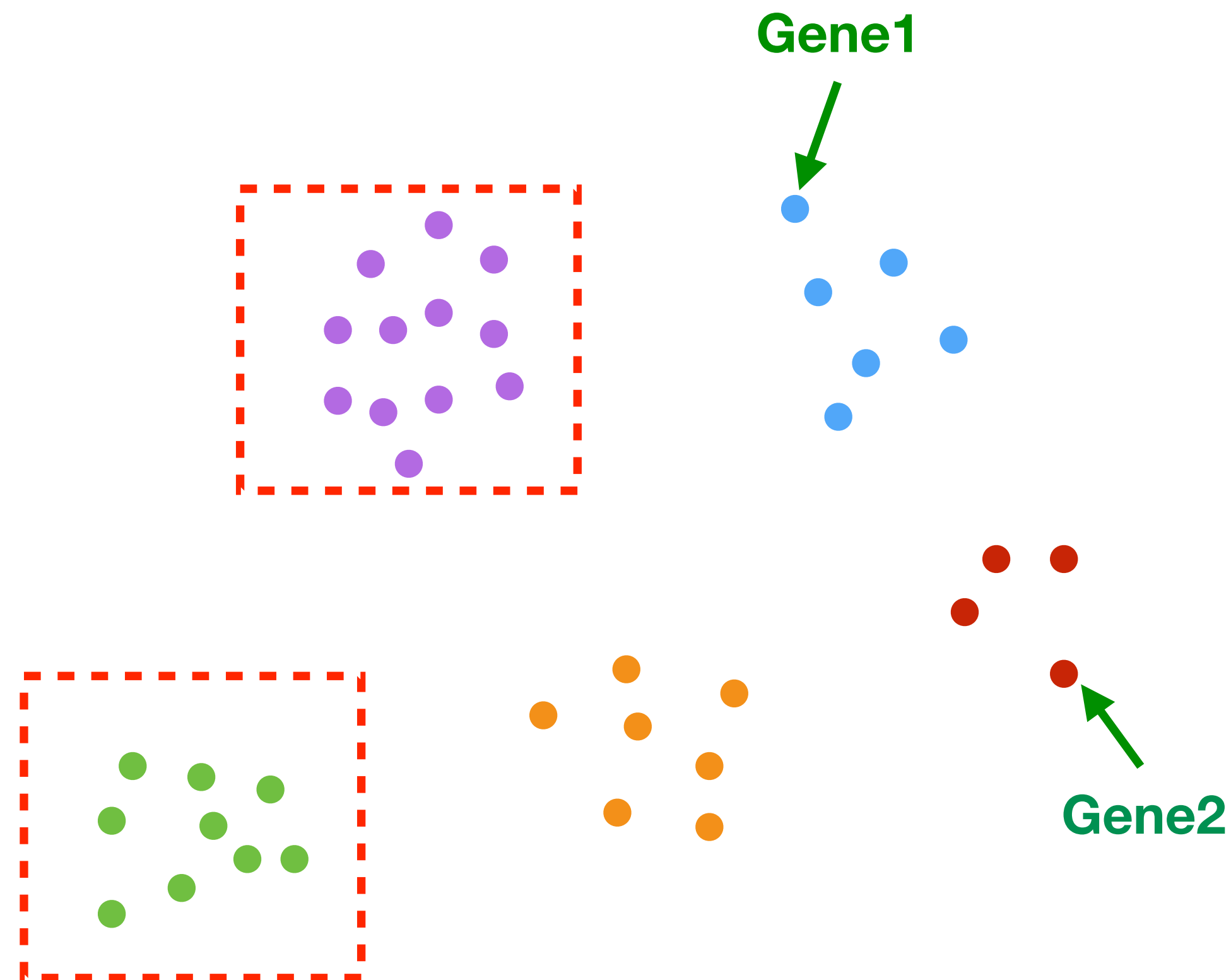
Find cluster markers

Pre-process

Reduce
dimension

Cluster

Learn graph



Compare expression
between clusters

Find cluster markers

Compare selected clusters

```
cds_subset <- choose_cells(cds)
```

