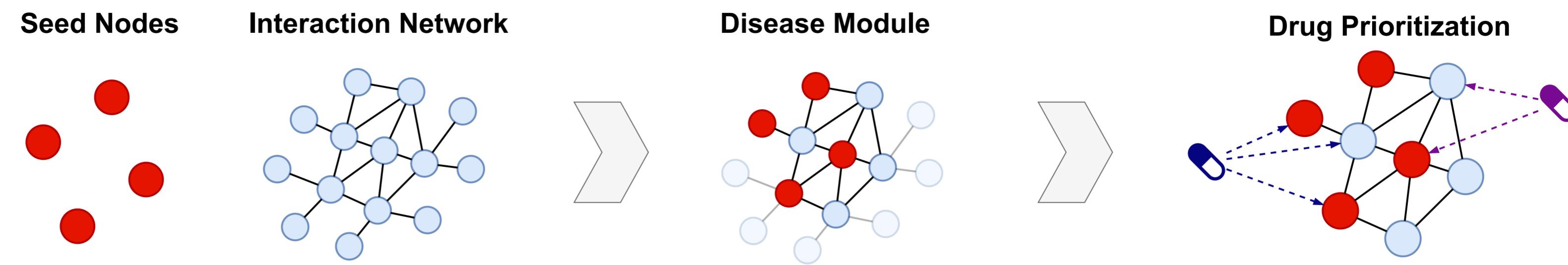
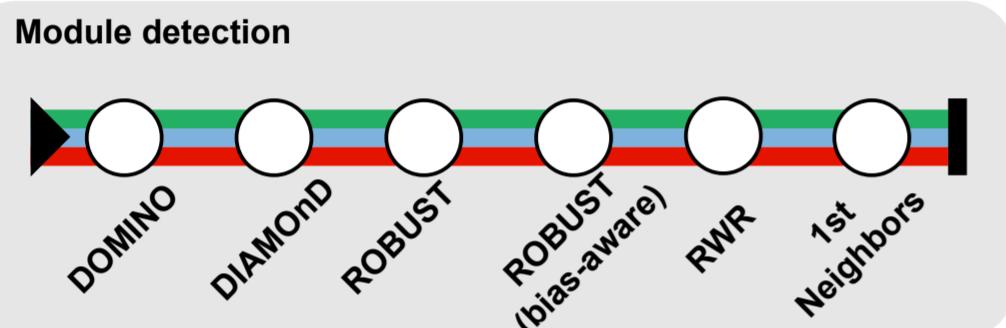


**A****B**

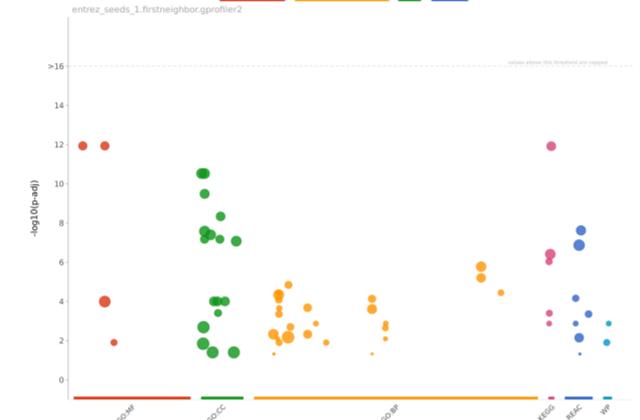
### Module Detection

- Six module detection **algorithms** included
- Subworkflows for input and output parsing



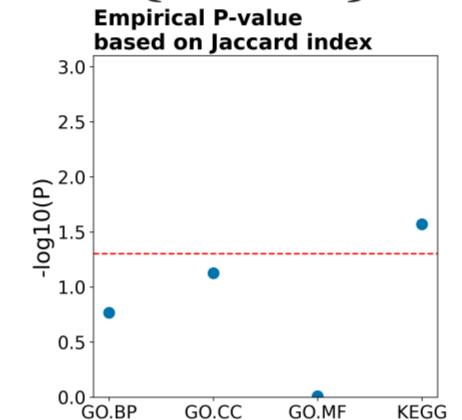
### Over-Representation

**g:Profiler**



### Evaluation

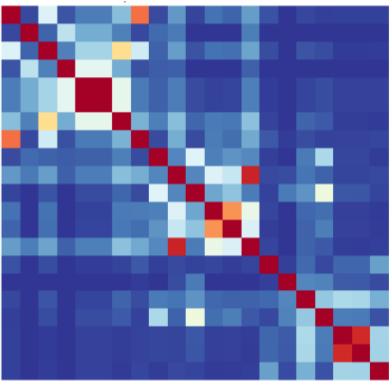
**DIGEST**



### Topology Measures

General Statistics				
	Nodes	Edges	Seeds	Diameter
entrez_seeds_1.diamond	210	696	10	8
entrez_seeds_1.domino	5	6	4	3
entrez_seeds_1.firstneighbor	83	264	10	9
entrez_seeds_1.robust	24	29	10	8
entrez_seeds_1.robust_bias_aware	24	31	10	8
entrez_seeds_2.diamond	207	672	7	8
entrez_seeds_2.domino	7	15	4	2
entrez_seeds_2.firstneighbor	54	207	7	6
entrez_seeds_2.robust	31	43	6	6
entrez_seeds_2.robust_bias_aware	31	43	6	1

### Module Overlaps



### Launch

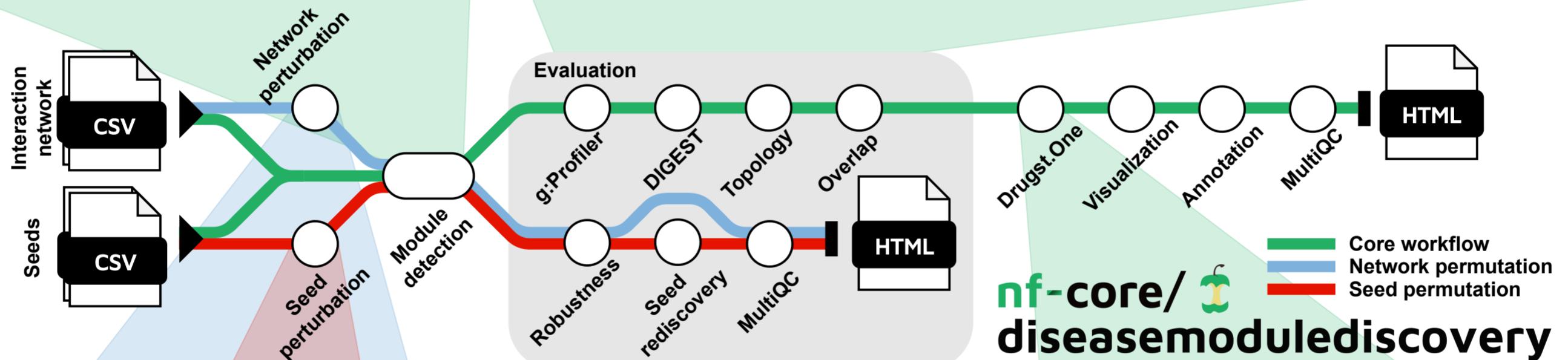
```

Run pipeline
nextflow run \
nf-core\diseasemodulediscovery \
-profile docker \
--network PPI.csv \
--seeds seed_genes.csv \
--id_space entrez \
--outdir results
  
```

**Interaction Network**  
Provide files or choose predefined

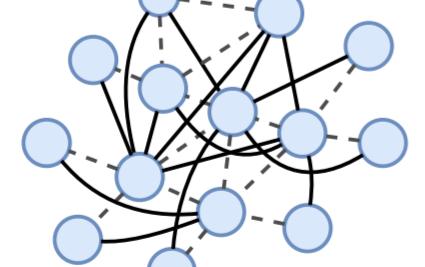
**Seeds**  
Provide files with seed nodes

### Software Deployment



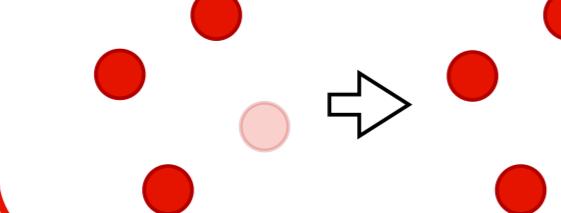
### Network Perturbation

Degree-preserving rewiring



### Seed Perturbation

Leave-one-out approach  
(repeat for every seed gene)



### Perturbation-Based Evaluation

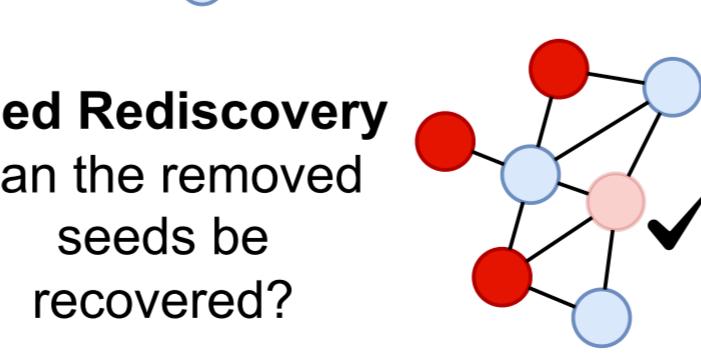
#### Robustness

How much do the modules change?



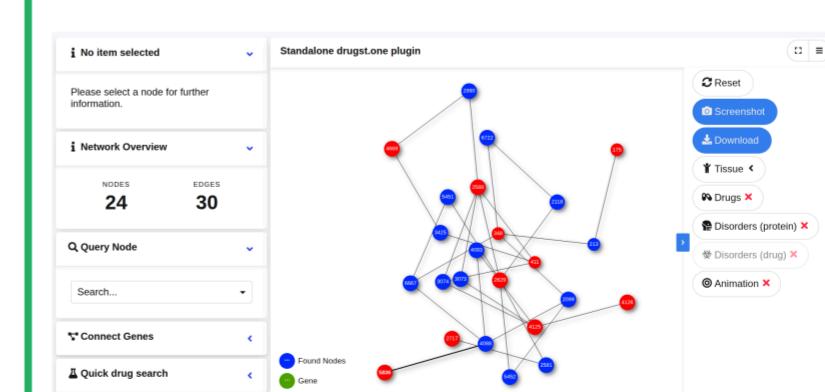
#### Seed Rediscovery

Can the removed seeds be recovered?



### Drugst.One

#### Web Export



#### Drug Prioritization

- TrustRank
- Degree Centrality
- Harmonic Centrality

### Output

#### Annotated Modules



- Targeting drugs
- Associated disorders
- Cellular localization

**Unified Output**  
Annotated modules saved in BioPAX format

**Pipeline Report**  
MultiQC report with summary statistics and figures

**Network Visualizations**