

A

Concept Overview

Seed Nodes

Interaction Network

Disease Module

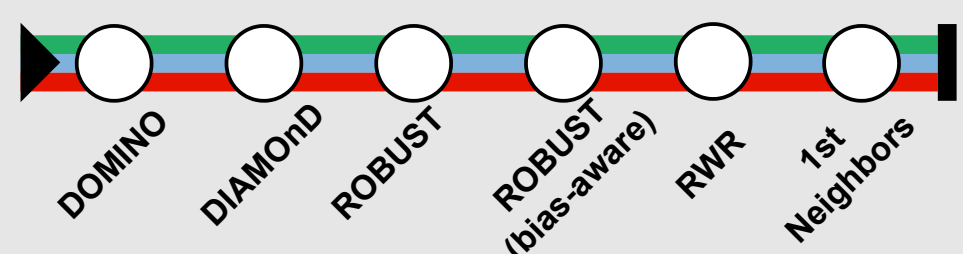
Drug Prioritization

B

Module Detection

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

Module detection



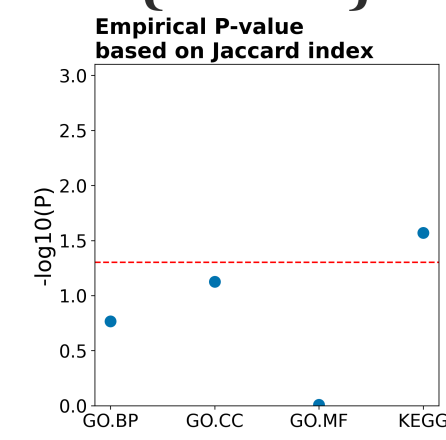
Evaluation

Over-Representation

g:Profiler



Functional Coherence

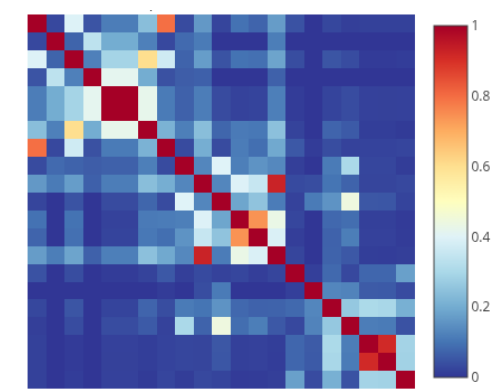
{DIGEST}_p

Topology Measures

General Statistics

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

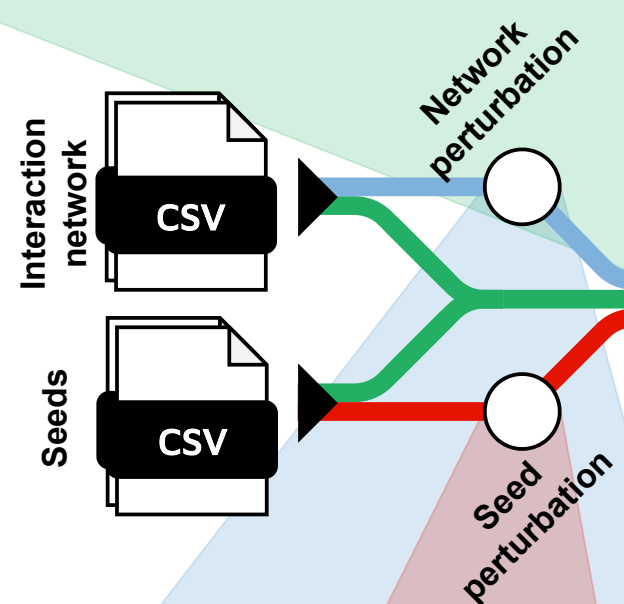
Provide files *or* choose predefined



Seeds

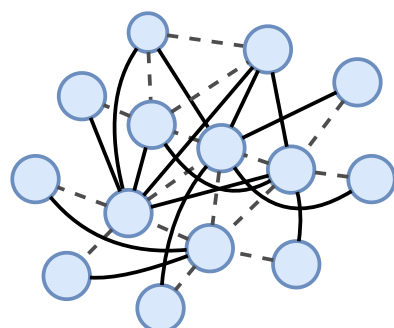
Provide files with seed nodes

Software Deployment



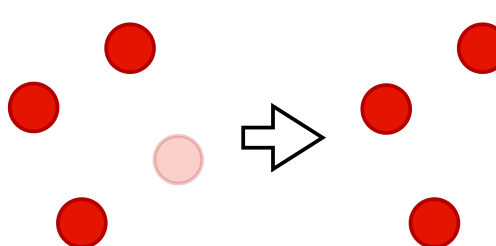
Network Perturbation

Degree-preserving rewiring

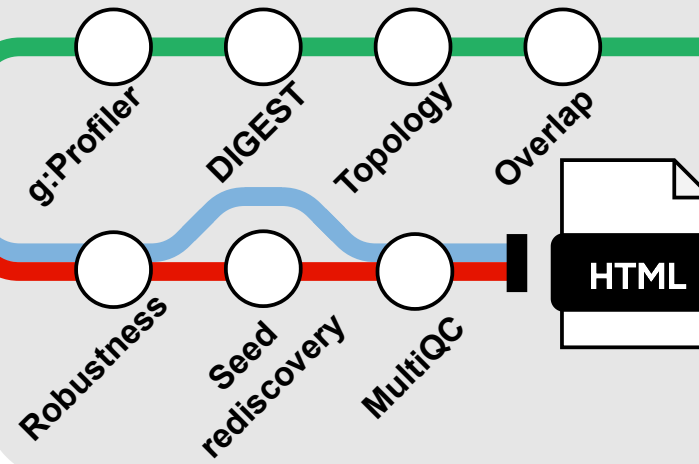


Seed Perturbation

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



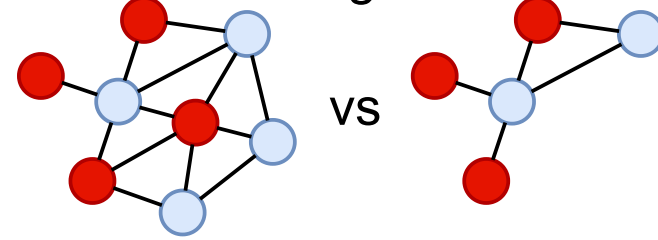
Evaluation



Perturbation-Based Evaluation

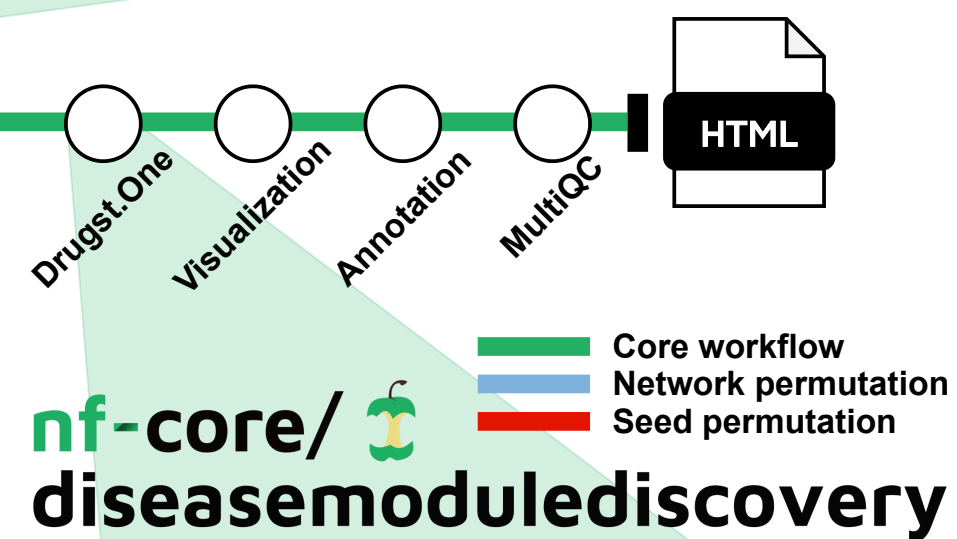
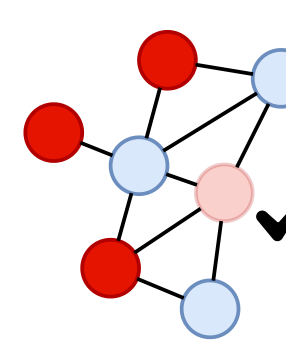
Robustness

How much do the modules change?



Seed Rediscovery

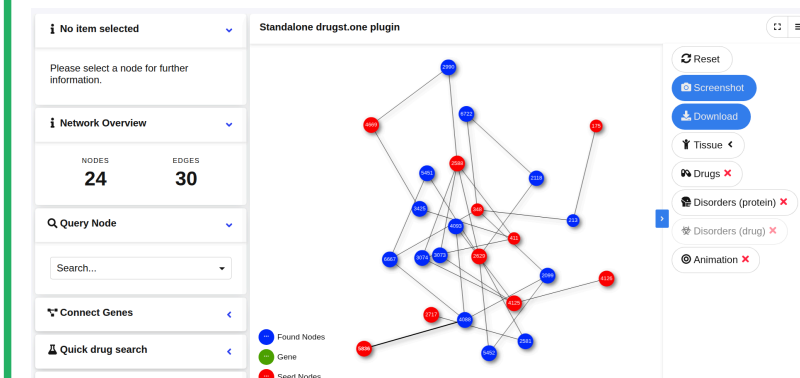
Can the removed seeds be recovered?



nf-core/ diseasemodulediscovery



Web Export



Drug Prioritization

- TrustRank
- Degree Centrality
- Harmonic Centrality

Output

Annotated Modules

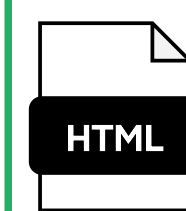


- Targeting drugs
- Associated disorders
- Cellular localization



Unified Output

Annotated modules saved in BioPAX format



Pipeline Report

MultiQC report with summary statistics and figures



Network Visualizations

