

Young-Rae Cho, et al.

"Semantic integration to identify overlapping functional modules in protein interaction networks"

Supplementary File 1.

Modularization results of the networks weighted by semantic similarity *before post-processing*

| number of informative proteins | min flow threshold | average size of modules | average <i>f</i> -measure | average $-\log(p\text{-value})$ |
|--------------------------------|--------------------|-------------------------|---------------------------|---------------------------------|
| 50 | 0.180 | 117.82 | 0.367 | 34.51 |
| 75 | 0.220 | 91.12 | 0.365 | 32.55 |
| 100 | 0.260 | 74.60 | 0.366 | 31.32 |
| 125 | 0.300 | 63.58 | 0.360 | 29.71 |
| 150 | 0.333 | 55.14 | 0.353 | 27.47 |
| 175 | 0.367 | 48.53 | 0.344 | 26.05 |
| 200 | 0.400 | 43.37 | 0.334 | 24.10 |
| 225 | 0.425 | 39.79 | 0.330 | 23.16 |
| 250 | 0.450 | 36.55 | 0.325 | 22.06 |
| 275 | 0.480 | 33.55 | 0.320 | 20.72 |

Modularization results of the networks weighted by semantic similarity *after post-processing*

| number of informative proteins | min flow threshold | merging threshold | number of modules | average size of modules | average <i>f</i> -measure | average $-\log(p\text{-value})$ |
|--------------------------------|--------------------|-------------------|-------------------|-------------------------|---------------------------|---------------------------------|
| 50 | 0.180 | 8.5 | 50 | 117.82 | 0.367 | 34.51 |
| 75 | 0.220 | 8.5 | 75 | 91.12 | 0.365 | 32.55 |
| 100 | 0.260 | 8.5 | 98 | 75.34 | 0.366 | 31.22 |
| 125 | 0.300 | 8.5 | 118 | 65.43 | 0.360 | 29.77 |
| 150 | 0.333 | 8.5 | 140 | 56.99 | 0.354 | 27.55 |
| 175 | 0.367 | 8.5 | 159 | 51.03 | 0.347 | 26.37 |
| 200 | 0.400 | 8.5 | 178 | 46.14 | 0.337 | 24.42 |
| 225 | 0.425 | 8.5 | 200 | 42.22 | 0.333 | 23.37 |
| 250 | 0.450 | 8.5 | 222 | 38.77 | 0.327 | 22.27 |
| 275 | 0.480 | 8.5 | 243 | 35.58 | 0.320 | 20.82 |