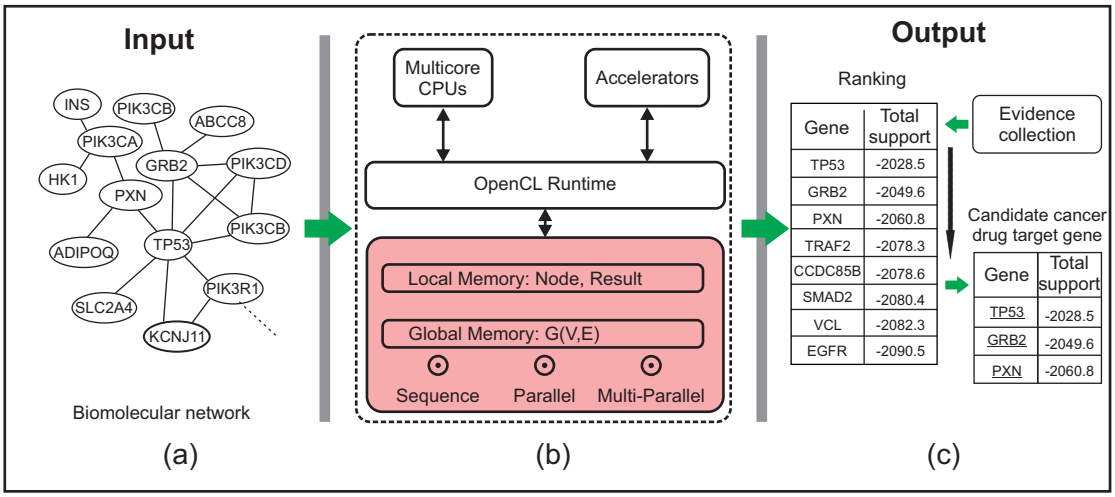
Novel method for competition-based controllability of large-scale complex networks

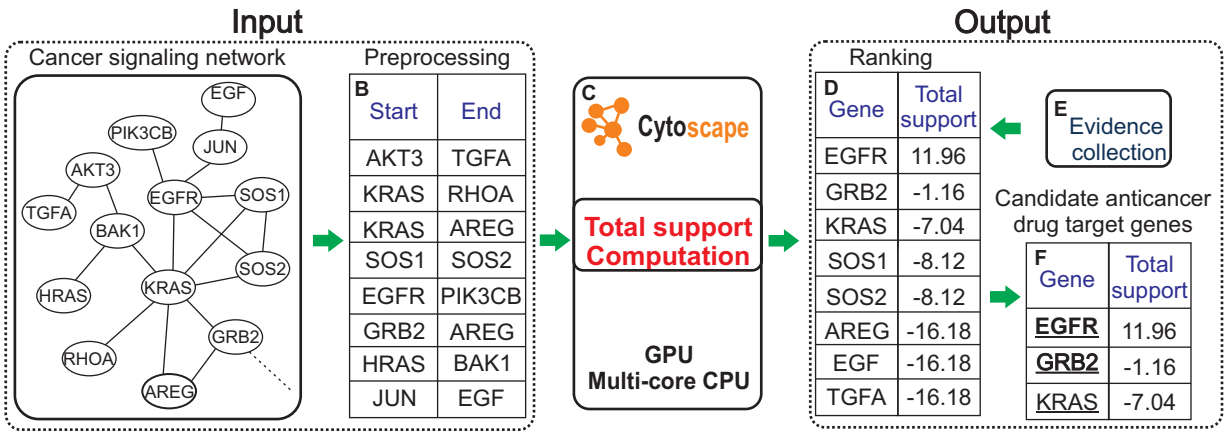


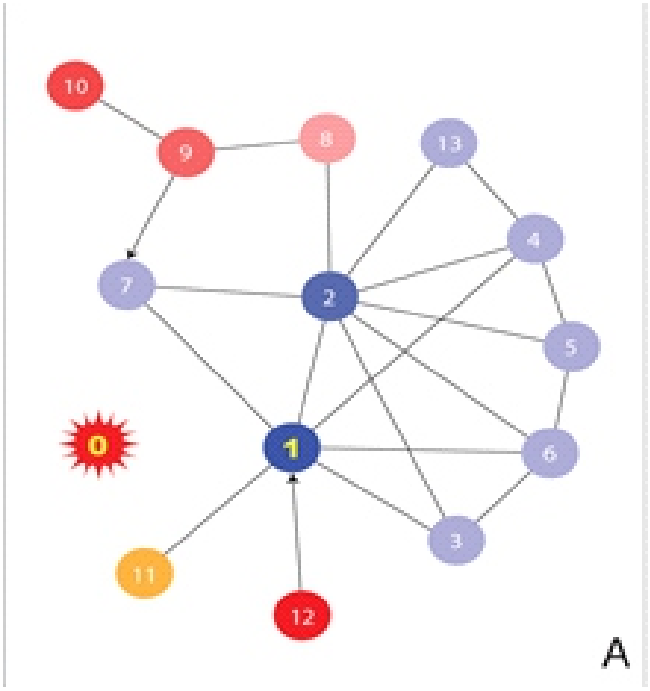
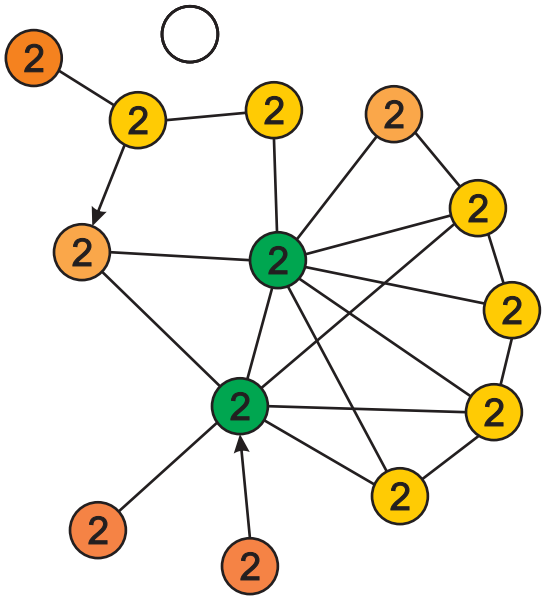
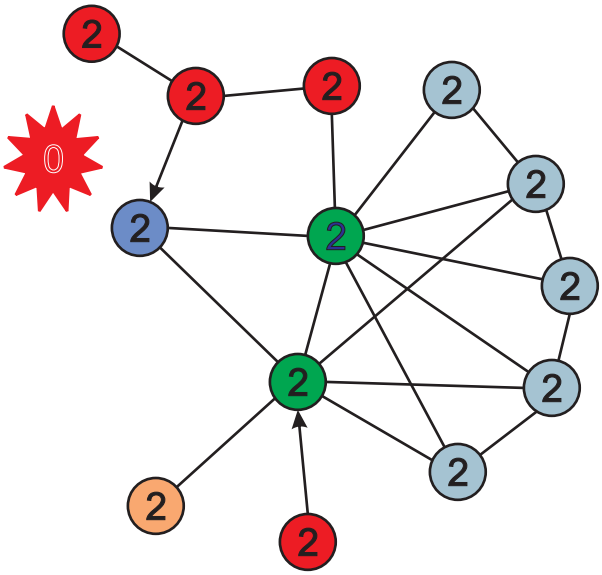
Outperforms

- Competition model
- Structural analysis of regulatory network
- Random Walk
- Network structure-based method
- Network distance-based method

HPC software

Case studies on large-scale molecular networks:
- Driver nodes are drug target genes
- Driver nodes reside at innermost K-core


Input
Cancer signaling network
EGF
PIK3CB
JUN
AKT3
EGFR
SOS1
TGFA
BAK1
SOS2
HRAS
KRAS
GRB2
RHOA
AREG
Preprocessing
B
Start
End
AKT3 TGFA
KRAS RHOA
KRAS AREG
SOS1 SOS2
EGFR PIK3CB
GRB2 AREG
HRAS BAK1
JUN EGF
C
Cytoscape
Total support Computation
GPU
Multi-core CPU
Output
Ranking
D
Gene
Total support
EGFR 11.96
GRB2 -1.16
KRAS -7.04
SOS1 -8.12
SOS2 -8.12
AREG -16.18
EGF -16.18
TGFA -16.18
E
Evidence collection
Candidate anticancer drug target genes
F
Gene
Total support
EGFR 11.96
GRB2 -1.16
KRAS -7.04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