

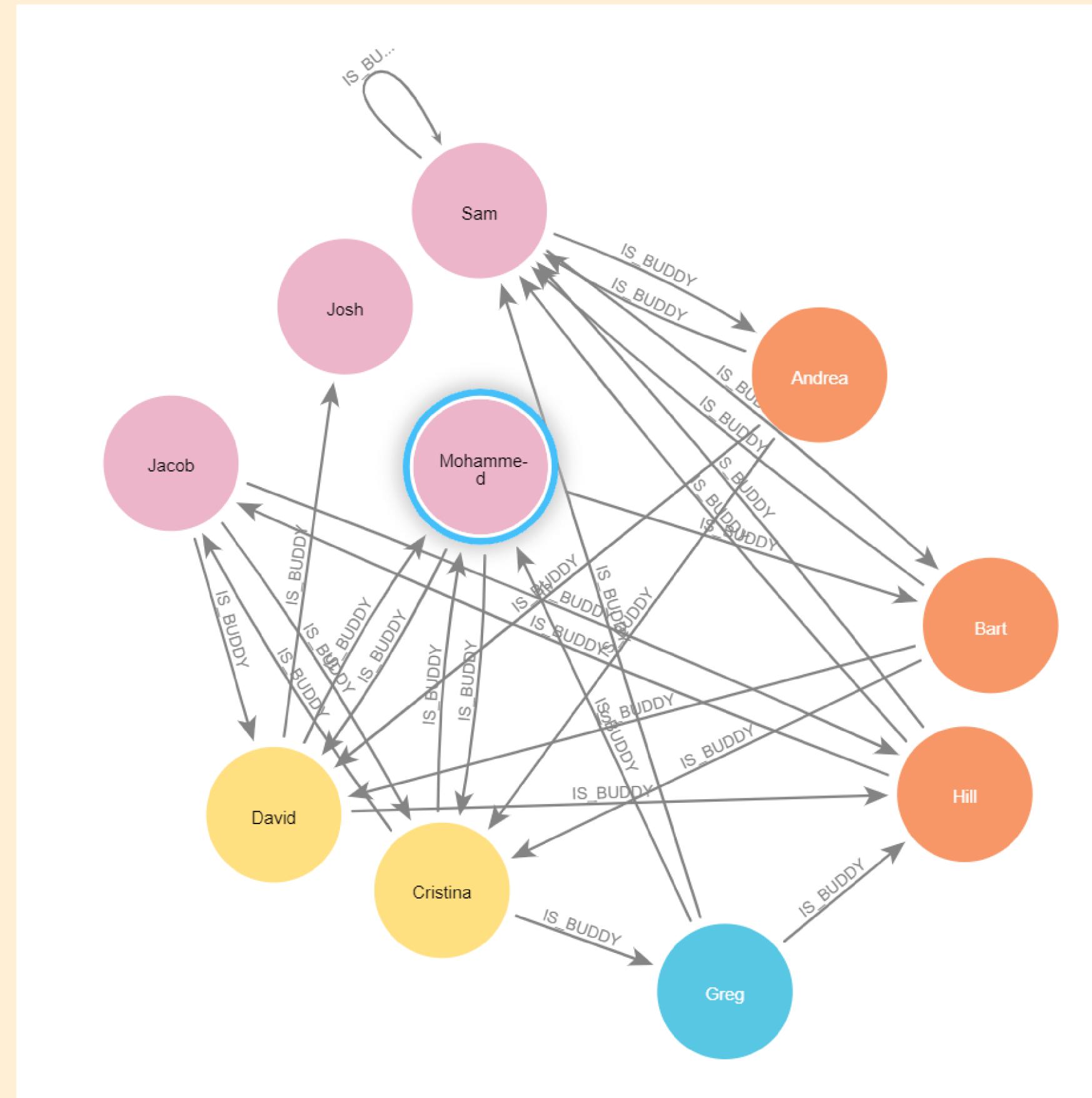
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NEO4J

K1 COLOUR

- Assigns a color to every node in the graph while aiming to optimize two objectives:
 - Every neighbor has a different color than the node itself.
 - As few colors as possible.
- NP-complete problem
- Uses Greedy Algorithm
 - Start with an empty list of colored vertices.
 - Sort the vertices
 - For each vertex:
 - Assign the lowest possible color that is not used by its adjacent vertices.
 - Add the vertex to the list of colored vertices.

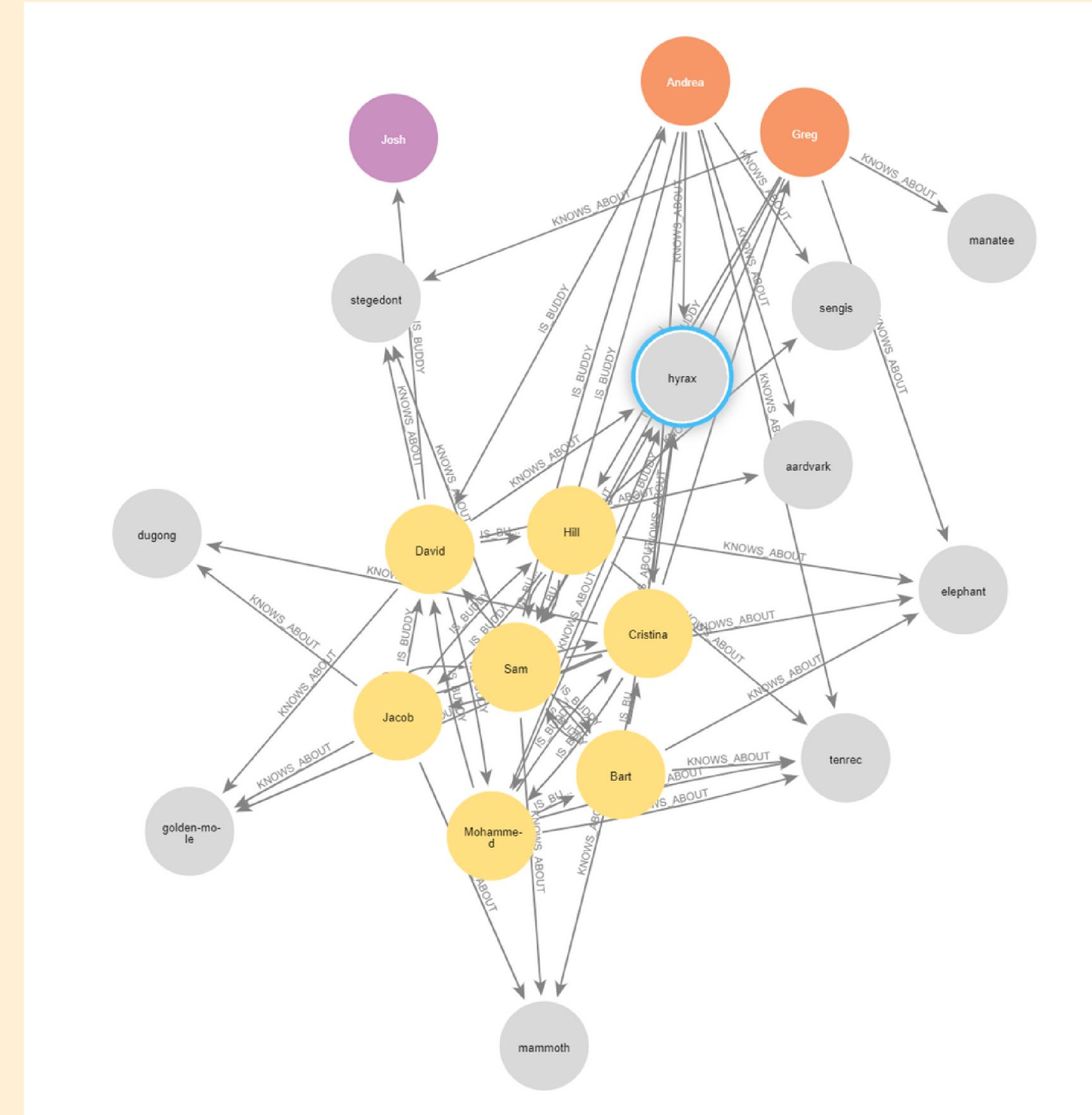
K1 COLOUR



K-CORE DECOMPOSITION

- Partitions nodes into groups based on the graph's degree sequence and topology.
- The i -core refers to a subgraph where every node has a degree of at least i . Nodes in the i -core also belong to the j -core for any $j < i$, but the reverse is not necessarily true.
- Each node in the graph is associated with a core value, which represents the largest value of i for which the node belongs to the i -core.
- Algorithm :
 - Iteratively remove nodes with the lowest degree, along with their relationships
 - Gradually different core groups in the graph are revealed.

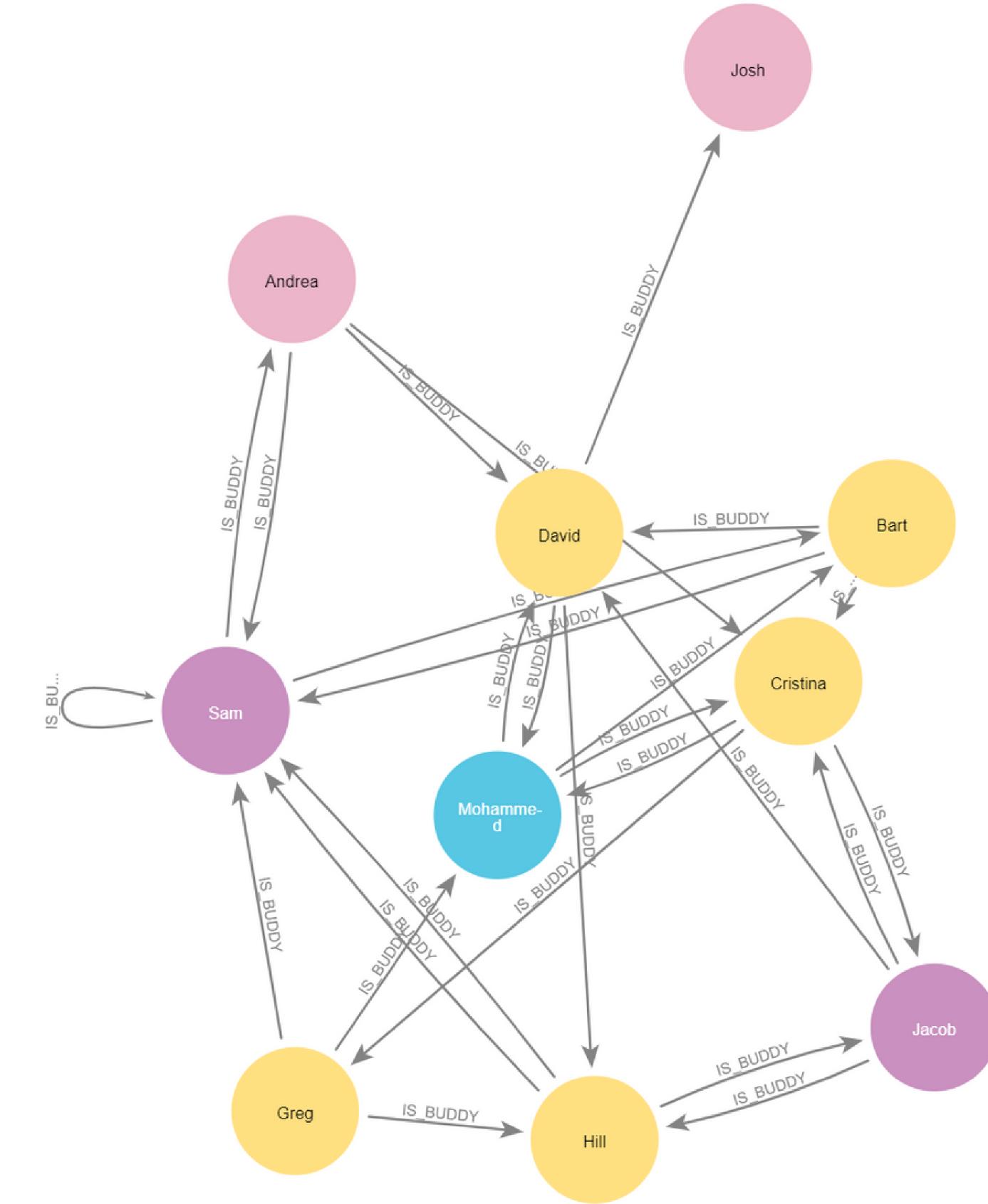
K-CORE DECOMPOSITION



TRIANGLE COUNT

- Calculates the number of triangles in a graph, specifically 3-cliques.
- Implemented in the GDS library and is designed for undirected graphs.
- Used in social network analysis - Communities and Cohesiveness.
- Stability of a graph
- Computing network indices, such as clustering coefficients.
- The algorithm is commonly employed in analyzing local clustering coefficients, which measure the degree of interconnectedness among a node's immediate neighbors.

TRIANGLE COUNT



HETIONET

- Hetnets - heterogeneous information networks
 - Additional dimension - nodes and edges can be multiple types\
- Hetionet - hetnet of biomedical knowledge
- Originally, to predict new uses for existing drug.
- Currently being used in the following:
 - Hetnet Connectivity Search
 - Drug Repurposing (Project Rephetio)
 - Prioritizing Disease-Associated Genes
 - XSwap Edge Probability Baselines
- Data in Hationet
 - 29 public databases
 - 47,031 nodes of 11 types
 - 2,250,197 edges of 24 types

CONNECTIVITY SEARCH

Node Info

Source Node

name	IQGAP3
source	Entrez Gene
identifier	128239
license	CC0 1.0

metanode	Gene
description	IQ motif containing GTPase activat...
id	0
chromosome	1

Target Node

name	small GTPase mediated signal trans...
source	Gene Ontology
id	46683

metanode	Biological Process
identifier	GO:0007264
license	CC BY 4.0

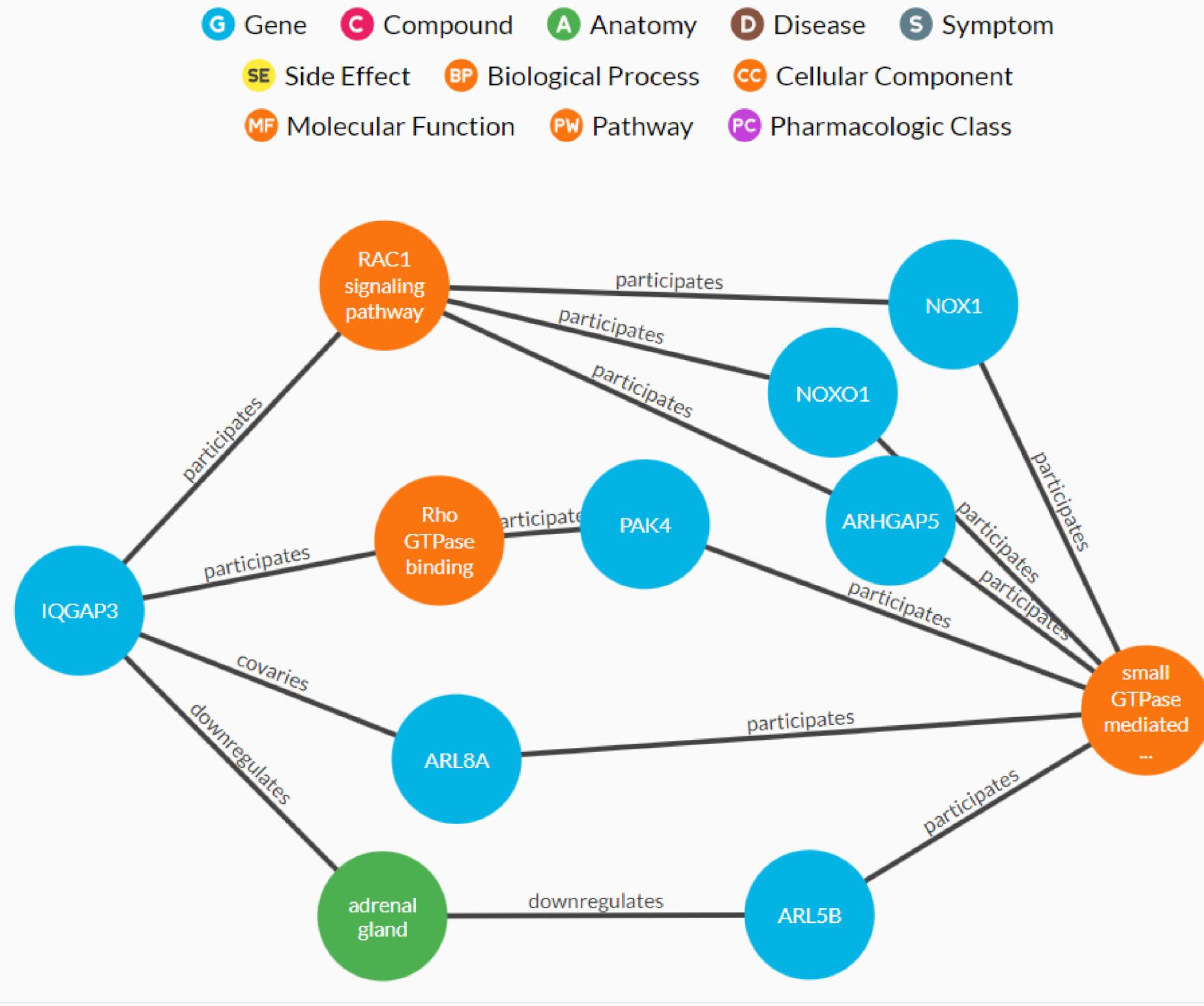
Metapaths

11 results, 5 selected

- ✓ metapath ↑
- ✓ **G e A e G p BP**
- ✓ **G p BP p G p BP**
- ✓ **G u A u G p BP**
- ✓ **G p MF p G p BP**
- ✓ **G u A d G p BP**
- ✓ **G u A e G p BP**
- ✓ **G p PW p G p BP**
- ✓ **G d A u G p BP**
- ✓ **G c G p BP**
- ✓ **G d A d G p BP**

.csv precomputed only expand

path count	adjusted p-value
3,574	2.5×10^{-46}
5,501	8.7×10^{-41}
814	2.7×10^{-30}
1,132	2.4×10^{-20}
898	6.0×10^{-7}
2,380	1.1×10^{-5}
72	1.2×10^{-4}
254	3.3×10^{-3}
3	5.1×10^{-3}
278	5.8×10^{-3}



HETIONET

QUERY RAN

```
match (n:Gene) UNWIND keys(n) AS property RETURN DISTINCT property, n[property] AS value
```

property	value
"license"	"CC0 1.0"
"chromosome"	"1"
"source"	"Entrez Gene"
"url"	"http://identifiers.org/ncbigene/128239"
"description"	"IQ motif containing GTPase activating protein 3"
"identifier"	128239
"name"	"IQGAP3"
"chromosome"	"16"
"description"	"Ion peptidase 2, peroxisomal"
"url"	"http://identifiers.org/ncbigene/83752"
"identifier"	83752
"name"	"LONP2"
"description"	"C1D nuclear receptor corepressor"
"url"	"http://identifiers.org/ncbigene/10438"
"chromosome"	"2"
"identifier"	10438

```
match (n:Gene) UNWIND keys(n) AS property RETURN DISTINCT property
```

property
"license"
"chromosome"
"source"
"url"
"description"
"identifier"
"name"

DANKESCHÖN



name	K-coreValue	triangleCount	K-1color
"Andrea"	4	0	2
"Bart"	5	2	2
"Cristina"	5	2	1
"David"	5	2	1
"Greg"	4	2	3
"Hill"	5	2	2
"Jacob"	5	1	0
"Josh"	1	0	0
"Mohammed"	5	3	0
"Sam"	5	1	0