

//CtGaD ALL Paths

MATCH p0 = (:Compound)-[:TARGETS]-(:Gene)-[:ASSOCIATES]-(:Disease)

RETURN p0 LIMIT 25

//CurGiGaD Path

MATCH p0 = (:Compound)-[:UPREGULATES]-(:Gene)-[:INTERACTS]-(:Gene)-

[:ASSOCIATES]-(:Disease {d_id:"DOID:5408"})

RETURN p0

//CtGaD Path

MATCH p0 = (:Compound {c_id:"DB00246"})-[:TARGETS]-(:Gene)-[:ASSOCIATES]-

(:Disease {d_id:"DOID:10652"})

RETURN p0

//CcSEtD Path

MATCH p0 = (:Compound {c_id:"DB00246"})-[:CAUSES]-(:SideEffect)-[:CAUSES]-

(:Compound)-[:TREATS]-(:Disease {d_id:"DOID:10652"})

RETURN p0

// Show meta-graph

CALL db.schema()

//CtGaD DWPC Degree's Path

MATCH p0 = (n0:Compound{c_id:"DB00246"})-[:TARGETS]-(n1:Gene)-

[:ASSOCIATES]-(n2:Disease{d_id:"DOID:10652"})

WITH

n0 AS source,

n1 AS intermediate,

n2 AS target,

p0,

[

size((n0)-[:TARGETS]-()),

size()-[:TARGETS]-(n1)),

size((n1)-[:ASSOCIATES]-()),

size()-[:ASSOCIATES]-(n2))

] AS degrees

RETURN degrees,

source.c_id AS compound_id,

source.name AS compound_name,
target.d_id AS disease_id,
target.name AS disease_name,
intermediate.name AS gene_name,
(reduce(pdp = 1.0, d in degrees| pdp * d ^ -0.5)) AS PDP

