**The EpiGeNet Framework – sample queries**

1. **To identify molecular conditional relationships, observed in adenoma, but not matched with the polyps phenotype (integrated data basis—StatEpigen curation):**

**MATCH** (m1:MolecularEvent)-[r:ADENOMA]->(m2:MolecularEvent) **where** not (m1)-[: POLYPS]->(m2) **RETURN** r

1. **To identify molecular conditional relationships, observed in adenoma, but not matched with polyps phenotype, and with probability value = T > 0.60 (based on StatEpigen curation):**

**MATCH** (m1:MolecularEvent)-[r:ADENOMA]->(m2:MolecularEvent) **where** not (m1)-[:POLYPS]->(m2) and r.CondProbValue > 0.60 **RETURN** r

1. **To identify molecular event neighborhood (in terms of connected nodes) in colon carcinoma:**

**MATCH** (m:MolecularEvent)-[:CARCINOMA]-(m2:MolecularEvent)

**WITH** m.GeneSymbol +" "+ m.EventName **as** MolecularEvent, collect(**distinct** m2.GeneSymbol +" "+ m2.EventName) **as** NeighbourSet, count(**distinct** m2.GeneSymbol +" "+ m2.EventName) **as** NeighbourNo

**RETURN** MolecularEvent, NeighbourNo, NeighbourSet

**ORDER** **BY** NeighbourNo **DESC**

**LIMIT** 3

1. **To identify the first 10 most plausible pathways for a maximum of 5 conditional relationships between KRAS mutation and APC hypermethylation in carcinoma.**

**MATCH** p=(m1:MolecularEvent)-[:CARCINOMA\*..5]-> (m2:MolecularEvent) **where** m1.GeneSymbol="KRAS" and m1.EventName="MUTATION" and m2.GeneSymbol="APC" and m2.EventName="HYPERMETH\_CPG"

**RETURN** p **AS** plausiblePath, REDUCE(score=1, r **in** relationships(p) | score\*r.CondProbValue) **AS** totalScore

**ORDER** **BY** totalScore **DESC**

**LIMIT** 10