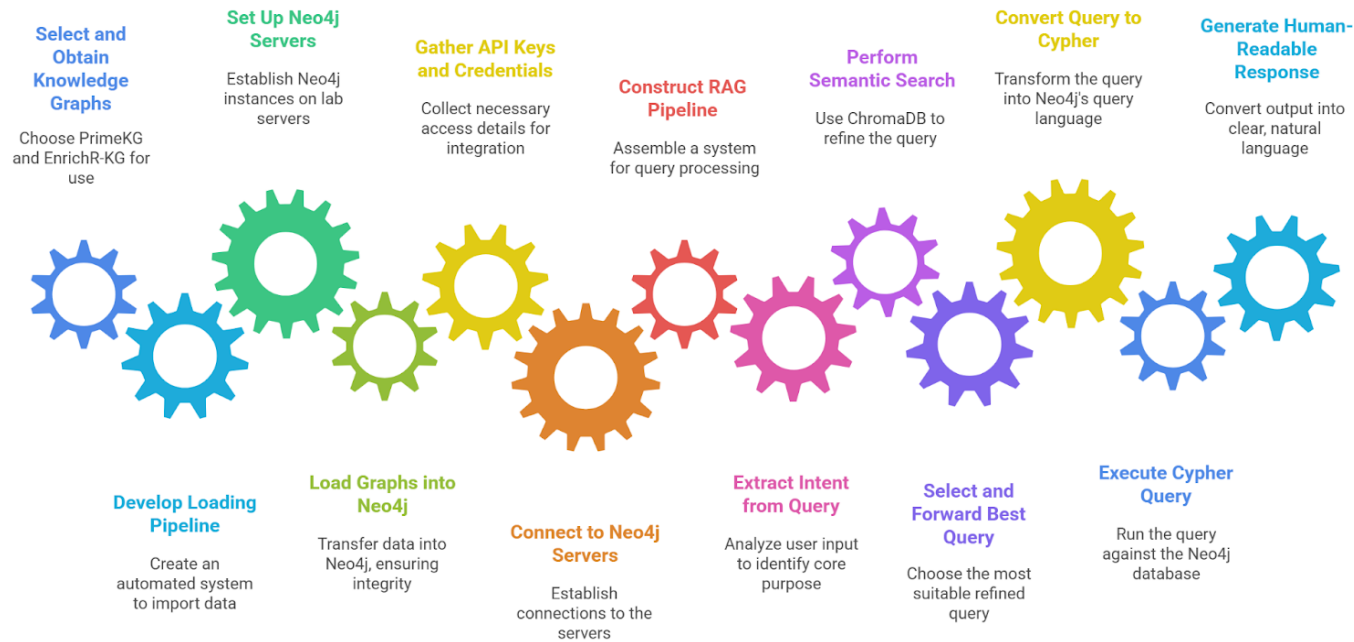


DETAILED FLOWCHART FOR THE LANGGRAPH APPROACH

Bio-Medical Knowledge Graph System Development



FLOWCHART
FOR
THE LANGCHAIN
APPROCH

Database Information

Use database

neo4j

Node labels

- (92,823) Biological_Process
- Cell_Line Cell_Type Disease
- Drug Gene
- Gene_Expression_State
- Kinase_Enzymes Pathway
- Pathway_Identifier Phenotype
- Protein_Domain Tissue
- Transcription_Factor Entity
- Incma_Deg_Gene

Relationship types

- (9,289,075) gene_bioprocess
- gene_cell_line
- gene_cell_line_fitness_decrease
- gene_cell_line_fitness_increase
- gene_cell_type gene_disease
- gene_drug_down

neo4j\$

neo4j\$ MATCH (n:Disease) RETURN n LIMIT 25

Node properties

Disease

<elementid>	41980
<id>	41980
name	Adenocarcinoma, Endometrioid
type	Disease

neo4j\$ MATCH (n:Gene) RETURN n LIMIT 25

Node properties

EnrichR KG

- 92823 nodes
- 9,289,075 relationships


```
ques = "What are the biological processes and mol function present in pediatric hepatocellular carcinoma ?"
solution(ques)
```

```
> Entering new GraphCypherQAChain chain...
Generated Cypher:
cypher
MATCH (d:Disease {name: 'pediatric hepatocellular carcinoma'})-[:associated_with]->(g:Gene)-[:bioprocess_interacts]->(bp:Biological_Process)
(g)-[:mol_func_interacts]->(mf:Molecular_Function)
RETURN DISTINCT bp.name AS Metabolic_Process, mf.name AS Molecular_Function

Full Context:
[{'Metabolic_Process': 'platelet degranulation', 'Molecular_Function': 'interleukin-1 binding'}, {'Metabolic_Process': 'negative regulation of endopeptidase activity'}]

> Finished chain.

The biological processes associated with pediatric hepatocellular carcinoma include platelet degranulation, negative regulation of endopeptidase activity, and
```

```
ques = "Tell me all the name of bp associated with liver cancer ."
```

```
> Finished chain.
The biological processes listed encompass a wide range of cellular functions and regulatory mechanisms. These include:

1. **Cellular Processes**:
  - Platelet degranulation
  - Stem cell differentiation
  - Cell adhesion and migration
  - Cell division and mitotic processes
  - Cellular response to DNA damage stimulus
  - Cellular response to various stimuli (e.g., calcium ion, drug, ethanol, oxidative stress)
  - Regulation of cell cycle phases (G1/S and G2/M transitions)
  - Apoptotic processes, including both positive and negative regulation
  - Regulation of cell differentiation and maturation
  - Protein phosphorylation and deubiquitination
  ...
  - Regulation of ion transport and homeostasis (e.g., calcium, sodium)
  - Response to stress conditions (e.g., heat, oxidative stress)

This comprehensive overview highlights the intricate network of biological processes that govern cellular function, development,
```

```
ans = vector_chain.invoke("Tell me all the genes of liver cancer")
ans

0%|          | 0/1 [00:00<?, ?it/s]
```

```
'According to the context, the genes associated with liver cancer are as follows:\n\n1. LINC00221\n2. MYC\n3. SLC25A47\n4. MEI\n5. NCAPG\n6. ORC1\n7. CTRN\n8. F2\n9. FAM111B\n10. CYP1A1\n11. CYP4A11\n12. TK1\n13. C14orf180\n14. CEP131\n15. BID\n16. FAM180A\n17. E2F1\n18. TTC39A\n19. CA2\n20. CLEC4G\n21. FST\n22. CYP2B6\n23. CYLD\n24. E2F8\n25. CDKN3\n26. MAGEC2\n27. FBXL18\n28. NR1H2\n29. LRRC59\n30. LILRB5\n31. PHB\n32. PKP1\n33. USP2\n34. CYP1A2\n35. PRC1\n36. PKMYT1\n37. CTSD\n38. LRRC1\n39. CDC6\n40. HSD3B2\n41. CYP17A1\n42. CETP\n43. AURKB\n44. KIF2C\n45. PGD\n46. CD163\n47. RUNX3\n48. XAGE1B\n49. FATE1\n50. MIR520B\n51. ERP29\n52. OIT3\n53. ABCB4\n54. CYP2E1\n55. MAPT\n56. GTSE1\n57. TICRR\n58. CDKN2A\n59. SLC26A6\n60. MIR885\n61. YTHDF2\n62. HOXD9\n63. MVK\n64. SLC2A1\n65. MOGAT2\n66. KMT2C\n67. NCAPH\n68. NMMT\n69. DNASE1L3\n70. SLC5A5\n71. ABCB1\n72. PLK1\n73. GPR182\n74. SHH\n75. ZIC4\n76. KIF4A\n77. CDKN2C\n78. DNAJC6\n79. NDC80\n80. PBK\n81. EXO1\n82. CCNF\n83. NR1H4\n84. SFN\n85. SLC22A1\n86. RB1\n87. GAPDH\n88. CDK14\n89. PLAC8\n90. CCNA1\n91. PTTG1\n92. WDR76\n93. AKR1C2\n94. BTG2\n95. GHR\n96. FAM83D\n97. GPC3\n98. GLUL\n99. HMMR\n100. DCN\n101. ASNS\n102. SIX3\n103. FCN3\n104. EF3H\n105. GJB1\n106. OAT\n107. DBH\n108. CELSR3\n109. SPRTN\n110. HSPA9\n111. DPYD\n112. FCN2\n113. NR1I3\n114. CPEB3\n115. CDCA3\n116. LCAT\n117. GNAO1\n118. FLVCR1\n119. FHIT\n120. THEM4\n121. CNTNAP4\n122. PDK4\n123. CKAP2L\n124. DLGAP5\n125. TCF4\n126. MTBP\n127. NEK2\n128. STAT4\n129. KMT2A\n130. KMT2C\n131. ZDHHC2\n132. TERT\n133. GWN\n134. TCIM\n135. UBE2C\n136. GBA3\n137. PTGS2\n138. STAB2\n139. GYS2\n140. MLXIPL\n141. SCAP\n142. ZIC2\n143. CYP2C8\n144. NAT2\n145. OLFML2B\n146. TOP2A\n147. SLIT2\n148. TPX2\n149. PCLAF\n150. IRF2\n151. ZWINT\n152. HRAS\n153. EGR2\n154. MICA\n155. HTATIP2\n156. KCNN2\n157. TEDC2\n158. CXCL14\n159. OLFML2A\n160. GMMT\n161. CENPW\n162. GPR158\n163. LILRB5\n164. MSH5\n165. GPM6A\n166. FABP5\n167. HERC5\n168. ZIC5\n169. AKR1B10\n170. CRP\n171. ISG15\n172. NKILA\n173. COP55\n174. CCR1\n\nThese genes are all associated with liver cancer as per the context provided.'
```

```
rag_chain.invoke({"question": "Give all the genes of triple negative breast carcinoma ."})
```

```
'The genes associated with triple negative breast carcinoma are:\n\n1. KRAS\n2. YAP1\n3. MIR873\n4. LRP6'
```

RESULTS