Network Visualization Tool

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SU WU LAB

MAKING ACCESSIBLE BIOINFORMATICS/COMPUTATIONAL BIOLOGY TOOLS

BioThings Explorer (BTE)

APIs

BioGPS

Wikidata

Citizen science

Transcriptomic atlases

BioThings Explorer allows users to query a vast amount of biological and chemical databases in a central place by calling APIs which distribute these data on the fly.

Example web interface

Making a tool to show connections between biological entities using BTE API

I.E. IMATINIB AND CHRONIC MYELOGENOUS LEUKEMIA

Assigned Tasks

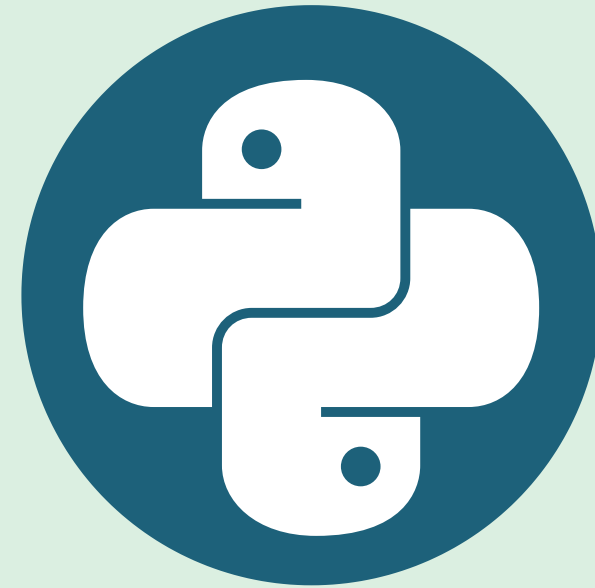find top 10 implicated pathways in literature

Color nodes based on type

Adjust line thickness based on how many times it was found in api query

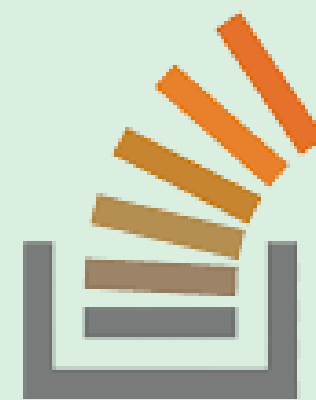# THE PROCESS

Learning to code in Python

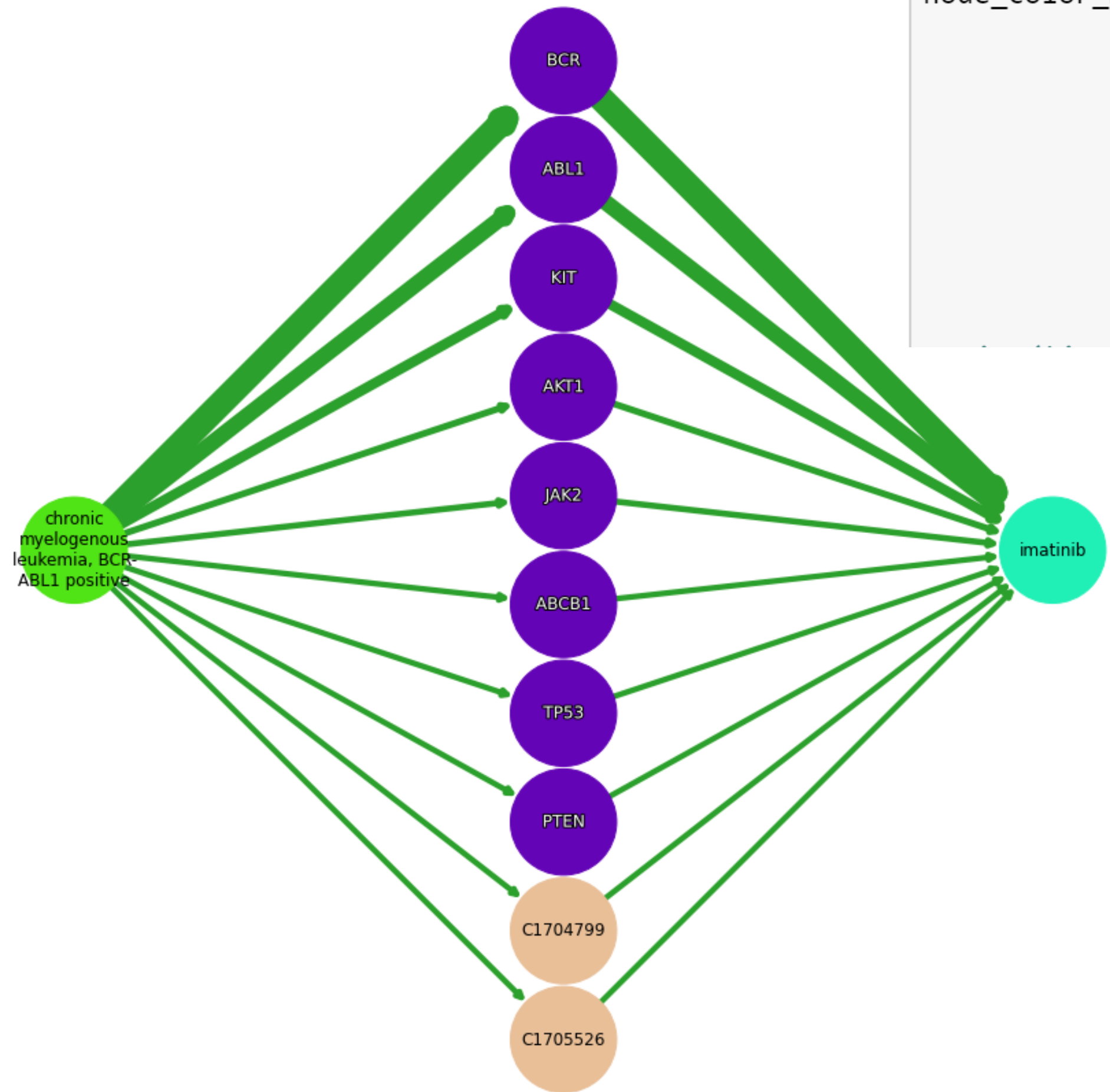Querying databases, manipulating output, sorting, ranking, coloring
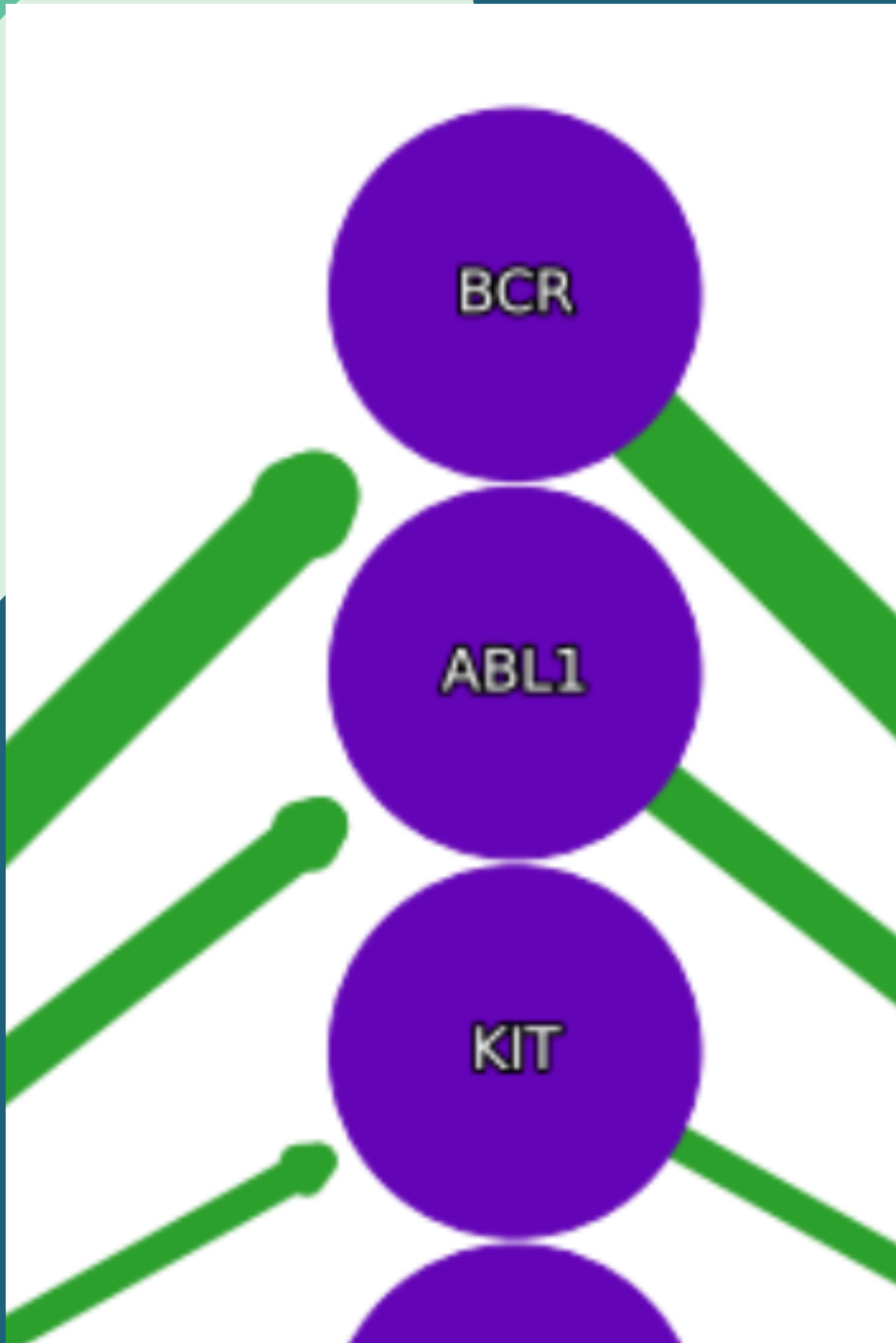
Cleaning up code and adding variables

TOOLS

node_color_map = {'AnatomicalEntity': '#5252b9',
                  'BiologicalProcessOrActivity': '#fc99d5',
                  'MacromolecularMachine': '#d032a3',
                  'Disease': '#50e316',
                  'Pathway': '#b7d165',
                  'PhenotypicFeature': '#165f28',
                  'Gene': '#6404b7',
                  'PhysiologicalProcess': '#ec102f',
                  'OrganismTaxon': '#e9bf98',
                  'ChemicalSubstance': '#21f0b6'}

```
for node in list_of_paths:
    if node[0] not in node_id_to_color.keys():
        node_id_to_color[node[0]] = node_color_map['Disease']
    if node[2] not in node_id_to_color.keys():
        node_id_to_color[node[2]] = node_color_map['ChemicalSubstance']
    node_hint = ht.query(node[1])
    d=node_hint
    print(d)
    if all([len(v) == 0 for v in d.values()]):
        node_id_to_color[node[1]] = node_color_map['OrganismTaxon']
    for key, value in d.items():
        if value:
            print(key)
            #print(node_color_map[key])
            print(node[1])
            #node_id_to_color = nodes.set_index('id')['Label'].map(node_color_map).to_dict()
            node_id_to_color[node[1]]= node_color_map[key]
            break
```

Some problems:
1. Paths didn't have class data
2. Some nodes didn't have any data
3. Original networkx too clunky

NEXT STEPS

Integrate into BioThings Explorer
Add path labels
Clickable nodes

THANK YOU SO MUCH

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