Lab11_Bonsai

April 10, 2025

[ ]:
```
!poetry run jupyter nbconvert --to pdf Lab11_Bonsai.ipynb
```

```
[NbConvertApp] WARNING | pattern 'Lab01_IBD_and_Genealogy_Intro.ipynb' matched
no files
This application is used to convert notebook files (*.ipynb)
        to various other formats.

        WARNING: THE COMMANDLINE INTERFACE MAY CHANGE IN FUTURE RELEASES.

Options
=======
The options below are convenience aliases to configurable class-options,
as listed in the "Equivalent to" description-line of the aliases.
To see all configurable class-options for some <cmd>, use:
    <cmd> --help-all

--debug
    set log level to logging.DEBUG (maximize logging output)
    Equivalent to: [--Application.log_level=10]
--show-config
    Show the application's configuration (human-readable format)
    Equivalent to: [--Application.show_config=True]
--show-config-json
    Show the application's configuration (json format)
    Equivalent to: [--Application.show_config_json=True]
--generate-config
    generate default config file
    Equivalent to: [--JupyterApp.generate_config=True]
-y
    Answer yes to any questions instead of prompting.
    Equivalent to: [--JupyterApp.answer_yes=True]
--execute
    Execute the notebook prior to export.
    Equivalent to: [--ExecutePreprocessor.enabled=True]
--allow-errors
    Continue notebook execution even if one of the cells throws an error and
include the error message in the cell output (the default behaviour is to abort
conversion). This flag is only relevant if '--execute' was specified, too.
```

```
    Equivalent to: [--ExecutePreprocessor.allow_errors=True]
--stdin
    read a single notebook file from stdin. Write the resulting notebook with
default basename 'notebook.*'
    Equivalent to: [--NbConvertApp.from_stdin=True]
--stdout
    Write notebook output to stdout instead of files.
    Equivalent to: [--NbConvertApp.writer_class=StdoutWriter]
--inplace
    Run nbconvert in place, overwriting the existing notebook (only
            relevant when converting to notebook format)
    Equivalent to: [--NbConvertApp.use_output_suffix=False
--NbConvertApp.export_format=notebook --FilesWriter.build_directory=]
--clear-output
    Clear output of current file and save in place,
            overwriting the existing notebook.
    Equivalent to: [--NbConvertApp.use_output_suffix=False
--NbConvertApp.export_format=notebook --FilesWriter.build_directory=
--ClearOutputPreprocessor.enabled=True]
--coalesce-streams
    Coalesce consecutive stdout and stderr outputs into one stream (within each
cell).
    Equivalent to: [--NbConvertApp.use_output_suffix=False
--NbConvertApp.export_format=notebook --FilesWriter.build_directory=
--CoalesceStreamsPreprocessor.enabled=True]
--no-prompt
    Exclude input and output prompts from converted document.
    Equivalent to: [--TemplateExporter.exclude_input_prompt=True
--TemplateExporter.exclude_output_prompt=True]
--no-input
    Exclude input cells and output prompts from converted document.
            This mode is ideal for generating code-free reports.
    Equivalent to: [--TemplateExporter.exclude_output_prompt=True
--TemplateExporter.exclude_input=True
--TemplateExporter.exclude_input_prompt=True]
--allow-chromium-download
    Whether to allow downloading chromium if no suitable version is found on the
system.
    Equivalent to: [--WebPDFExporter.allow_chromium_download=True]
--disable-chromium-sandbox
    Disable chromium security sandbox when converting to PDF..
    Equivalent to: [--WebPDFExporter.disable_sandbox=True]
--show-input
    Shows code input. This flag is only useful for dejavu users.
    Equivalent to: [--TemplateExporter.exclude_input=False]
--embed-images
    Embed the images as base64 dataurls in the output. This flag is only useful
for the HTML/WebPDF/Slides exports.
```

```
    Equivalent to: [--HTMLExporter.embed_images=True]
--sanitize-html
    Whether the HTML in Markdown cells and cell outputs should be sanitized..
    Equivalent to: [--HTMLExporter.sanitize_html=True]
--log-level=<Enum>
    Set the log level by value or name.
    Choices: any of [0, 10, 20, 30, 40, 50, 'DEBUG', 'INFO', 'WARN', 'ERROR',
'CRITICAL']
    Default: 30
    Equivalent to: [--Application.log_level]
--config=<Unicode>
    Full path of a config file.
    Default: ''
    Equivalent to: [--JupyterApp.config_file]
--to=<Unicode>
    The export format to be used, either one of the built-in formats
            ['asciidoc', 'custom', 'html', 'latex', 'markdown', 'notebook',
'pdf', 'python', 'qtpdf', 'qtpng', 'rst', 'script', 'slides', 'webpdf']
            or a dotted object name that represents the import path for an
            ``Exporter`` class
    Default: ''
    Equivalent to: [--NbConvertApp.export_format]
--template=<Unicode>
    Name of the template to use
    Default: ''
    Equivalent to: [--TemplateExporter.template_name]
--template-file=<Unicode>
    Name of the template file to use
    Default: None
    Equivalent to: [--TemplateExporter.template_file]
--theme=<Unicode>
    Template specific theme(e.g. the name of a JupyterLab CSS theme distributed
    as prebuilt extension for the lab template)
    Default: 'light'
    Equivalent to: [--HTMLExporter.theme]
--sanitize_html=<Bool>
    Whether the HTML in Markdown cells and cell outputs should be sanitized.This
    should be set to True by nbviewer or similar tools.
    Default: False
    Equivalent to: [--HTMLExporter.sanitize_html]
--writer=<DottedObjectName>
    Writer class used to write the
                                        results of the conversion
    Default: 'FilesWriter'
    Equivalent to: [--NbConvertApp.writer_class]
--post=<DottedOrNone>
    PostProcessor class used to write the
                                        results of the conversion
```

```
    Default: ''
    Equivalent to: [--NbConvertApp.postprocessor_class]
--output=<Unicode>
    Overwrite base name use for output files.
                Supports pattern replacements '{notebook_name}'.
    Default: '{notebook_name}'
    Equivalent to: [--NbConvertApp.output_base]
--output-dir=<Unicode>
    Directory to write output(s) to. Defaults
                                    to output to the directory of each notebook.
To recover
                                    previous default behaviour (outputting to the
current
                                    working directory) use . as the flag value.
    Default: ''
    Equivalent to: [--FilesWriter.build_directory]
--reveal-prefix=<Unicode>
    The URL prefix for reveal.js (version 3.x).
            This defaults to the reveal CDN, but can be any url pointing to a
copy
            of reveal.js.
            For speaker notes to work, this must be a relative path to a local
            copy of reveal.js: e.g., "reveal.js".
            If a relative path is given, it must be a subdirectory of the
            current directory (from which the server is run).
            See the usage documentation
            (https://nbconvert.readthedocs.io/en/latest/usage.html#reveal-js-
html-slideshow)
            for more details.
    Default: ''
    Equivalent to: [--SlidesExporter.reveal_url_prefix]
--nbformat=<Enum>
    The nbformat version to write.
            Use this to downgrade notebooks.
    Choices: any of [1, 2, 3, 4]
    Default: 4
    Equivalent to: [--NotebookExporter.nbformat_version]

Examples
--------

    The simplest way to use nbconvert is

            > jupyter nbconvert mynotebook.ipynb --to html

            Options include ['asciidoc', 'custom', 'html', 'latex', 'markdown',
'notebook', 'pdf', 'python', 'qtpdf', 'qtpng', 'rst', 'script', 'slides',
'webpdf'].
```

```
            > jupyter nbconvert --to latex mynotebook.ipynb

            Both HTML and LaTeX support multiple output templates. LaTeX
includes
            'base', 'article' and 'report'.  HTML includes 'basic', 'lab' and
            'classic'. You can specify the flavor of the format used.

            > jupyter nbconvert --to html --template lab mynotebook.ipynb

            You can also pipe the output to stdout, rather than a file

            > jupyter nbconvert mynotebook.ipynb --stdout

            PDF is generated via latex

            > jupyter nbconvert mynotebook.ipynb --to pdf

            You can get (and serve) a Reveal.js-powered slideshow

            > jupyter nbconvert myslides.ipynb --to slides --post serve

            Multiple notebooks can be given at the command line in a couple of
            different ways:

            > jupyter nbconvert notebook*.ipynb
            > jupyter nbconvert notebook1.ipynb notebook2.ipynb

            or you can specify the notebooks list in a config file, containing::

                c.NbConvertApp.notebooks = ["my_notebook.ipynb"]

            > jupyter nbconvert --config mycfg.py

To see all available configurables, use `--help-all`.
```

1 Environment Setup

[46]:
```
!poetry install --no-root
```

```
Installing dependencies from lock file

No dependencies to install or update
```

[47]:
```
import os
from collections import Counter
```

```
import logging
import sys
from pathlib import Path
import subprocess
import os
import matplotlib.pyplot as plt
import seaborn as sns
from IPython.display import display, HTML
import IPython
import pandas as pd
import boto3
import importlib.util
import ast
import numpy as np
import networkx as nx
from scipy.stats import poisson
import json
import pygraphviz as pgv
import matplotlib.pyplot as plt
import matplotlib.image as mpimg

from dotenv import load_dotenv
```

[48]:
```
def find_comp_gen_dir():
    """Find the computational_genetic_genealogy directory by searching up from␣
 ↪current directory."""
    current = Path.cwd()

    # Search up through parent directories
    while current != current.parent:
        # Check if target directory exists in current path
        target = current / 'computational_genetic_genealogy'
        if target.is_dir():
            return target
        # Move up one directory
        current = current.parent

    raise FileNotFoundError("Could not find computational_genetic_genealogy␣
 ↪directory")

def load_env_file():
    """Find and load the .env file from the computational_genetic_genealogy␣
 ↪directory."""
    try:
        # Find the computational_genetic_genealogy directory
        comp_gen_dir = find_comp_gen_dir()
```

```
        # Look for .env file
        env_path = comp_gen_dir / '.env'
        if not env_path.exists():
            print(f"Warning: No .env file found in {comp_gen_dir}")
            return None

        # Load the .env file
        load_dotenv(env_path, override=True)
        print(f"Loaded environment variables from: {env_path}")
        return env_path

    except FileNotFoundError as e:
        print(f"Error: {e}")
        return None

# Use the function
env_path = load_env_file()

working_directory = os.getenv('PROJECT_WORKING_DIR', default=None)
data_directory = os.getenv('PROJECT_DATA_DIR', default=None)
references_directory = os.getenv('PROJECT_REFERENCES_DIR', default=None)
results_directory = os.getenv('PROJECT_RESULTS_DIR', default=None)
utils_directory = os.getenv('PROJECT_UTILS_DIR', default=None)

os.environ["WORKING_DIRECTORY"] = working_directory
os.environ["DATA_DIRECTORY"] = data_directory
os.environ["REFERENCES_DIRECTORY"] = references_directory
os.environ["RESULTS_DIRECTORY"] = results_directory
os.environ["UTILS_DIRECTORY"] = utils_directory

print(f"Working Directory: {working_directory}")
print(f"Data Directory: {data_directory}")
print(f"References Directory: {references_directory}")
print(f"Results Directory: {results_directory}")
print(f"Utils Directory: {utils_directory}")

os.chdir(working_directory)
print(f"The current directory is {os.getcwd()}")
```

```
Loaded environment variables from:
/home/lakishadavid/computational_genetic_genealogy/.env
Working Directory: /home/lakishadavid/computational_genetic_genealogy
Data Directory: /home/lakishadavid/computational_genetic_genealogy/data
References Directory:
/home/lakishadavid/computational_genetic_genealogy/references
Results Directory: /home/lakishadavid/computational_genetic_genealogy/results
Utils Directory: /home/lakishadavid/computational_genetic_genealogy/utils
The current directory is /home/lakishadavid/computational_genetic_genealogy
```

1.1 Prepare Data

Bonsai requires data on the age and sex of each individual. However, when we simulated data, we did not get an age. Bonsai also requires the the individual name to be an integer, which is not how our simulated data outputs names. This section of code will assign a random integer ID and age based on certain parameters and output this bioinfo variable as needed for Bonsai.

[49]:
```
import random
import os
import pandas as pd

# Read the seg file and extract unique individual IDs
seg_file = os.path.join(data_directory, "class_data/ped_sim_run2.seg")
seg_df = pd.read_csv(seg_file, sep="\t", header=None)
seg_df.columns = ["sample1", "sample2", "chrom", "phys_start", "phys_end",␣
 ↪"ibd_type", "gen_start", "gen_end", "gen_seg_len"]
unique_individuals = set(seg_df["sample1"]).union(set(seg_df["sample2"]))
unique_individuals = sorted(list(unique_individuals))
print("Number of individuals:", len(unique_individuals))
```

```
Number of individuals: 520
```

[50]:
```
# Read the fam file
with open(os.path.join(data_directory, "class_data/ped_sim_run2-everyone.fam"),␣
 ↪'r') as file:
    fam_lines = file.readlines()

# Create a dictionary to store individual information and Bonsai IDs
individuals = {}
bonsai_ids = {}

# Process each line in the fam file
for line in fam_lines:
    fields = line.strip().split()
    individual_id = fields[1]

    # Skip individuals not present in the seg file
    if individual_id not in unique_individuals:
        continue

    father_id = fields[2]
    mother_id = fields[3]
    sex = 'M' if fields[4] == '1' else 'F'

    # Extract the generation number from the individual ID
    generation = int(individual_id.split('-')[0].split('_')[-1][1:])

    # Store the individual information in the dictionary
```

```
    individuals[individual_id] = {
        'father_id': father_id,
        'mother_id': mother_id,
        'sex': sex,
        'generation': generation
    }

print("First 10 individuals:")
print({k: v for k, v in list(individuals.items())[:10]})
```

```
First 10 individuals:
{'FAM1_g1-b1-s1': {'father_id': '0', 'mother_id': '0', 'sex': 'F', 'generation':
1}, 'FAM1_g1-b1-i1': {'father_id': '0', 'mother_id': '0', 'sex': 'M',
'generation': 1}, 'FAM1_g2-b1-s1': {'father_id': '0', 'mother_id': '0', 'sex':
'F', 'generation': 2}, 'FAM1_g2-b1-i1': {'father_id': 'FAM1_g1-b1-i1',
'mother_id': 'FAM1_g1-b1-s1', 'sex': 'M', 'generation': 2}, 'FAM1_g2-b2-s1':
{'father_id': '0', 'mother_id': '0', 'sex': 'M', 'generation': 2},
'FAM1_g2-b2-i1': {'father_id': 'FAM1_g1-b1-i1', 'mother_id': 'FAM1_g1-b1-s1',
'sex': 'F', 'generation': 2}, 'FAM1_g3-b1-s1': {'father_id': '0', 'mother_id':
'0', 'sex': 'M', 'generation': 3}, 'FAM1_g3-b1-i1': {'father_id':
'FAM1_g2-b1-i1', 'mother_id': 'FAM1_g2-b1-s1', 'sex': 'F', 'generation': 3},
'FAM1_g3-b2-s1': {'father_id': '0', 'mother_id': '0', 'sex': 'F', 'generation':
3}, 'FAM1_g3-b2-i1': {'father_id': 'FAM1_g2-b1-i1', 'mother_id':
'FAM1_g2-b1-s1', 'sex': 'M', 'generation': 3}}
```

[51]:
```
# Get the earliest and latest generation numbers
generation_numbers = [info['generation'] for info in individuals.values()]
earliest_generation = min(generation_numbers)
latest_generation = max(generation_numbers)
print(f"Earliest generation: {earliest_generation}, Latest generation:␣
 ↪{latest_generation}")
```

```
Earliest generation: 1, Latest generation: 6
```

This code block retrieves the earliest and latest generation numbers from the `individuals` dictionary. It creates a list comprehension to extract the 'generation' values from the dictionary values. The `min` and `max` functions are used to find the earliest and latest generation numbers, respectively.

[52]:
```
# Assign ages to individuals based on their generation
for generation in range(latest_generation, earliest_generation - 1, -1):
    for individual_id, info in individuals.items():
        if info['generation'] == generation:
            if generation == latest_generation:
                # Assign ages between 18 and 40 for the latest generation
                age = random.randint(18, 40)
            else:
                # Assign ages based on the descendants' ages
                child_ages = []
                for child_id, child_info in individuals.items():
```

```
                    if child_info['father_id'] == individual_id or␣
↪child_info['mother_id'] == individual_id:
                        child_ages.append(child_info['age'])

                if child_ages:
                    min_child_age = min(child_ages)
                    age = min_child_age + random.randint(12, 40)
                else:
                    # If no child information is available, assign a random age␣
↪based on the generation gap
                    age_gap = (latest_generation - generation) * random.
↪randint(12, 40)
                    age = random.randint(18, 40) + age_gap

            individuals[individual_id]['age'] = age


print("First 10 individuals with ages:")
print({k: v for k, v in list(individuals.items())[:10]})
print("\n")
print("The age range is:", min([info['age'] for info in individuals.values()]),␣
↪"-", max([info['age'] for info in individuals.values()]))
```

```
First 10 individuals with ages:
{'FAM1_g1-b1-s1': {'father_id': '0', 'mother_id': '0', 'sex': 'F', 'generation':
1, 'age': 131}, 'FAM1_g1-b1-i1': {'father_id': '0', 'mother_id': '0', 'sex':
'M', 'generation': 1, 'age': 139}, 'FAM1_g2-b1-s1': {'father_id': '0',
'mother_id': '0', 'sex': 'F', 'generation': 2, 'age': 99}, 'FAM1_g2-b1-i1':
{'father_id': 'FAM1_g1-b1-i1', 'mother_id': 'FAM1_g1-b1-s1', 'sex': 'M',
'generation': 2, 'age': 101}, 'FAM1_g2-b2-s1': {'father_id': '0', 'mother_id':
'0', 'sex': 'M', 'generation': 2, 'age': 110}, 'FAM1_g2-b2-i1': {'father_id':
'FAM1_g1-b1-i1', 'mother_id': 'FAM1_g1-b1-s1', 'sex': 'F', 'generation': 2,
'age': 107}, 'FAM1_g3-b1-s1': {'father_id': '0', 'mother_id': '0', 'sex': 'M',
'generation': 3, 'age': 72}, 'FAM1_g3-b1-i1': {'father_id': 'FAM1_g2-b1-i1',
'mother_id': 'FAM1_g2-b1-s1', 'sex': 'F', 'generation': 3, 'age': 72},
'FAM1_g3-b2-s1': {'father_id': '0', 'mother_id': '0', 'sex': 'F', 'generation':
3, 'age': 120}, 'FAM1_g3-b2-i1': {'father_id': 'FAM1_g2-b1-i1', 'mother_id':
'FAM1_g2-b1-s1', 'sex': 'M', 'generation': 3, 'age': 101}}


The age range is: 18 - 162
```

This code block assigns ages to individuals based on their generation. It iterates over the generations in reverse order, starting from the latest generation and going backward to the earliest generation.

For each generation:

- If it's the latest generation, ages between 18 and 40 are randomly assigned using random.randint(18, 40).

- For earlier generations, ages are assigned based on the descendants' ages. It iterates over the individuals and checks if the current individual is the father or mother of any other individual. If so, the age of the child is appended to the child_ages list.
  - If the child_ages list is not empty, the minimum age among the children is found using min(child_ages), and the individual's age is assigned by adding a random value between 12 and 40 to the minimum child age.
  - If the child_ages list is empty (i.e., the individual has no children), a random age is assigned based on the generation gap. The generation gap is calculated by subtracting the current generation from the latest generation, and then multiplying it by a random value between 12 and 40. The individual's age is then assigned by adding this age gap to a base age range of 18 to 40.
- The assigned age is stored in the individuals dictionary under the 'age' key for each individual.

[53]:
```
# Create Genotype IDs for individuals
for index, individual_id in enumerate(individuals.keys(), start=1000):
    bonsai_id = str(index)
    individuals[individual_id]['genotype_id'] = bonsai_id

print("First 10 individuals with Genotype IDs:")
print({k: v for k, v in list(individuals.items())[:10]})
```

```
First 10 individuals with Genotype IDs:
{'FAM1_g1-b1-s1': {'father_id': '0', 'mother_id': '0', 'sex': 'F', 'generation':
1, 'age': 131, 'genotype_id': '1000'}, 'FAM1_g1-b1-i1': {'father_id': '0',
'mother_id': '0', 'sex': 'M', 'generation': 1, 'age': 139, 'genotype_id':
'1001'}, 'FAM1_g2-b1-s1': {'father_id': '0', 'mother_id': '0', 'sex': 'F',
'generation': 2, 'age': 99, 'genotype_id': '1002'}, 'FAM1_g2-b1-i1':
{'father_id': 'FAM1_g1-b1-i1', 'mother_id': 'FAM1_g1-b1-s1', 'sex': 'M',
'generation': 2, 'age': 101, 'genotype_id': '1003'}, 'FAM1_g2-b2-s1':
{'father_id': '0', 'mother_id': '0', 'sex': 'M', 'generation': 2, 'age': 110,
'genotype_id': '1004'}, 'FAM1_g2-b2-i1': {'father_id': 'FAM1_g1-b1-i1',
'mother_id': 'FAM1_g1-b1-s1', 'sex': 'F', 'generation': 2, 'age': 107,
'genotype_id': '1005'}, 'FAM1_g3-b1-s1': {'father_id': '0', 'mother_id': '0',
'sex': 'M', 'generation': 3, 'age': 72, 'genotype_id': '1006'}, 'FAM1_g3-b1-i1':
{'father_id': 'FAM1_g2-b1-i1', 'mother_id': 'FAM1_g2-b1-s1', 'sex': 'F',
'generation': 3, 'age': 72, 'genotype_id': '1007'}, 'FAM1_g3-b2-s1':
{'father_id': '0', 'mother_id': '0', 'sex': 'F', 'generation': 3, 'age': 120,
'genotype_id': '1008'}, 'FAM1_g3-b2-i1': {'father_id': 'FAM1_g2-b1-i1',
'mother_id': 'FAM1_g2-b1-s1', 'sex': 'M', 'generation': 3, 'age': 101,
'genotype_id': '1009'}}
```

This code block creates Bonsai IDs for each individual. It uses the enumerate function to iterate over the keys of the individuals dictionary, starting the index from 1000. For each individual ID, a corresponding Bonsai ID is created by converting the index to a string. The Bonsai ID is then stored in the bonsai_ids dictionary using the individual ID as the key.

[54]:
```
# Write the individual information to a new file
with open(os.path.join(results_directory, 'individual_info.txt'), 'w') as file:
```

```
    file.write("Individual ID\tBonsai ID\tAge\tSex\n")
    for individual_id, info in individuals.items():
        genotype_id = info['genotype_id']
        age = info['age']
        sex = info['sex']
        file.write(f"{individual_id}\t{genotype_id}\t{age}\t{sex}\n")
```

This code block writes the individual information to a new file named "individual_info.txt" in the results_directory. It opens the file in write mode ('w').

The header line `"Individual ID\tBonsai ID\tAge\tSex\n"` is written to the file first.

Then, it iterates over the `individuals` dictionary items. For each individual:

- The corresponding Bonsai ID is retrieved from the `bonsai_ids` dictionary using the individual ID as the key.
- The age and sex information is retrieved from the `individuals` dictionary.
- The individual information is written to the file in the format `"Individual ID\tBonsai ID\tAge\tSex\n"` using an f-string.

Take a look at the `individual_info.txt` file in your results directory.

[55]:
```
# Create the bioinfo value in the desired format
bioinfo = []
for individual_id, info in individuals.items():
    genotype_id = int(info['genotype_id'])
    age = info['age']
    sex = info['sex']
    bioinfo.append({'genotype_id': genotype_id, 'age': age, 'sex': sex})

print("The first 10 bioinfo values:")
for i in range(10):
    print(bioinfo[i])
```

```
The first 10 bioinfo values:
{'genotype_id': 1000, 'age': 131, 'sex': 'F'}
{'genotype_id': 1001, 'age': 139, 'sex': 'M'}
{'genotype_id': 1002, 'age': 99, 'sex': 'F'}
{'genotype_id': 1003, 'age': 101, 'sex': 'M'}
{'genotype_id': 1004, 'age': 110, 'sex': 'M'}
{'genotype_id': 1005, 'age': 107, 'sex': 'F'}
{'genotype_id': 1006, 'age': 72, 'sex': 'M'}
{'genotype_id': 1007, 'age': 72, 'sex': 'F'}
{'genotype_id': 1008, 'age': 120, 'sex': 'F'}
{'genotype_id': 1009, 'age': 101, 'sex': 'M'}
```

This code block creates the bioinfo value in the desired format. It initializes an empty list called `bioinfo`.

It iterates over the `individuals` dictionary items. For each individual:

- The corresponding Bonsai ID is retrieved from the `bonsai_ids` dictionary using the individual ID as the key.
- The Bonsai ID is converted to an integer and assigned to the `genotype_id` variable.
- The age and sex information is retrieved from the `individuals` dictionary.
- A dictionary containing the `genotype_id`, `age`, and `sex` is appended to the `bioinfo` list.

Remember that Bonsai is designed to read the individal names as integers. We already assigned integer IDs for each individual in our segments file in the earlier code. Let's use those assignments to update our segments file by replacing the individual names with their integer IDs.

NOTE: The following code block can't run more than once unless you change the existing .seg_orig to .seg

[56]:
```
import pandas as pd
import os

seg_file_orig = seg_file + "_orig"

# Check for .seg_orig and .seg files in the results directory
if os.path.exists(seg_file_orig) and os.path.exists(seg_file):
    os.remove(seg_file)
    os.rename(seg_file_orig, seg_file)
elif os.path.exists(seg_file_orig):
    os.rename(seg_file_orig, seg_file)

segments = seg_df.copy()

# New file paths
seg_file_new = seg_file
dict_file = seg_file + "_dict.txt"

# Read the individual_info.txt file
individual_info = pd.read_csv(os.path.join(results_directory, 'individual_info.
 ↪txt'), sep='\t')

# Create a dictionary to map individual IDs to Bonsai IDs
individual_to_bonsai = dict(zip(individual_info['Individual ID'],␣
 ↪individual_info['Bonsai ID']))

# Replace sample names with their corresponding Bonsai IDs
segments['sample1'] = segments['sample1'].map(individual_to_bonsai)
segments['sample2'] = segments['sample2'].map(individual_to_bonsai)

# Save the modified segments as .seg
segments.to_csv(seg_file_new, sep='\t', index=False, header=False)

# Save the dictionary
with open(dict_file, 'w') as f:
```

```
    for individual, bonsai_id in individual_to_bonsai.items():
        f.write(f"{individual}\t{bonsai_id}\n")

print("Segments and dictionary saved successfully.")
display(segments.head())
```

```
Segments and dictionary saved successfully.
```

	sample1	sample2	chrom	phys_start	phys_end	ibd_type	gen_start	gen_end	gen_seg_len
0	1000	1003	1	817341	44617788	IBD1	0.000000	68.343071	68.343071
1	1000	1003	1	44617789	205983275	IBD1	68.343113	200.153155	131.810042
2	1000	1003	1	205983276	242249428	IBD1	200.153157	250.580913	50.427756
3	1000	1003	1	242249429	248876512	IBD1	250.580914	261.713366	11.132452
4	1000	1003	2	118913	4929466	IBD1	0.000000	8.741841	8.741841

Create the segment list

[58]:
```
def create_unphased_ibd_seg_list(segments):
    """
    Creates an unphased IBD segment list from the given DataFrame.

    Parameters:
        segments_ibd (pd.DataFrame): DataFrame containing the IBD segments with␣
 ↪columns:
                                     ['id1', 'id2', 'chromosome',␣
 ↪'physical_position_start',
                                      'physical_position_end', 'IBD_type',␣
 ↪'genetic_length'].
        numeric_ids (dict): Mapping of sample IDs (str) to numeric IDs (int).

    Returns:
        list: A list of unphased IBD segments in the specified format:
              [[id1, id2, chrom, start_bp, end_bp, is_full, len_cm], ...].
    """
    unphased_ibd_seg_list = []

    for _, row in segments.iterrows():
        try:
            id1 = int(row['sample1'])
            id2 = int(row['sample2'])
```

```
            chrom = str(row['chrom'])  # Convert chromosome to string if␣
 ↪necessary
            start_bp = float(row['phys_start'])
            end_bp = float(row['phys_end'])
            is_full = row['ibd_type'] == 2  # Assuming IBD2 indicates "full"
            len_cm = float(row['gen_seg_len'])

            unphased_ibd_seg_list.append([id1, id2, chrom, start_bp, end_bp,␣
 ↪is_full, len_cm])
        except KeyError as e:
            print(f"Error mapping ID: {e}")
        except ValueError as e:
            print(f"Error converting row data: {e}")

    return unphased_ibd_seg_list

unphased_ibd_seg_list = create_unphased_ibd_seg_list(segments)

print("First 10 unphased IBD segments:")
for i in range(10):
    print(unphased_ibd_seg_list[i])
```

```
First 10 unphased IBD segments:
[1000, 1003, '1', 817341.0, 44617788.0, False, 68.343071]
[1000, 1003, '1', 44617789.0, 205983275.0, False, 131.810042]
[1000, 1003, '1', 205983276.0, 242249428.0, False, 50.427756]
[1000, 1003, '1', 242249429.0, 248876512.0, False, 11.132452]
[1000, 1003, '2', 118913.0, 4929466.0, False, 8.741841]
[1000, 1003, '2', 4929467.0, 67922741.0, False, 77.365229]
[1000, 1003, '2', 67922742.0, 242101808.0, False, 162.599718]
[1000, 1003, '3', 66543.0, 42375917.0, False, 63.832452]
[1000, 1003, '3', 42375918.0, 198073373.0, False, 153.016539]
[1000, 1003, '4', 173807.0, 108049728.0, False, 107.960655]
```

1.2 Run Bonsai

[ ]:
```
from utils.bonsaitree.bonsaitree.v3 import bonsai

up_dict_log_like_list = bonsai.build_pedigree(
    bio_info=bioinfo,
    unphased_ibd_seg_list=unphased_ibd_seg_list,
    min_seg_len=3
)
```

1.3 Louvain communities

Louvain communities is a community detection algorithm that helps identify groups of nodes that are more densely connected to each other than to nodes in other groups. In the context of our

problem, using Louvain communities allows us to partition the large network of individuals into smaller, more manageable communities.

The Louvain algorithm is a hierarchical clustering algorithm that optimizes the modularity score of the network. Modularity is a measure of the strength of division of a network into communities. A high modularity score indicates that the nodes within a community have more connections among themselves than with nodes in other communities.

By applying the Louvain algorithm to our network of individuals, we can identify communities of individuals that are more closely related to each other based on their shared IBD segments. This allows us to focus our analysis on smaller subsets of the data, reducing the computational burden and memory requirements.

By leveraging Louvain communities, we can partition our large network into smaller communities and run Bonsai on each community separately. This approach enables us to work with larger datasets and overcome the memory limitations of the free version of Google Colab.

[59]:
```
import pandas as pd
import networkx as nx
from tqdm import tqdm

# Create a graph from the hapibd_df DataFrame
G = nx.Graph()

with tqdm(total=len(segments), desc="Adding edges to the graph") as pbar:
    for _, row in segments.iterrows():
        first_sample = row["sample1"]
        second_sample = row["sample2"]
        gen_seg_len = row["gen_seg_len"]
        G.add_edge(first_sample, second_sample, weight=gen_seg_len)
        pbar.update(1)

# Find Louvain communities
communities = nx.community.louvain_communities(G, weight='weight')

print(len(communities))
```

```
Adding edges to the graph: 100%|      | 183061/183061 [00:08<00:00,
20407.82it/s]

10
```

[60]:
```
# Print the members of each community
for i, community in enumerate(communities[:5], start=1):
    print(f"Community {i}:")
    print(list(community))
    print()
```

```
Community 1:
[1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036,
1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049,
```

```
1050, 1051, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010,
1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023]

Community 2:
[1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064,
1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077,
1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090,
1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103]

Community 3:
[1152, 1153, 1154, 1155, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112,
1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125,
1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138,
1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151]

Community 4:
[1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168,
1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181,
1182, 1183, 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194,
1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, 1207]

Community 5:
[1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220,
1221, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233,
1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246,
1247, 1248, 1249, 1250, 1251, 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259]
```

To make the Louvain communities smaller, you can adjust the `resolution` parameter in the `louvain_communities` function. The `resolution` parameter controls the size of the communities detected by the algorithm. By default, it is set to 1.0.

- Decreasing the `resolution` parameter (e.g., setting it to a value less than 1.0) will result in larger communities. The algorithm will favor merging smaller communities into larger ones.
- Increasing the `resolution` parameter (e.g., setting it to a value greater than 1.0) will result in smaller communities. The algorithm will favor splitting larger communities into smaller ones.

Here's how you can modify the code to make the communities smaller:

[ ]:
```python
with tqdm(total=len(segments), desc="Adding edges to the graph") as pbar:
    for _, row in segments.iterrows():
        first_sample = row["sample1"]
        second_sample = row["sample2"]
        gen_seg_len = row["gen_seg_len"]
        G.add_edge(first_sample, second_sample, weight=gen_seg_len)
        pbar.update(1)

# Find Louvain communities with a smaller resolution value
```

```
resolution = 100  # Adjust this value to control the size of the communities
communities_v2 = nx.community.louvain_communities(G, resolution=resolution,␣
↪weight='weight')
print(len(communities_v2))
```

[ ]:
```
# Print the members of each community
for i, community in enumerate(communities_v2[:5], start=1):
    print(f"Community {i}:")
    print(list(community))
    print()
```

NOTE: It could be that you find Bonsai is more accurate for smaller, more related groups of individuals than for larger, more distantly related individuals. Bonsai has a `seed_pedigree_list` parameter that is an "optional [list] of seed pedigrees to use as starting points for building the pedigree". It also has a `validated_node_set_list` parameter where you can identify the nodes in the pedigrees in the `seed_pedigree_list` where you know the genealogical relationship.

2 Run Bonsai

Rather than running Bonsai on our entire dataset, we can now run it on a Louvain community where we know there is relatedness among the members of the community. Because of this, we need to reduce our ibd_seg_list and bioinfo variables to only the inviduals in the community.

[61]:
```
# Choose the community you want to focus on (e.g., community 0)
target_community = communities[0]
```

[62]:
```
target_community
```

[62]:
```
{1000,
 1001,
 1002,
 1003,
 1004,
 1005,
 1006,
 1007,
 1008,
 1009,
 1010,
 1011,
 1012,
 1013,
 1014,
 1015,
 1016,
 1017,
 1018,
```

```
1019,
1020,
1021,
1022,
1023,
1024,
1025,
1026,
1027,
1028,
1029,
1030,
1031,
1032,
1033,
1034,
1035,
1036,
1037,
1038,
1039,
1040,
1041,
1042,
1043,
1044,
1045,
1046,
1047,
1048,
1049,
1050,
1051}
```

[63]:
```python
def filter_ibd_seg_list(ibd_seg_list, community_ids, both_in_community=True):
    if both_in_community:
        filtered_ibd_seg_list = [
            seg for seg in ibd_seg_list
            if seg[0] in community_ids and seg[1] in community_ids
        ]
    # else:
    #     filtered_ibd_seg_list = [
    #         seg for seg in ibd_seg_list
    #         if seg[0] in community_ids or seg[1] in community_ids
    #     ]
    return filtered_ibd_seg_list
```

```
# Filter the ibd_seg_list based on the community IDs
filtered_ibd_seg_list_v1 = filter_ibd_seg_list(unphased_ibd_seg_list,␣
 ↪target_community, both_in_community=True)
# filtered_ibd_seg_list_v2 = filter_ibd_seg_list(ibd_seg_list,␣
 ↪target_community, both_in_community=False)

# Filter the bioinfo based on the community IDs
filtered_bioinfo = [info for info in bioinfo if info['genotype_id'] in␣
 ↪target_community]
filtered_bioinfo
```

[63]:
```
[{'genotype_id': 1000, 'age': 131, 'sex': 'F'},
 {'genotype_id': 1001, 'age': 139, 'sex': 'M'},
 {'genotype_id': 1002, 'age': 99, 'sex': 'F'},
 {'genotype_id': 1003, 'age': 101, 'sex': 'M'},
 {'genotype_id': 1004, 'age': 110, 'sex': 'M'},
 {'genotype_id': 1005, 'age': 107, 'sex': 'F'},
 {'genotype_id': 1006, 'age': 72, 'sex': 'M'},
 {'genotype_id': 1007, 'age': 72, 'sex': 'F'},
 {'genotype_id': 1008, 'age': 120, 'sex': 'F'},
 {'genotype_id': 1009, 'age': 101, 'sex': 'M'},
 {'genotype_id': 1010, 'age': 98, 'sex': 'F'},
 {'genotype_id': 1011, 'age': 90, 'sex': 'M'},
 {'genotype_id': 1012, 'age': 116, 'sex': 'F'},
 {'genotype_id': 1013, 'age': 112, 'sex': 'M'},
 {'genotype_id': 1014, 'age': 53, 'sex': 'F'},
 {'genotype_id': 1015, 'age': 52, 'sex': 'M'},
 {'genotype_id': 1016, 'age': 118, 'sex': 'F'},
 {'genotype_id': 1017, 'age': 102, 'sex': 'M'},
 {'genotype_id': 1018, 'age': 79, 'sex': 'M'},
 {'genotype_id': 1019, 'age': 81, 'sex': 'F'},
 {'genotype_id': 1020, 'age': 73, 'sex': 'M'},
 {'genotype_id': 1021, 'age': 82, 'sex': 'F'},
 {'genotype_id': 1022, 'age': 65, 'sex': 'M'},
 {'genotype_id': 1023, 'age': 77, 'sex': 'F'},
 {'genotype_id': 1024, 'age': 79, 'sex': 'M'},
 {'genotype_id': 1025, 'age': 78, 'sex': 'F'},
 {'genotype_id': 1026, 'age': 53, 'sex': 'M'},
 {'genotype_id': 1027, 'age': 39, 'sex': 'F'},
 {'genotype_id': 1028, 'age': 32, 'sex': 'F'},
 {'genotype_id': 1029, 'age': 32, 'sex': 'M'},
 {'genotype_id': 1030, 'age': 75, 'sex': 'F'},
 {'genotype_id': 1031, 'age': 80, 'sex': 'M'},
 {'genotype_id': 1032, 'age': 45, 'sex': 'F'},
 {'genotype_id': 1033, 'age': 46, 'sex': 'M'},
 {'genotype_id': 1034, 'age': 37, 'sex': 'M'},
 {'genotype_id': 1035, 'age': 51, 'sex': 'F'},
```

```
 {'genotype_id': 1036, 'age': 42, 'sex': 'F'},
 {'genotype_id': 1037, 'age': 52, 'sex': 'M'},
 {'genotype_id': 1038, 'age': 40, 'sex': 'F'},
 {'genotype_id': 1039, 'age': 45, 'sex': 'M'},
 {'genotype_id': 1040, 'age': 72, 'sex': 'M'},
 {'genotype_id': 1041, 'age': 65, 'sex': 'F'},
 {'genotype_id': 1042, 'age': 32, 'sex': 'F'},
 {'genotype_id': 1043, 'age': 19, 'sex': 'M'},
 {'genotype_id': 1044, 'age': 20, 'sex': 'F'},
 {'genotype_id': 1045, 'age': 40, 'sex': 'M'},
 {'genotype_id': 1046, 'age': 29, 'sex': 'M'},
 {'genotype_id': 1047, 'age': 25, 'sex': 'F'},
 {'genotype_id': 1048, 'age': 35, 'sex': 'M'},
 {'genotype_id': 1049, 'age': 30, 'sex': 'M'},
 {'genotype_id': 1050, 'age': 24, 'sex': 'F'},
 {'genotype_id': 1051, 'age': 39, 'sex': 'M'}]
```

2.0.1 Option 1

Run Bonsai without selecting a focal_id

[ ]:
```
from utils.bonsaitree.bonsaitree.v3 import bonsai

up_dict_log_like_list = bonsai.build_pedigree(
    bio_info=filtered_bioinfo,
    unphased_ibd_seg_list=filtered_ibd_seg_list_v1,
    min_seg_len=3
)

# Takes about 5 - 10 mintues
```

```
/home/lakishadavid/computational_genetic_genealogy/utils/bonsaitree/bonsaitree/v
3/druid.py:221: RuntimeWarning: divide by zero encountered in log
  log_term = np.log(1 - np.exp(-np.exp(log_mu_amt)))
/home/lakishadavid/computational_genetic_genealogy/.venv/lib/python3.12/site-
packages/scipy/stats/_distn_infrastructure.py:2068: RuntimeWarning: divide by
zero encountered in divide
  x = np.asarray((x - loc)/scale, dtype=dtyp)
/home/lakishadavid/computational_genetic_genealogy/.venv/lib/python3.12/site-
packages/scipy/stats/_distn_infrastructure.py:2068: RuntimeWarning: invalid
value encountered in divide
  x = np.asarray((x - loc)/scale, dtype=dtyp)
```

[65]:
```
for element in up_dict_log_like_list:
    print(f"pedigree {element[0]}")
    print(f"likelihood {element[1]}")
```

```
pedigree {1050: {-2: 1, -5: 1}, -2: {-3: 1, -4: 1}, 1038: {-3: 1, -4: 1}, -5:
{-6: 1, -7: 1}, 1049: {-10: 1, -11: 1}, 1036: {-10: 1, -12: 1}, -11: {-13: 1,
```

-14: 1}, 1035: {-17: 1, -24: 1}, -17: {-14: 1, -13: 1}, 1020: {-13: 1, -23: 1},
1037: {-13: 1, -14: 1}, 1048: {-17: 1, -28: 1}, 1034: {-31: 1, -32: 1}, 1047:
{-31: 1, -33: 1}, -31: {-17: 1, -28: 1}, 1022: {-7: 1, -37: 1}, 1039: {-7: 1,
-6: 1}, -6: {-39: 1, -14: 1}, 1025: {-43: 1, -46: 1}, -43: {-44: 1, -45: 1},
1012: {-44: 1, -45: 1}, 1024: {-49: 1, -50: 1}, 1041: {-49: 1, -51: 1}, 1040:
{-54: 1, -55: 1}, 1051: {-58: 1, -59: 1}, -58: {-54: 1, -55: 1}, -59: {-51: 1,
-49: 1}, -51: {-46: 1, -43: 1}, 1017: {-62: 1, 1006: 1}, 1033: {-66: 1, -69: 1},
-66: {-67: 1, -68: 1}, 1018: {-67: 1, -68: 1}, -69: {-70: 1, -71: 1}, 1011:
{-46: 1, -75: 1}, 1004: {-46: 1, -76: 1}, 1013: {-46: 1, -80: 1}, 1028: {-83: 1,
-84: 1}, 1044: {-83: 1, -85: 1}, 1026: {}, 1043: {-90: 1, -93: 1}, -90: {1026:
1, -92: 1}, 1042: {1026: 1, -92: 1}, 1009: {-96: 1, -97: 1}, 1000: {1001: 1,
-101: 1}, 1003: {-96: 1, -105: 1}, -96: {1001: 1, -101: 1}, 1001: {}, 1005:
{-46: 1, -113: 1}, -46: {1001: 1, -101: 1}, 1029: {-85: 1, -125: 1}, -85: {1006:
1, -62: 1}, 1027: {-92: 1, -124: 1}, -92: {-62: 1, 1006: 1}, 1014: {-62: 1,
1006: 1}, 1006: {}, 1015: {1006: 1, -62: 1}, -62: {-97: 1, -96: 1}, 1002: {-136:
1, -137: 1}, 1007: {-97: 1, -96: 1}, -97: {-136: 1, -137: 1}, 1008: {-140: 1,
-141: 1}, 1019: {-71: 1, -70: 1}, -71: {-140: 1, -141: 1}, -70: {-97: 1, -96:
1}, 1010: {-14: 1, -149: 1}, 1023: {-14: 1, -39: 1}, 1021: {-14: 1, -13: 1},
-14: {-75: 1, -46: 1}, 1045: {-157: 1, -160: 1}, -157: {-158: 1, -159: 1}, 1030:
{-158: 1, -159: 1}, -160: {-85: 1, -162: 1}, 1016: {-165: 1, -166: 1}, 1031:
{-162: 1, -85: 1}, -162: {-165: 1, -166: 1}, 1032: {-169: 1, -170: 1}, 1046:
{-169: 1, -171: 1}, -171: {-69: 1, -66: 1}}
likelihood -18203.296223544945
pedigree {1050: {-2: 1, -5: 1}, -2: {-3: 1, -4: 1}, 1038: {-3: 1, -4: 1}, -5:
{-6: 1, -7: 1}, 1049: {-10: 1, -11: 1}, 1036: {-10: 1, -12: 1}, -11: {-13: 1,
-14: 1}, 1035: {-17: 1, -24: 1}, -17: {-14: 1, -13: 1}, 1020: {-13: 1, -23: 1},
1037: {-13: 1, -14: 1}, 1048: {-17: 1, -28: 1}, 1034: {-31: 1, -32: 1}, 1047:
{-31: 1, -33: 1}, -31: {-17: 1, -28: 1}, 1022: {-7: 1, -37: 1}, 1039: {-7: 1,
-6: 1}, -6: {-39: 1, -14: 1}, 1025: {-43: 1, -46: 1}, -43: {-44: 1, -45: 1},
1012: {-44: 1, -45: 1}, 1024: {-49: 1, -50: 1}, 1041: {-49: 1, -51: 1}, 1040:
{-54: 1, -55: 1}, 1051: {-58: 1, -59: 1}, -58: {-54: 1, -55: 1}, -59: {-51: 1,
-49: 1}, -51: {-46: 1, -43: 1}, 1017: {-62: 1, 1006: 1}, 1033: {-66: 1, -69: 1},
-66: {-67: 1, -68: 1}, 1018: {-67: 1, -68: 1}, -69: {-70: 1, -71: 1}, 1011:
{-46: 1, -75: 1}, 1004: {-46: 1, -76: 1}, 1013: {-46: 1, -80: 1}, 1028: {-83: 1,
-84: 1}, 1044: {-83: 1, -85: 1}, 1026: {}, 1043: {-90: 1, -93: 1}, -90: {1026:
1, -92: 1}, 1042: {1026: 1, -92: 1}, 1009: {-96: 1, -97: 1}, 1000: {1001: 1,
-101: 1}, 1003: {-96: 1, -105: 1}, -96: {1001: 1, -101: 1}, 1001: {}, 1005:
{-46: 1, -113: 1}, -46: {1001: 1, -101: 1}, 1029: {-85: 1, -125: 1}, -85: {1006:
1, -62: 1}, 1027: {-92: 1, -124: 1}, -92: {-62: 1, 1006: 1}, 1014: {-62: 1,
1006: 1}, 1006: {}, 1015: {1006: 1, -62: 1}, -62: {-97: 1, -96: 1}, 1002: {-136:
1, -137: 1}, 1007: {-97: 1, -96: 1}, -97: {-136: 1, -137: 1}, 1008: {-140: 1,
-141: 1}, 1019: {-71: 1, -70: 1}, -71: {-140: 1, -141: 1}, -70: {-97: 1, -96:
1}, 1010: {-14: 1, -149: 1}, 1023: {-14: 1, -39: 1}, 1021: {-14: 1, -13: 1},
-14: {-75: 1, -46: 1}, 1045: {-157: 1, -160: 1}, -157: {-158: 1, -159: 1}, 1030:
{-158: 1, -159: 1}, -160: {-85: 1, -162: 1}, 1016: {-165: 1, -166: 1}, 1031:
{-162: 1, -85: 1}, -162: {-165: 1, -166: 1}, 1032: {-169: 1, -170: 1}, 1046:
{-169: 1, -171: 1}, -171: {-69: 1, -66: 1}}
likelihood -18203.296223544945

```
pedigree {1050: {-2: 1, -5: 1}, -2: {-3: 1, -4: 1}, 1038: {-3: 1, -4: 1}, -5:
{-6: 1, -7: 1}, 1049: {-10: 1, -11: 1}, 1036: {-10: 1, -12: 1}, -11: {-13: 1,
-14: 1}, 1035: {-17: 1, -24: 1}, -17: {-14: 1, -13: 1}, 1020: {-13: 1, -23: 1},
1037: {-13: 1, -14: 1}, 1048: {-17: 1, -28: 1}, 1034: {-31: 1, -32: 1}, 1047:
{-31: 1, -33: 1}, -31: {-17: 1, -28: 1}, 1022: {-7: 1, -37: 1}, 1039: {-7: 1,
-6: 1}, -6: {-39: 1, -14: 1}, 1025: {-43: 1, -46: 1}, -43: {-44: 1, -45: 1},
1012: {-44: 1, -45: 1}, 1024: {-49: 1, -50: 1}, 1041: {-49: 1, -51: 1}, 1040:
{-54: 1, -55: 1}, 1051: {-58: 1, -59: 1}, -58: {-54: 1, -55: 1}, -59: {-51: 1,
-49: 1}, -51: {-46: 1, -43: 1}, 1017: {-62: 1, 1006: 1}, 1033: {-66: 1, -69: 1},
-66: {-67: 1, -68: 1}, 1018: {-67: 1, -68: 1}, -69: {-70: 1, -71: 1}, 1011:
{-46: 1, -75: 1}, 1004: {-46: 1, -76: 1}, 1013: {-46: 1, -80: 1}, 1028: {-83: 1,
-84: 1}, 1044: {-83: 1, -85: 1}, 1026: {}, 1043: {-90: 1, -93: 1}, -90: {1026:
1, -92: 1}, 1042: {1026: 1, -92: 1}, 1009: {-96: 1, -97: 1}, 1000: {1001: 1,
-101: 1}, 1003: {-96: 1, -105: 1}, -96: {1001: 1, -101: 1}, 1001: {}, 1005:
{-46: 1, -113: 1}, -46: {1001: 1, -101: 1}, 1029: {-85: 1, -125: 1}, -85: {1006:
1, -62: 1}, 1027: {-92: 1, -124: 1}, -92: {-62: 1, 1006: 1}, 1014: {-62: 1,
1006: 1}, 1006: {}, 1015: {1006: 1, -62: 1}, -62: {-97: 1, -96: 1}, 1002: {-136:
1, -137: 1}, 1007: {-97: 1, -96: 1}, -97: {-136: 1, -137: 1}, 1008: {-140: 1,
-141: 1}, 1019: {-71: 1, -70: 1}, -71: {-140: 1, -141: 1}, -70: {-97: 1, -96:
1}, 1010: {-14: 1, -149: 1}, 1023: {-14: 1, -39: 1}, 1021: {-14: 1, -13: 1},
-14: {-75: 1, -46: 1}, 1045: {-157: 1, -160: 1}, -157: {-158: 1, -159: 1}, 1030:
{-158: 1, -159: 1}, -160: {-85: 1, -162: 1}, 1016: {-165: 1, -166: 1}, 1031:
{-162: 1, -85: 1}, -162: {-165: 1, -166: 1}, 1032: {-169: 1, -170: 1}, 1046:
{-169: 1, -171: 1}, -171: {-69: 1, -66: 1}}
likelihood -18203.296223544945
```

[66]:
```python
import json
import os

def save_pedigrees(up_dict_log_like_list, results_directory):
    """
    Save pedigrees from up_dict_log_like_list to JSON files.

    Parameters:
    up_dict_log_like_list -- List of tuples (pedigree_dict, log_likelihood)
    results_directory -- Directory to save results
    """
    for i, (pedigree, log_likelihood) in enumerate(up_dict_log_like_list):
        # Convert all dictionary keys to strings for JSON compatibility
        str_pedigree = {}
        for key, value in pedigree.items():
            str_key = str(key)

            if isinstance(value, dict):
                str_value = {}
                for sub_key, sub_value in value.items():
                    str_value[str(sub_key)] = sub_value
```

```
            else:
                str_value = value

            str_pedigree[str_key] = str_value

        # Save the pedigree
        file_path = os.path.join(results_directory,␣
↪f'bonsai_normed_pedigree_{i+1}.json')
        with open(file_path, 'w') as f:
            json.dump(str_pedigree, f)

        # Save the likelihood in a separate file
        likelihood_path = os.path.join(results_directory,␣
↪f'bonsai_likelihood_{i+1}.txt')
        with open(likelihood_path, 'w') as f:
            f.write(str(log_likelihood))

        print(f"Saved pedigree {i+1} to {file_path}")
        print(f"Saved likelihood for pedigree {i+1} to {likelihood_path}")

# Example usage:
save_pedigrees(up_dict_log_like_list, results_directory)
```

```
Saved pedigree 1 to /home/lakishadavid/computational_genetic_genealogy/results/b
onsai_normed_pedigree_1.json
Saved likelihood for pedigree 1 to /home/lakishadavid/computational_genetic_gene
alogy/results/bonsai_likelihood_1.txt
Saved pedigree 2 to /home/lakishadavid/computational_genetic_genealogy/results/b
onsai_normed_pedigree_2.json
Saved likelihood for pedigree 2 to /home/lakishadavid/computational_genetic_gene
alogy/results/bonsai_likelihood_2.txt
Saved pedigree 3 to /home/lakishadavid/computational_genetic_genealogy/results/b
onsai_normed_pedigree_3.json
Saved likelihood for pedigree 3 to /home/lakishadavid/computational_genetic_gene
alogy/results/bonsai_likelihood_3.txt
```

[67]:
```
import networkx as nx
import matplotlib.pyplot as plt
import json
import os

def graph_pedigree(pedigree_file, output_file=None):
    # Load the pedigree
    with open(pedigree_file, 'r') as f:
        pedigree = json.load(f)

    # Create a directed graph
```

```
    G = nx.DiGraph()

    # Add nodes and edges
    for child, parents in pedigree.items():
        G.add_node(child)
        for parent in parents:
            G.add_node(parent)
            G.add_edge(parent, child)  # Direction from parent to child

    # Set node colors: green for real individuals (positive IDs), white for␣
 ↪latent (negative IDs)
    node_colors = ['green' if not str(node).startswith('-') else 'white' for␣
 ↪node in G.nodes()]

    # Calculate layout
    pos = nx.nx_agraph.graphviz_layout(G, prog='dot')

    # Create figure
    plt.figure(figsize=(15, 10))

    # Draw the graph
    nx.draw(G, pos, with_labels=True, node_color=node_colors, node_size=500,␣
 ↪arrows=True)

    # Save or display
    if output_file:
        plt.savefig(output_file, dpi=300)
        print(f"Saved graph to {output_file}")
    else:
        plt.show()

    plt.close()
    return G

# Create directory for plots
plot_dir = os.path.join(results_directory, 'pedigree_plots')
os.makedirs(plot_dir, exist_ok=True)

# Graph each saved pedigree
for i in range(len(up_dict_log_like_list)):
    pedigree_file = os.path.join(results_directory,␣
 ↪f'bonsai_normed_pedigree_{i+1}.json')
    output_file = os.path.join(plot_dir, f'pedigree_{i+1}.png')
    graph_pedigree(pedigree_file, output_file)
```

```
Saved graph to /home/lakishadavid/computational_genetic_genealogy/results/pedigr
ee_plots/pedigree_1.png
```

```
Saved graph to /home/lakishadavid/computational_genetic_genealogy/results/pedigr
ee_plots/pedigree_2.png
Saved graph to /home/lakishadavid/computational_genetic_genealogy/results/pedigr
ee_plots/pedigree_3.png
```

2.1 Plot the true graph

[68]:
```python
# Creates the true graph (does not display)

import pandas as pd
import networkx as nx

# Load the fam file into a DataFrame
fam_df = pd.read_csv(f"{data_directory}/class_data/ped_sim_run2-everyone.fam",␣
 ↪sep=" ", header=None)
fam_df.columns = ["family_id", "individual_id", "father_id", "mother_id",␣
 ↪"sex", "phenotype"]

# Load the seg_dict file into a DataFrame
seg_dict_df = pd.read_csv(f"{data_directory}/class_data/ped_sim_run2.seg_dict.
 ↪txt", sep="\t", header=None)
seg_dict_df.columns = ["individual_id", "bonsai_id"]

# Create a dictionary to map individual_id to bonsai_id
individual_to_bonsai = dict(zip(seg_dict_df["individual_id"],␣
 ↪seg_dict_df["bonsai_id"]))

# Create a graph using the fam data
fam_graph = nx.DiGraph()
for _, row in fam_df.iterrows():
    individual_id = row["individual_id"]
    father_id = row["father_id"]
    mother_id = row["mother_id"]

    # Use Bonsai ID if available, otherwise use the original name
    individual_node = individual_to_bonsai.get(individual_id, individual_id)
    fam_graph.add_node(individual_node)

    if father_id != "0":
        father_node = individual_to_bonsai.get(father_id, father_id)
        fam_graph.add_edge(father_node, individual_node)

    if mother_id != "0":
        mother_node = individual_to_bonsai.get(mother_id, mother_id)
        fam_graph.add_edge(mother_node, individual_node)
```

[69]:
```
# Check the number of nodes and edges in the graph
print("Number of nodes:", fam_graph.number_of_nodes())
print("Number of edges:", fam_graph.number_of_edges())

# Print a few nodes
print("\nNodes:")
for node in list(fam_graph.nodes())[:5]:
    print(node)

# Print a few edges
print("\nEdges:")
for edge in list(fam_graph.edges())[:5]:
    print(edge)
```

```
Number of nodes: 520
Number of edges: 600

Nodes:
1000
1001
1002
1003
1004

Edges:
(1000, 1003)
(1000, 1005)
(1001, 1003)
(1001, 1005)
(1002, 1007)
```

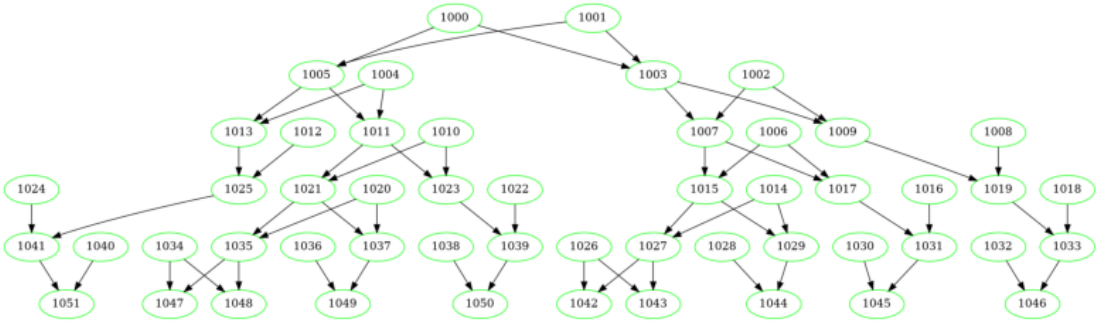
[70]:
```
# Find the target community individuals
target_community_individual_ids = [seg_dict_df.loc[seg_dict_df["bonsai_id"] ==␣
 ↪int(bonsai_id), "individual_id"].values[0] for bonsai_id in target_community]

# Find all connected individuals (relatives and ancestors) of the target␣
 ↪community
connected_individuals = set()
for individual_id in target_community_individual_ids:
    connected_individuals.update(nx.descendants(fam_graph, individual_to_bonsai.
 ↪get(individual_id, individual_id)))
    connected_individuals.update(nx.ancestors(fam_graph, individual_to_bonsai.
 ↪get(individual_id, individual_id)))
connected_individuals.update(target_community_individual_ids)

# Create the true graph for the target community and their connected individuals
```

```
true_graph = nx.subgraph(fam_graph, [individual_to_bonsai.get(individual_id,␣
 ↪individual_id) for individual_id in connected_individuals])

# Check the number of nodes and edges in the graph
print("Number of nodes:", true_graph.number_of_nodes())
print("Number of edges:", true_graph.number_of_edges())

# Print a few nodes
print("\nNodes:")
for node in list(true_graph.nodes())[:5]:
    print(node)

# Print a few edges
print("\nEdges:")
for edge in list(true_graph.edges())[:5]:
    print(edge)
```

```
Number of nodes: 52
Number of edges: 60

Nodes:
1024
1025
1026
1027
1028

Edges:
(1024, 1041)
(1025, 1041)
(1026, 1042)
(1026, 1043)
(1027, 1042)
```

[71]:
```
# Create a PyGraphviz graph
A = pgv.AGraph(directed=True)

# Add nodes and edges to the PyGraphviz graph
for node in true_graph.nodes():
    A.add_node(node)
    if node in [individual_to_bonsai.get(individual_id, individual_id) for␣
 ↪individual_id in target_community_individual_ids]:
        A.get_node(node).attr['color'] = 'green'
    else:
        A.get_node(node).attr['color'] = 'white'

for edge in true_graph.edges():
```

```
    parent, child = edge
    A.add_edge(parent, child)

# Set Graphviz layout options
A.layout(prog='dot')

# Save and display the graph
graph_filename = f"{results_directory}/true_graph_target_community.png"
A.draw(graph_filename, format='png')

# Load and display the image
img = mpimg.imread(graph_filename)
plt.figure(figsize=(10, 10))
plt.imshow(img)
plt.axis('off')
plt.show()
```



How does Bonsai compare to the ground truth?

2.2 Exploring Bonsai

[ ]:
```
# 1. Basic pedigree construction with different parameters
from utils.bonsaitree.bonsaitree.v3 import bonsai, constants

# Try building with different minimum segment lengths
up_dict_log_like_list_7cm = bonsai.build_pedigree(
    bio_info=filtered_bioinfo,
    unphased_ibd_seg_list=filtered_ibd_seg_list_v1,
    min_seg_len=7  # More stringent minimum segment length
)

# Try with restricted connections
up_dict_log_like_list_restricted = bonsai.build_pedigree(
    bio_info=filtered_bioinfo,
```

```
    unphased_ibd_seg_list=filtered_ibd_seg_list_v1,
    min_seg_len=3,
    restrict_connection_points=True
)

print(f"Number of pedigrees with 3cM threshold: {len(up_dict_log_like_list)}")
print(f"Number of pedigrees with 7cM threshold:␣
 ↪{len(up_dict_log_like_list_7cm)}")
print(f"Number of pedigrees with restricted connections:␣
 ↪{len(up_dict_log_like_list_restricted)}")
```

[73]:
```
# 2. Examine pedigree likelihood differences
if len(up_dict_log_like_list) > 1:
    for i, (pedigree, log_like) in enumerate(up_dict_log_like_list):
        print(f"Pedigree {i+1} log likelihood: {log_like}")

    # Calculate likelihood ratio between best and second best
    if len(up_dict_log_like_list) >= 2:
        best_ll = up_dict_log_like_list[0][1]
        second_best_ll = up_dict_log_like_list[1][1]
        likelihood_ratio = np.exp(best_ll - second_best_ll)
        print(f"Likelihood ratio between best and second-best pedigree:␣
 ↪{likelihood_ratio:.2f}")
```

```
Pedigree 1 log likelihood: -18203.296223544945
Pedigree 2 log likelihood: -18203.296223544945
Pedigree 3 log likelihood: -18203.296223544945
Likelihood ratio between best and second-best pedigree: 1.00
```

[74]:
```
# 4. Analyze the top pedigree from Bonsai
if up_dict_log_like_list:
    top_pedigree = up_dict_log_like_list[0][0]

    # Count individuals by type
    real_individuals = [node for node in top_pedigree.keys() if␣
 ↪isinstance(node, int) and node > 0]
    inferred_ancestors = [node for node in top_pedigree.keys() if␣
 ↪isinstance(node, int) and node < 0]

    print(f"Top pedigree has {len(real_individuals)} real individuals")
    print(f"Top pedigree has {len(inferred_ancestors)} inferred ancestors")

    # Analyze pedigree depth (maximum generations)
    max_depth = 0
    for node in real_individuals:
        depth = 0
        current = node
```

```
        while current in top_pedigree and top_pedigree[current]:
            parent = list(top_pedigree[current].keys())[0]  # Get first parent
            current = parent
            depth += 1
        max_depth = max(max_depth, depth)

    print(f"Maximum depth in the pedigree: {max_depth} generations")
```

```
Top pedigree has 52 real individuals
Top pedigree has 26 inferred ancestors
Maximum depth in the pedigree: 4 generations
```

[ ]:
```
# 5. Find potential siblings in the pedigree
def find_siblings(pedigree):
    # Group children by their parents
    parent_to_children = {}
    for child, parents in pedigree.items():
        if not parents:  # Skip nodes with no parents
            continue

        # Convert parents dict to a frozenset for use as dictionary key
        parent_key = frozenset(parents.keys())
        if parent_key not in parent_to_children:
            parent_to_children[parent_key] = []
        parent_to_children[parent_key].append(child)

    # Return sibling groups (only those with at least 2 siblings)
    sibling_groups = [children for children in parent_to_children.values() if␣
 ↪len(children) >= 2]
    return sibling_groups

if up_dict_log_like_list:
    top_pedigree = up_dict_log_like_list[0][0]
    sibling_groups = find_siblings(top_pedigree)

    print(f"Found {len(sibling_groups)} sibling groups:")
    for i, group in enumerate(sibling_groups):
        real_siblings = [s for s in group if isinstance(s, int) and s > 0]
        print(f"Group {i+1}: {real_siblings}")
```

[ ]:
```
# 6. Compare multiple communities using Bonsai
def compare_communities(communities, bioinfo, ibd_seg_list):
    results = {}

    for i, community in enumerate(communities[:3]):  # Compare first 3␣
 ↪communities
        print(f"Analyzing community {i+1} with {len(community)} members")
```

```
        # Filter bioinfo and IBD segments for this community
        community_bioinfo = [info for info in bioinfo if info['genotype_id'] in␣
↪community]

        community_ibd = [
            seg for seg in ibd_seg_list
            if seg[0] in community and seg[1] in community
        ]

        # Run Bonsai
        up_dict_log_like_list = bonsai.build_pedigree(
            bio_info=community_bioinfo,
            unphased_ibd_seg_list=community_ibd,
            min_seg_len=3
        )

        if up_dict_log_like_list:
            top_pedigree = up_dict_log_like_list[0][0]
            top_likelihood = up_dict_log_like_list[0][1]

            results[i] = {
                "size": len(community),
                "pedigree": top_pedigree,
                "likelihood": top_likelihood,
                "real_individuals": len([n for n in top_pedigree.keys() if␣
↪isinstance(n, int) and n > 0]),
                "inferred_ancestors": len([n for n in top_pedigree.keys() if␣
↪isinstance(n, int) and n < 0])
            }

    return results

compare_communities(communities_v2, bioinfo, unphased_ibd_seg_list)
```

[75]:
```
# 7. Analyze specific relationships in the pedigree
def analyze_relationship(pedigree, id1, id2):
    """Find the relationship between two individuals in the pedigree"""

    # Find path from id1 to root
    path1 = []
    current = id1
    while current in pedigree and pedigree[current]:
        parent = list(pedigree[current].keys())[0]  # Get first parent
        path1.append((current, parent))
        current = parent
```

```
    # Find path from id2 to root
    path2 = []
    current = id2
    while current in pedigree and pedigree[current]:
        parent = list(pedigree[current].keys())[0]  # Get first parent
        path2.append((current, parent))
        current = parent

    # Find common ancestor
    common_ancestors = set([p for _, p in path1]) & set([p for _, p in path2])
    if not common_ancestors:
        return "No relationship found"

    # Find closest common ancestor
    degrees = {}
    for ancestor in common_ancestors:
        degree1 = [p for _, p in path1].index(ancestor)
        degree2 = [p for _, p in path2].index(ancestor)
        degrees[ancestor] = (degree1, degree2)

    closest = min(degrees.items(), key=lambda x: sum(x[1]))
    ancestor, (deg1, deg2) = closest

    # Interpret relationship
    if deg1 == 0 and deg2 > 0:
        return f"{id1} is an ancestor of {id2}, {deg2} generations removed"
    elif deg2 == 0 and deg1 > 0:
        return f"{id2} is an ancestor of {id1}, {deg1} generations removed"
    elif deg1 == 1 and deg2 == 1:
        return f"{id1} and {id2} are siblings"
    elif deg1 == 1 and deg2 == 2:
        return f"{id1} is an aunt/uncle of {id2}"
    elif deg1 == 2 and deg2 == 1:
        return f"{id2} is an aunt/uncle of {id1}"
    elif deg1 == 2 and deg2 == 2:
        return f"{id1} and {id2} are first cousins"
    else:
        return f"{id1} and {id2} are related with common ancestor {ancestor},␣
↪{deg1} and {deg2} generations removed"

# Example usage
if up_dict_log_like_list:
    top_pedigree = up_dict_log_like_list[0][0]

    # Find relationships between several pairs of individuals
    id_pairs = [(1000, 1003), (1005, 1007), (1010, 1015)]
    for id1, id2 in id_pairs:
```

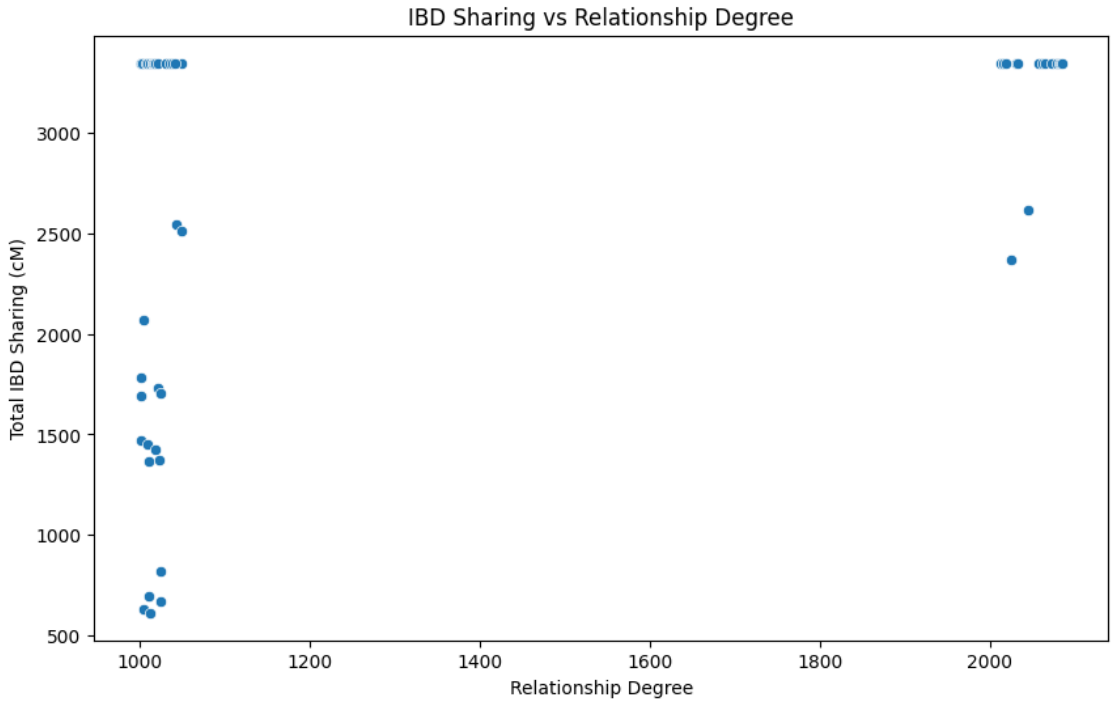
```
        relationship = analyze_relationship(top_pedigree, id1, id2)
        print(f"Relationship between {id1} and {id2}: {relationship}")
```

```
Relationship between 1000 and 1003: 1000 is an ancestor of 1003, 1 generations
removed
Relationship between 1005 and 1007: No relationship found
Relationship between 1010 and 1015: No relationship found
```

[ ]:
```
# 8. Validate Bonsai pedigree against truth (if available)
def compare_to_truth(inferred_pedigree, truth_pedigree):
    """Compare the inferred pedigree to ground truth"""

    # Get all real individuals in both pedigrees
    inferred_real_ids = [id for id in inferred_pedigree.keys() if␣
 ↪isinstance(id, int) and id > 0]
    truth_real_ids = [id for id in truth_pedigree.keys() if isinstance(id, int)␣
 ↪and id > 0]

    common_ids = set(inferred_real_ids) & set(truth_real_ids)
    print(f"Common individuals: {len(common_ids)}")

    # Check parent-child relationships
    correct_relationships = 0
    incorrect_relationships = 0

    for child in common_ids:
        if child in inferred_pedigree and child in truth_pedigree:
            inferred_parents = set(inferred_pedigree[child].keys())
            truth_parents = set(truth_pedigree[child].keys())

            # In the inferred pedigree, parents are often inferred ancestors
            # So we need to trace up to find real parents for comparison

            # This is a simplified approach:
            if any(p in truth_parents for p in inferred_parents):
                correct_relationships += 1
            else:
                incorrect_relationships += 1

    print(f"Correctly inferred relationships: {correct_relationships}")
    print(f"Incorrectly inferred relationships: {incorrect_relationships}")

    accuracy = correct_relationships / (correct_relationships +␣
 ↪incorrect_relationships) if (correct_relationships +␣
 ↪incorrect_relationships) > 0 else 0
    print(f"Accuracy: {accuracy:.2%}")
```

```
compare_to_truth(top_pedigree, truth_pedigree)
```

[76]:
```
# 9. Plot IBD sharing vs relationship degree in the pedigree
import seaborn as sns

def plot_ibd_vs_relationship(pedigree, ibd_seg_list):
    """Plot the relationship between IBD sharing and relationship degree"""
    # Calculate total IBD sharing between all pairs
    ibd_sharing = {}
    for seg in ibd_seg_list:
        id1, id2 = seg[0], seg[1]
        pair = tuple(sorted([id1, id2]))
        ibd_sharing[pair] = ibd_sharing.get(pair, 0) + seg[6]  # Add segment␣
 ↪length

    # Analyze relationships in the pedigree
    relationships = []
    ibd_amounts = []

    for pair, ibd_amount in ibd_sharing.items():
        id1, id2 = pair
        if id1 in pedigree and id2 in pedigree:
            relationship = analyze_relationship(pedigree, id1, id2)
            # Extract degree from relationship string (simplified)
            if "generations removed" in relationship:
                try:
                    degree = sum([int(s) for s in relationship.split() if s.
 ↪isdigit()])
                    relationships.append(degree)
                    ibd_amounts.append(ibd_amount)
                except:
                    pass

    # Plot
    plt.figure(figsize=(10, 6))
    sns.scatterplot(x=relationships, y=ibd_amounts)
    plt.xlabel("Relationship Degree")
    plt.ylabel("Total IBD Sharing (cM)")
    plt.title("IBD Sharing vs Relationship Degree")
    plt.show()

plot_ibd_vs_relationship(top_pedigree, filtered_ibd_seg_list_v1)
```



[77]:
```python
# 10. Export pedigree in a standard format (e.g., GEDCOM-like)
def export_pedigree(pedigree, bioinfo, output_file):
    """Export the pedigree in a standard format"""
    # Create a mapping of ID to sex and age
    id_to_info = {info['genotype_id']: (info['sex'], info['age']) for info in␣
↪bioinfo}

    with open(output_file, 'w') as f:
        f.write("# Exported Pedigree\n")
        f.write("# Format: ID Sex Age Parent1 Parent2\n")

        # Process all individuals, starting with real ones
        real_ids = sorted([id for id in pedigree.keys() if isinstance(id, int)␣
↪and id > 0])
        inferred_ids = sorted([id for id in pedigree.keys() if isinstance(id,␣
↪int) and id < 0])

        # Write real individuals first
        for id in real_ids:
            sex, age = id_to_info.get(id, ('U', 0))
            parents = list(pedigree.get(id, {}).keys())
            parent1 = parents[0] if len(parents) > 0 else 0
            parent2 = parents[1] if len(parents) > 1 else 0
```

```
            f.write(f"{id} {sex} {age} {parent1} {parent2}\n")

        # Then write inferred individuals
        for id in inferred_ids:
            # For inferred individuals, we can assume they're one generation␣
 ↪older than their children
            children = [child for child, parents in pedigree.items() if id in␣
 ↪parents]

            # Infer sex based on placement if possible
            inferred_sex = 'U'  # Unknown

            # Infer approximate age based on children's ages if possible
            inferred_age = 0
            for child in children:
                if child in id_to_info:
                    child_age = id_to_info[child][1]
                    if inferred_age == 0 or child_age + 20 < inferred_age:
                        inferred_age = child_age + 20

            parents = list(pedigree.get(id, {}).keys())
            parent1 = parents[0] if len(parents) > 0 else 0
            parent2 = parents[1] if len(parents) > 1 else 0

            f.write(f"{id} {inferred_sex} {inferred_age} {parent1} {parent2}\n")

    print(f"Pedigree exported to {output_file}")

# Example usage
if up_dict_log_like_list:
    export_pedigree(
        up_dict_log_like_list[0][0],
        filtered_bioinfo,
        os.path.join(results_directory, 'exported_pedigree.txt')
    )
```

```
Pedigree exported to
/home/lakishadavid/computational_genetic_genealogy/results/exported_pedigree.txt
```