Group 19: Pedigree Analysis

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Course Modelling Project

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Abstract

When given a pedigree chart, our model will track the family members to their previous generations with all possibilities triats. As they are affected by a trait to determine if a trait is: dominant or recessive, and autosomal or X-linked.
A pedigree chart is a diagram that documents how a genetic trait is pass on in a family, from one generation to another.
A trait can be determined as either dominant or recessive:
- Dominant traits only need one affected allele to be expressed.
- Recessives traits are only expressed when both alleles are affected.
Autosomal or x-linked:
- Autosomal traits are located on all the chromosomes except the X or Y chromosome
- X-linked traits are located on the X chromosomes; are more likely to affect males

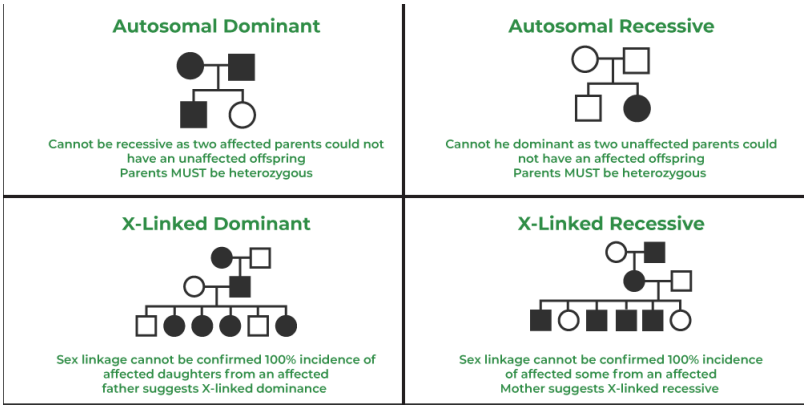


Figure 1: Image from `https://www.geeksforgeeks.org/pedigree-analysis/`

Propositions

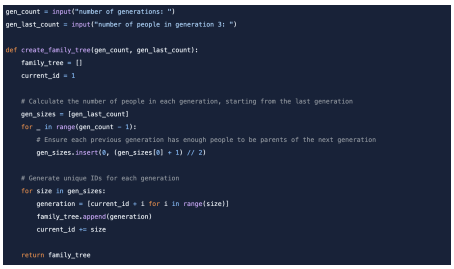
- Drafts
  - Characteristics of each family member
    - F(i), is true if a family member at position i is female
    - A(i): is true if a family member at position i is affected
    - R(i): is true if a family member at position i is a blood relative
  - Relationship between family members
    - C(i,j,k): is true if a family member at position i is the child of family members at position j and k
    - S(i,j): is true if a family member at position i is the sibling of someone at position j
  - Inheritance Pattern
    - M(g): is true if more male family members are affected in a generation
  - Inheritance mode of trait passed down
    - R: is true if a disease is recessive and false if it is not
    - X: is true if a disease is x linked and false if it is autosomal

Constraints

- Drafts:
  - Two family members are siblings if and only if they have the same parents:
    - $C(a, c, d) \land C(b, c, d) \iff S(a, b)$
  - If both parents of an affected family member are unaffected, then the disease is recessive
    - $(A(a) \land C(a, b, c)) \land (\neg A(b) \land \neg A(c)) \implies R$
  - There must be one male and one female parent
    - $C(i, a, b) \iff (F(a) \land \neg F(b)) \lor (\neg F(a) \land F(b))$
  - Parents cannot be blood relatives
    - $C(i, a, b) \iff (R(a) \land \neg R(b) \lor (R(b) \land \neg R(a))$
- To do:
  - If there are more males in a generation than females the M(g) is true
  - If M(g) is true for at least half of the generations then, X is true

Model Exploration

- building pedigree
  1. First draft: 2d array based on number of gen and the number of ppl in last gen



```
gen_count = input("number of generations: ")
gen_last_count = input("number of people in generation 3: ")

def create_family_tree(gen_count, gen_last_count):
    family_tree = []
    current_id = 1

    # Calculate the number of people in each generation, starting from the last generation
    gen_sizes = [gen_last_count]
    for _ in range(gen_count - 1):
        # Ensure each previous generation has enough people to be parents of the next generation
        gen_sizes.insert(0, (gen_sizes[0] + 1) // 2)

    # Generate unique IDs for each generation
    for size in gen_sizes:
        generation = [current_id + i for i in range(size)]
        family_tree.append(generation)
        current_id += size

    return family_tree
```

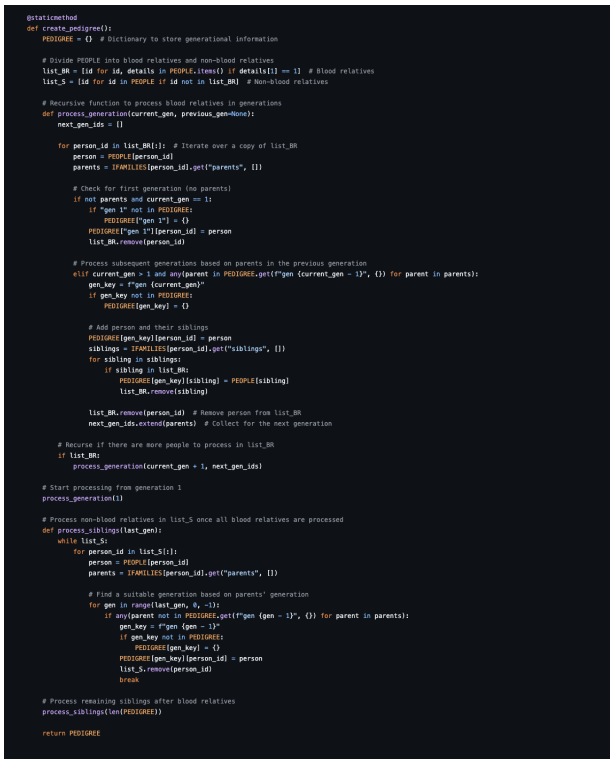
     – Issue with model: too restrictive, limits the amount of generations and how many children the older generations have
  2. Second Draft: Recursive 2d dictionary that build up a person, then siblings then parents

```
def create_family_tree(person_id, num_siblings, parents, family_tree, generation=0):
    # Check if the person already exists in the tree
    if person_id not in family_tree:
        # Initialize the person's data
        family_tree[person_id] = {
            "generation": generation,
            "siblings": set(),
            "parents": [],
            "spouse": None
        }

    # Add siblings based on num_siblings count
    siblings = []
    for i in range(num_siblings):
        sibling_id = person_id + i + 1
        if sibling_id not in family_tree:
            create_family_tree(sibling_id, 0, [], family_tree, generation)
        siblings.append(sibling_id)
        family_tree[person_id]["siblings"].add(sibling_id)
        family_tree[sibling_id]["siblings"].add(person_id)

    # Add parents if provided
    if parents:
        parent1, parent2 = parents
        if parent1 not in family_tree:
            # Recursively add each parent and establish spousal relationship
            create_family_tree(parent1, 0, [], family_tree, generation + 1)
        if parent2 not in family_tree:
            create_family_tree(parent2, 0, [], family_tree, generation + 1)

        # Link the parents as spouses and set them as the person's parents
        family_tree[parent1]["spouse"] = parent2
        family_tree[parent2]["spouse"] = parent1
        family_tree[person_id]["parents"] = [parent1, parent2]

        # Assign siblings' parents to the same parents
        for sibling_id in siblings:
            family_tree[sibling_id]["parents"] = [parent1, parent2]

    return family_tree
```

     – Issue with model: the function does not follow the format of our propositions and constraints
  3. Current draft: a dictionary of individual family members with their IDs as the key. Assign values to their keys by giving them characteristics (affected, gender, blood relation) using Char propositions. Then create a dictionary using for immediate families (siblings+parents) by linking individual family members using Rel propositions, then create a recursive function that builds the pedigree up using the dictionaries

```
PEDIGREE={}
#dictionary to store immediate family (siblings+parents)
IFAMILIES=[]
#dictionary to store individual family member (id, chars)
PEOPLE={}
#amount of people in the family
FAMNUM=20

#generate a dictionary represent each family member as an unique integer
def create_people(FAMNUM):
    i=1
    while i <=FAMNUM:
        id=i
        PEOPLE.update({id: [0,0,0]})
        i+=1


@proposition(E)
class Char(object):
    def assign_person(id, char):

        characteristic=[0,0,0] #char[0]: bool for female, char[1]: bool for blood relative, char[2]: bool for a
        if char=="Female":
            characteristic[0]=1
        elif char=="Blood Relative":
            characteristic[1]=1
        elif char=="Affected":
            characteristic[2]=1
        PEOPLE["id"]=characteristic
    def get_person():
        if id in PEOPLE:
            if id <=FAMNUM:
                return PEOPLE["id"]
    def _prop_name(self):
        return f"Char.{self.id}={self.char}"
```

```
@proposition(E)
class Rel(object):
    def create_ifam(id1, id2, id3=None):
        # Initialize a family structure
        ifamily = {"parents": [], "siblings": []}

        # Helper function to add a person to a list without duplicates
        def add_to_list(person_id, list_name):
            person = PEOPLE[person_id]
            if person not in ifamily[list_name]:
                ifamily[list_name].append(person)

        # Two arguments case: add both to siblings
        if id3 is None:
            add_to_list(id1, "siblings")
            add_to_list(id2, "siblings")
        else:
            # Three arguments case: first goes to siblings, second and third go to parents
            add_to_list(id1, "siblings")
            add_to_list(id2, "parents")
            add_to_list(id3, "parents")

        # Add the completed family dictionary to IFAMILIES
        IFAMILIES.append(ifamily)
```



```
@staticmethod
def create_pedigree():
    PEDIGREE = {}  # Dictionary to store generational information

    # Divide PEOPLE into blood relatives and non-blood relatives
    list_BR = [id for id, details in PEOPLE.items() if details[1] == 1]  # Blood relatives
    list_S = [id for id in PEOPLE if id not in list_BR]  # Non-blood relatives

    # Recursive function to process blood relatives in generations
    def process_generation(current_gen, previous_gen=None):
        next_gen_ids = []

        for person_id in list_BR[:]:  # Iterate over a copy of list_BR
            person = PEOPLE[person_id]
            parents = IFAMILIES[person_id].get("parents", [])

            # Check for first generation (no parents)
            if not parents and current_gen == 1:
                if "gen 1" not in PEDIGREE:
                    PEDIGREE["gen 1"] = {}
                PEDIGREE["gen 1"][person_id] = person
                list_BR.remove(person_id)

            # Process subsequent generations based on parents in the previous generation
            elif current_gen > 1 and any(parent in PEDIGREE.get(f"gen {current_gen - 1}", {}) for parent in parents):
                gen_key = f"gen {current_gen}"
                if gen_key not in PEDIGREE:
                    PEDIGREE[gen_key] = {}

                # Add person and their siblings
                PEDIGREE[gen_key][person_id] = person
                siblings = IFAMILIES[person_id].get("siblings", [])
                for sibling in siblings:
                    if sibling in list_BR:
                        PEDIGREE[gen_key][sibling] = PEOPLE[sibling]
                        list_BR.remove(sibling)

                list_BR.remove(person_id)  # Remove person from list_BR
                next_gen_ids.extend(parents)  # Collect for the next generation

        # Recurse if there are more people to process in list_BR
        if list_BR:
            process_generation(current_gen + 1, next_gen_ids)

    # Start processing from generation 1
    process_generation(1)

    # Process non-blood relatives in list_S once all blood relatives are processed
    def process_siblings(last_gen):
        while list_S:
            for person_id in list_S[:]:
                person = PEOPLE[person_id]
                parents = IFAMILIES[person_id].get("parents", [])

                # Find a suitable generation based on parents' generation
                for gen in range(last_gen, 0, -1):
                    if any(parent not in PEDIGREE.get(f"gen {gen - 1}", {}) for parent in parents):
                        gen_key = f"gen {gen - 1}"
                        if gen_key not in PEDIGREE:
                            PEDIGREE[gen_key] = {}
                        PEDIGREE[gen_key][person_id] = person
                        list_S.remove(person_id)
                        break

    # Process remaining siblings after blood relatives
    process_siblings(len(PEDIGREE))

    return PEDIGREE
```

Jape Proof Ideas

- A person is affected and their parents are not. This must mean the parents are carriers of the trait and the trait is recessive
- In a family, one parent is affected, and one is not. They have more than one kid but not all of them are affected. This must mean either one parent has a dominant gene and the other doesn't have this gene or the parent has two recessive genes and the other is a carrier.

Requested Feedback

- Ideas for how to implement, the constraints in our to-dos (If there are more males in a generation than females the M(g) is true & If M(g) is true for at least half of the generations then, X is true). We are trying to do this recursively but are struggling to count the amount of people and generations with only logic.