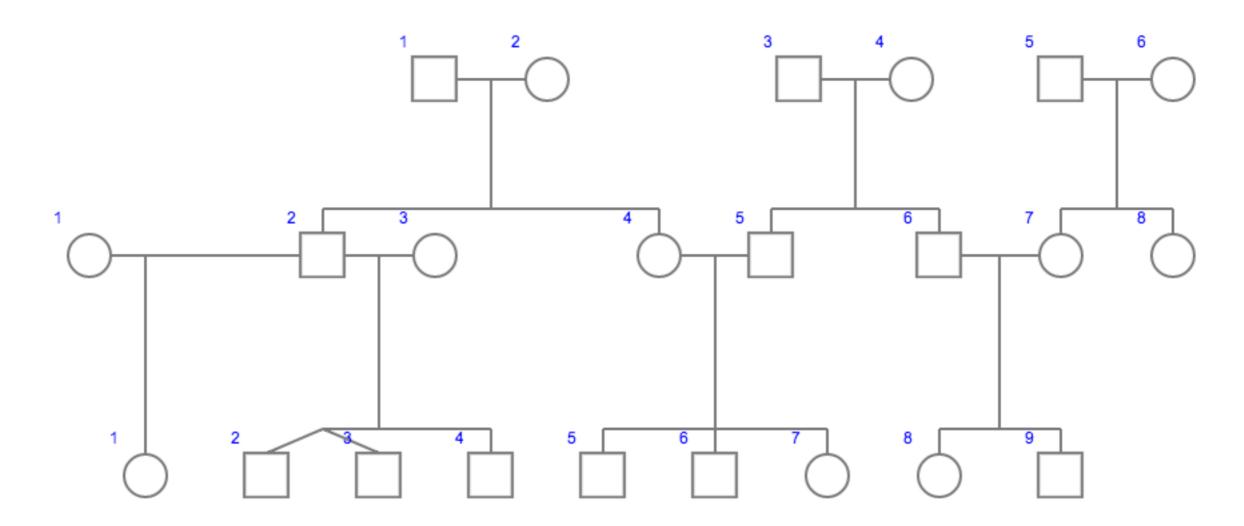
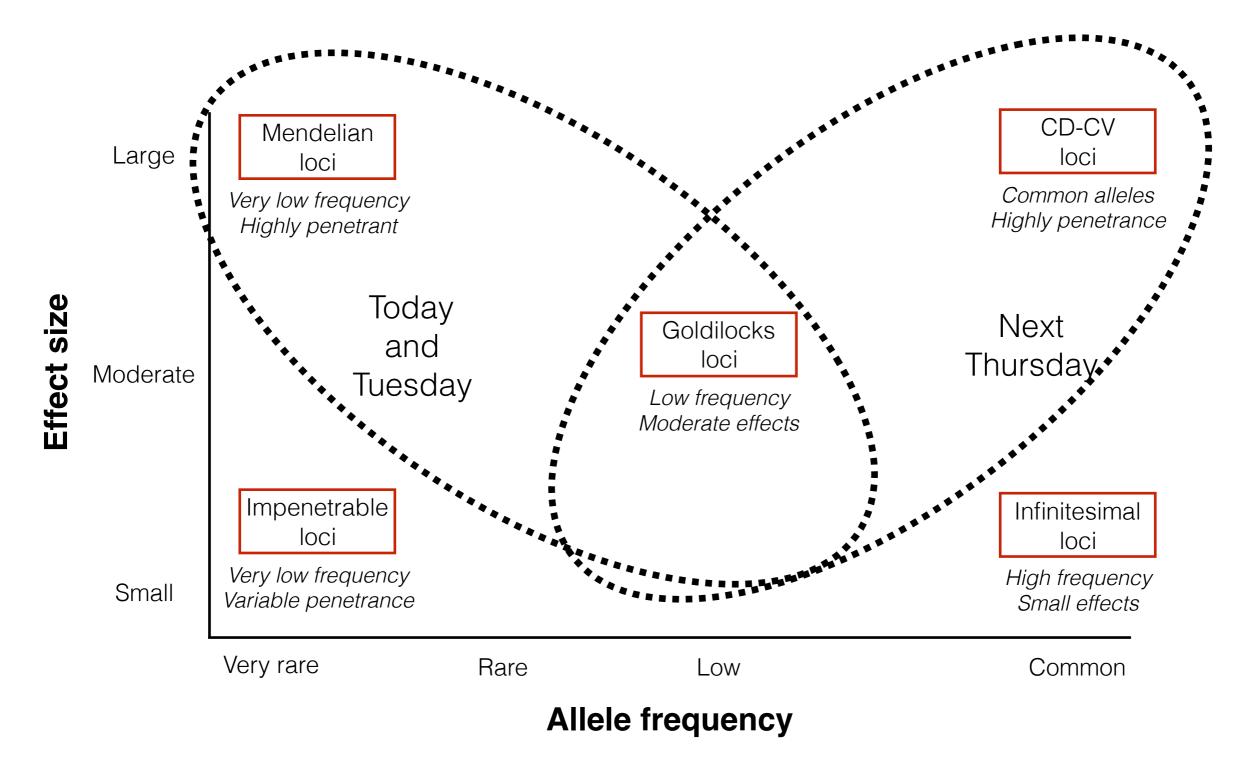
Bio393: Genetic Analysis

Family-based analysis, Modes of inheritance, Phase

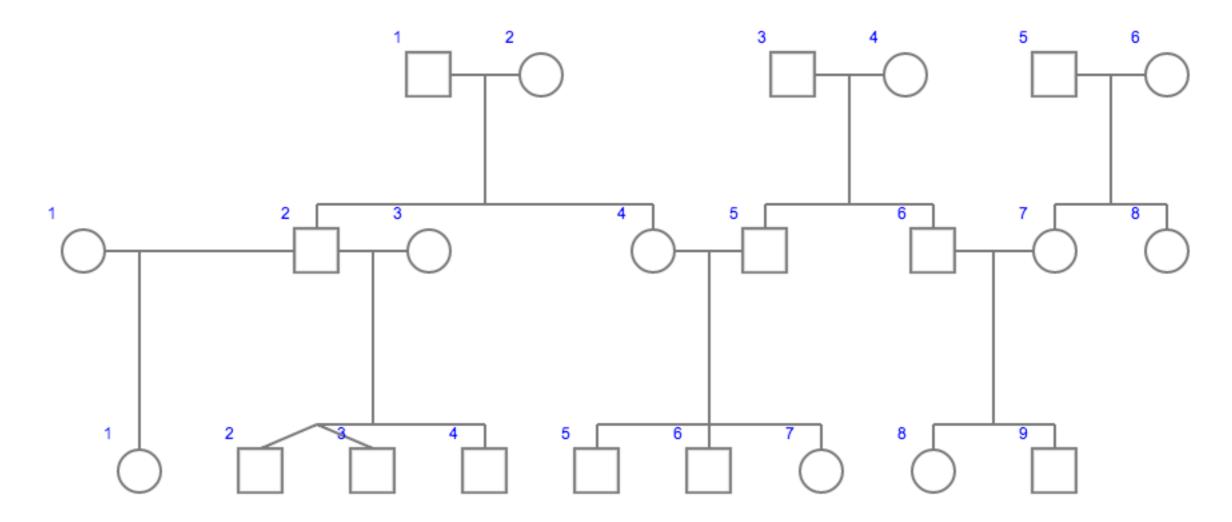


The spectrum of how variation contributes to disease



Linkage mapping studies or family-based mapping studies

Why do we study inheritance in families?



Correlating genetic variants with disease tells us the disease gene is near that variant (or is that variant)

Human pedigree analysis allows us to follow traits in families

| Male

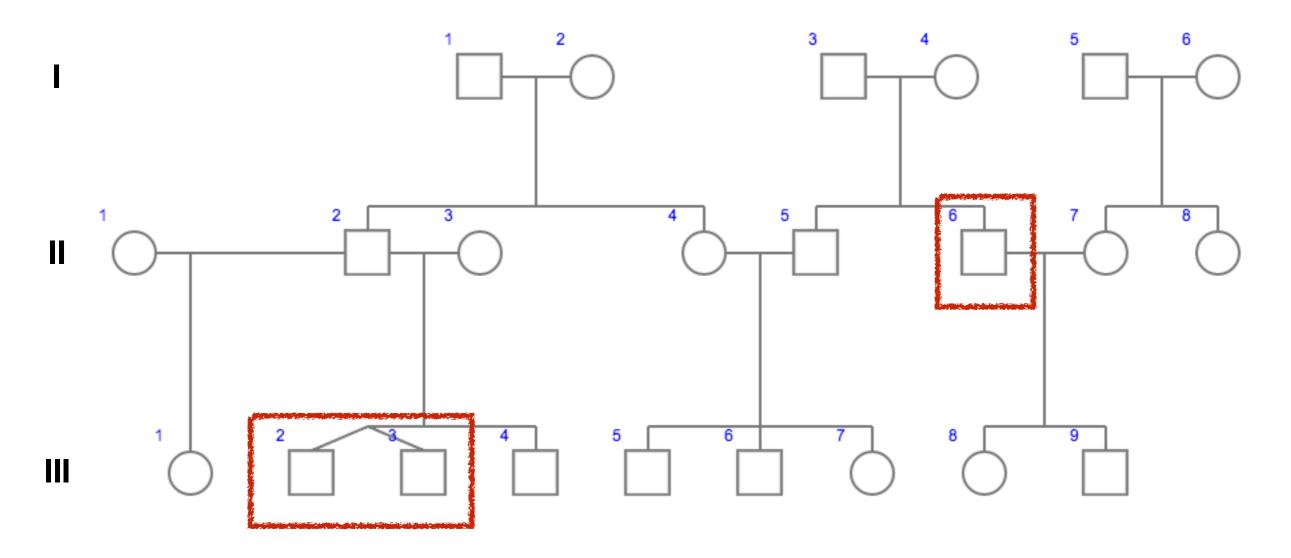
() Female

Affected male

Affected female

Remember that humans are diploid.

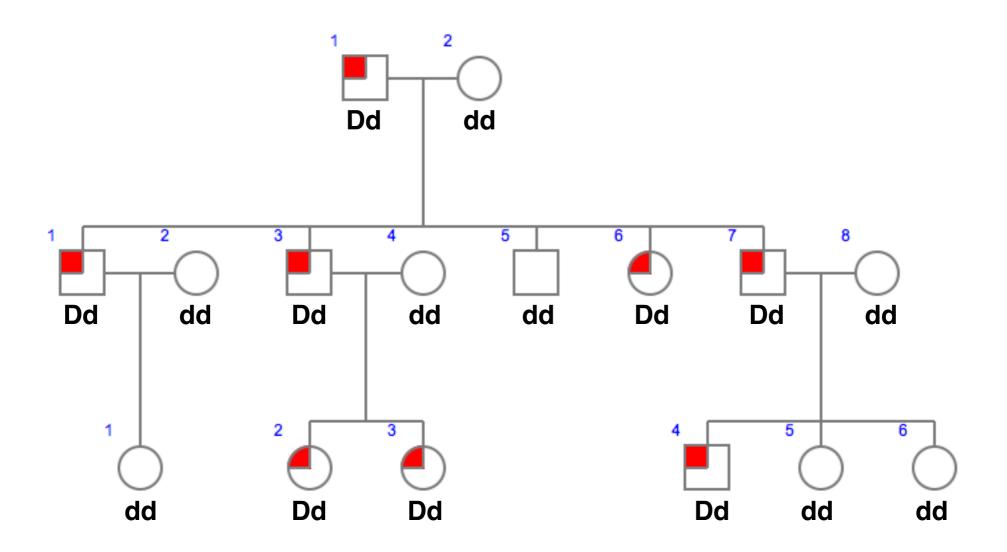
Human pedigree analysis allows us to follow traits in families



Individuals are numbered from left to right

Generations are numbered from top to bottom in Roman numerals

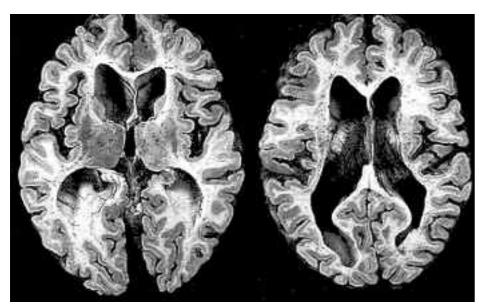
Most diseases are rare, individuals breeding into families are usually unaffected



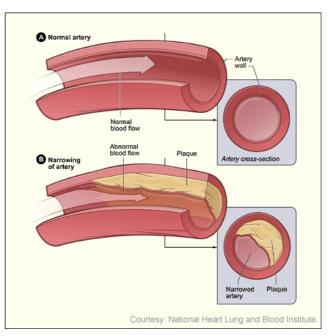
- How many individuals are affected?
- In each generation?
- Are males preferentially affected from affected mothers?
- Are females preferentially affected from affected fathers?

Autosomal dominant

Examples of human autosomal dominant disorders



Huntington's Disease chr. 4



Familial Hypercholesterolemia chr. 19

Caused by loss-of-function or gain-of-function?

Most affected individuals are heterozygotes

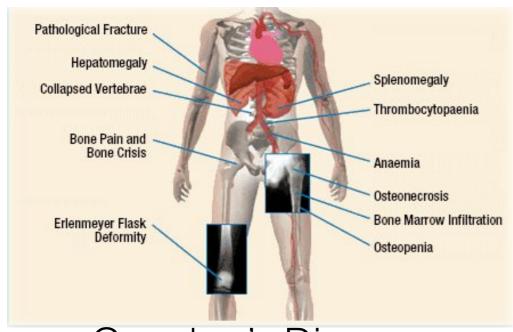
What is the chance that a child is affected?

Modes of inheritance AA **AA** aa Aa

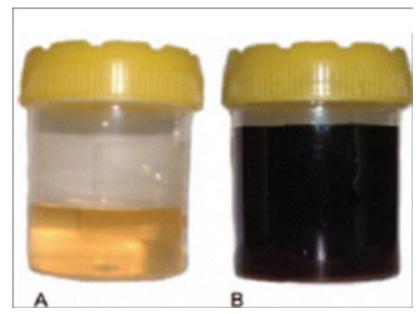
- How many individuals are affected?
- In each generation?
- Are males preferentially affected from affected mothers?
- Are females preferentially affected from affected fathers?

Autosomal recessive

Examples of human autosomal recessive disorders



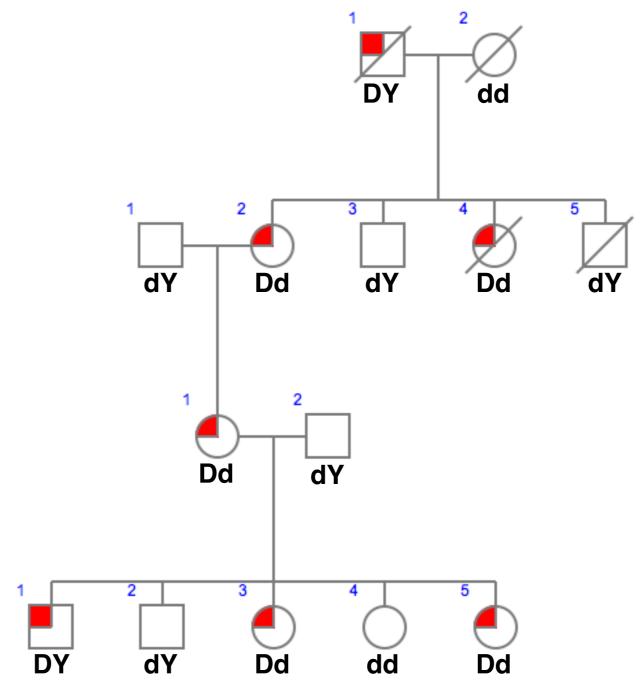
Gaucher's Disease chr. 1



Maple Syrup Urine Disease chr. 1, 6, or 19

Caused by loss-of-function or gain-of-function?

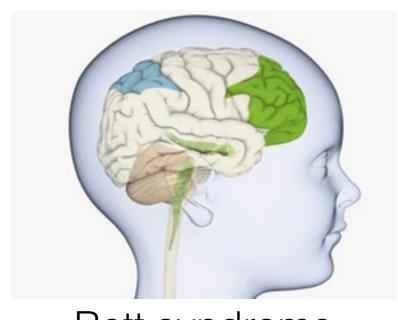
All affected individuals are homozygotes



- How many individuals are affected?
- In each generation?
- Are males preferentially affected from affected mothers?
- Are females preferentially affected from affected fathers?

X-linked dominant

Examples of human X-linked dominant disorders

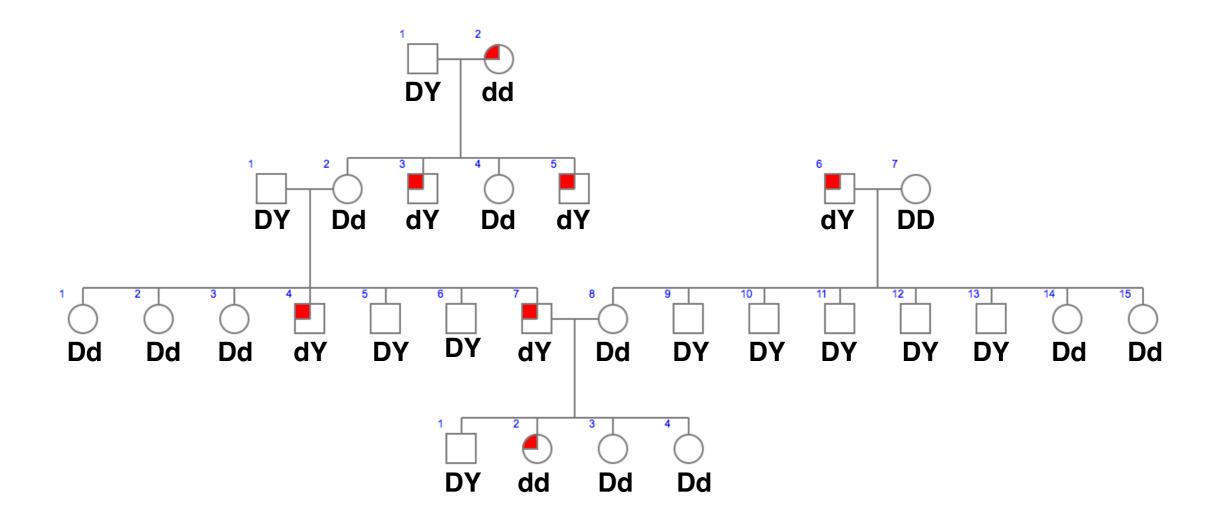


Rett syndrome



Fragile X syndrome

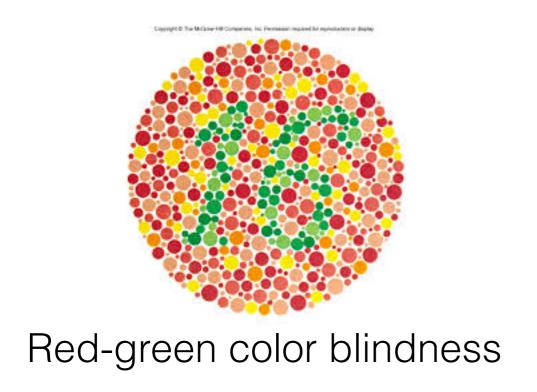
All daughters of affected fathers are affected

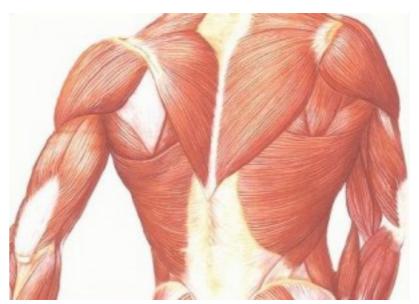


- How many individuals are affected?
- In each generation?
- Are males preferentially affected from affected mothers?
- Are females preferentially affected from affected fathers?

X-linked recessive

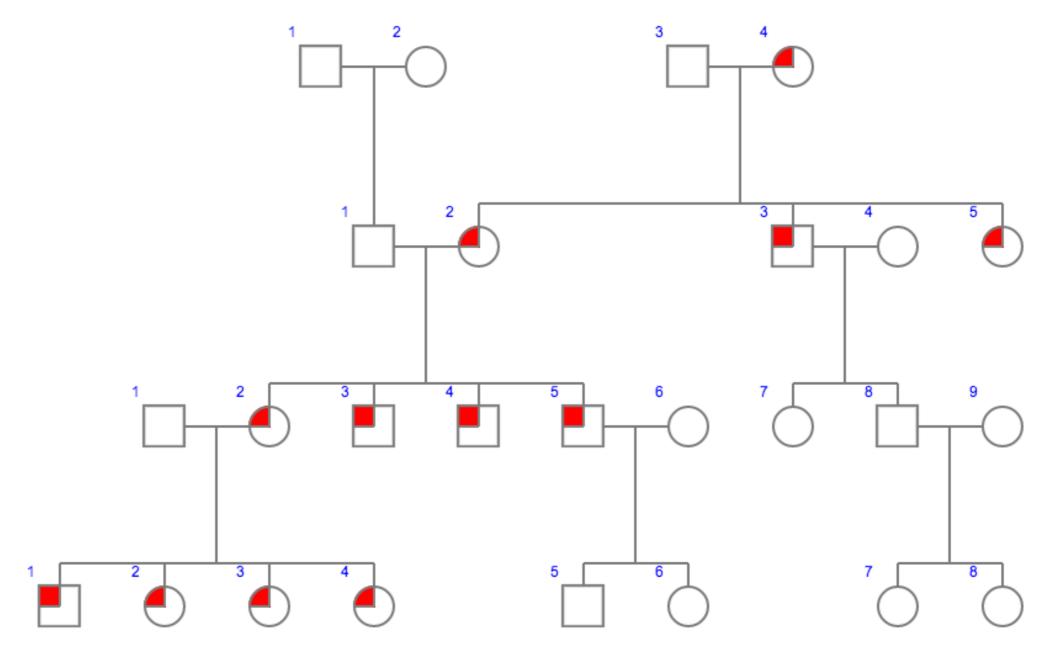
Examples of human X-linked recessive disorders





Duchenne muscular dystrophy

All sons of affected mothers are affected



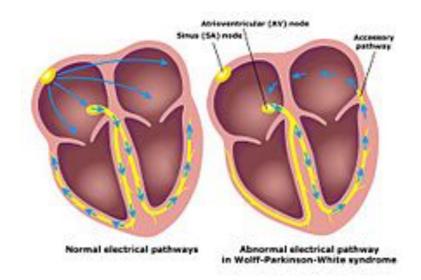
- How many individuals are affected?
- In each generation?
- Are males preferentially affected from affected mothers?
- Are females preferentially affected from affected fathers?

Cytoplasmic inheritance

Examples of human cytoplasmic inheritance disorders

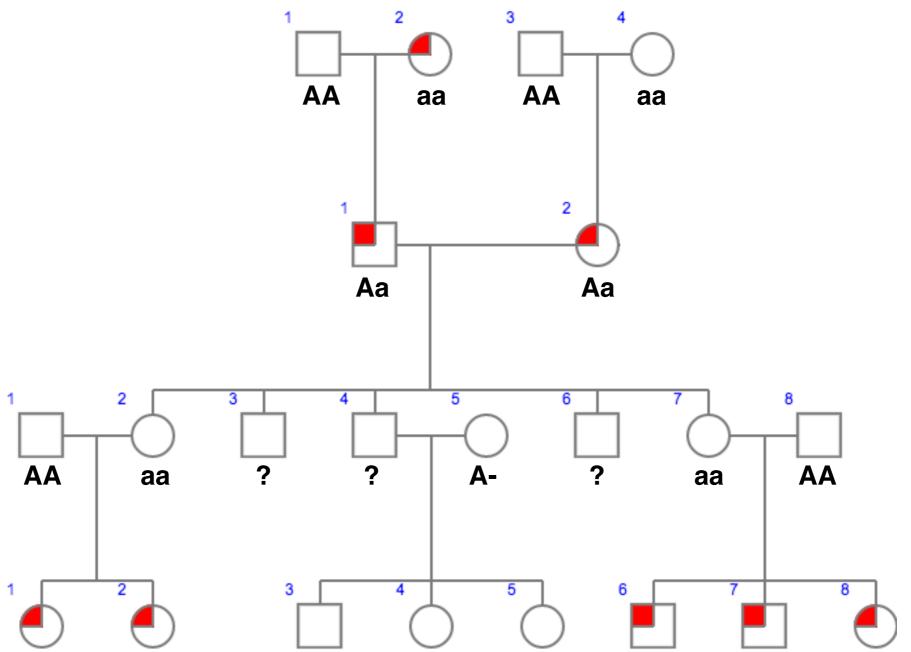


Mitochondrial myopathy



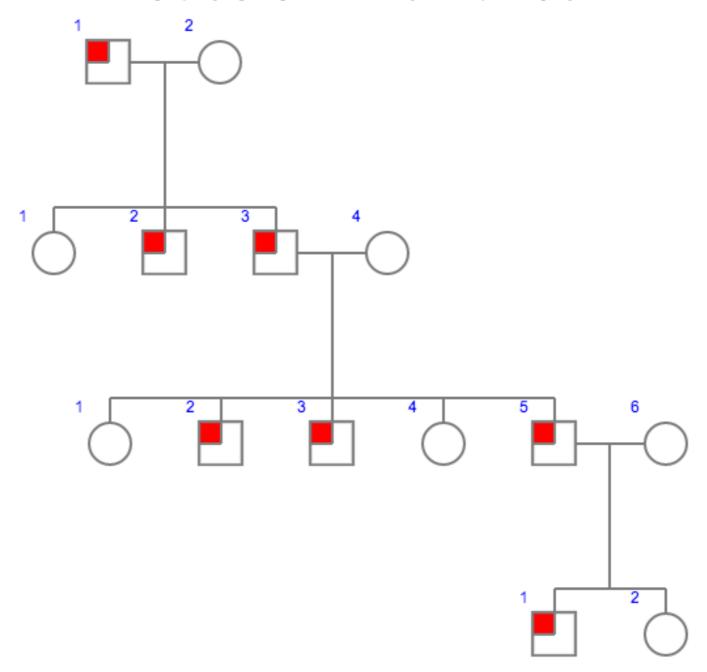
Wolff-Parkinson-White syndrome

All children of affected mothers are affected



- How many individuals are affected?
- In each generation?
- Are males preferentially affected from affected mothers?
- Are females preferentially affected from affected fathers?

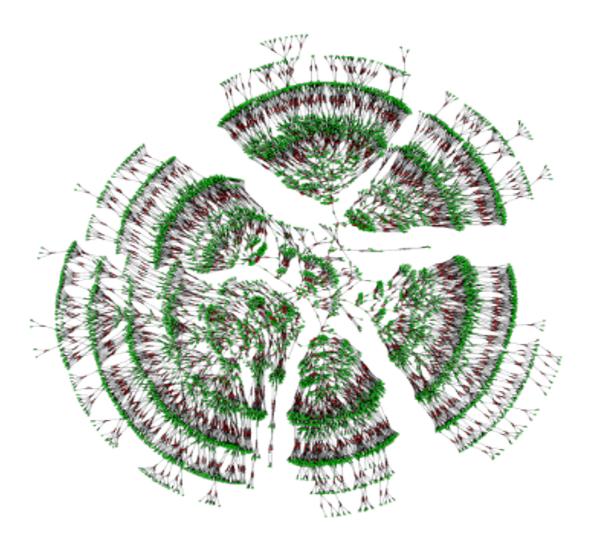
Recessive maternal-effect inheritance

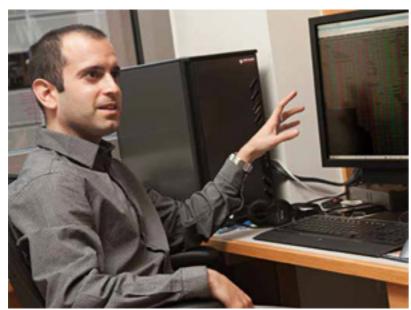


- How many individuals are affected?
- In each generation?
- Are males preferentially affected from affected mothers?
- Are females preferentially affected from affected fathers?

Y-linked inheritance

Some pedigrees can contain millions of individuals



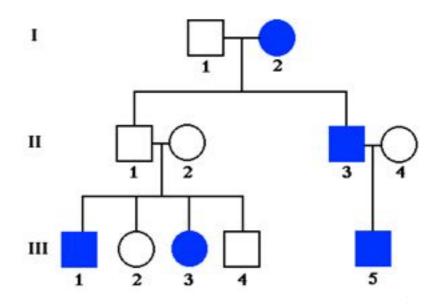


Yaniv Erlich

Ancestry websites offer rich family data



Remember all of the genetics we've learned so far



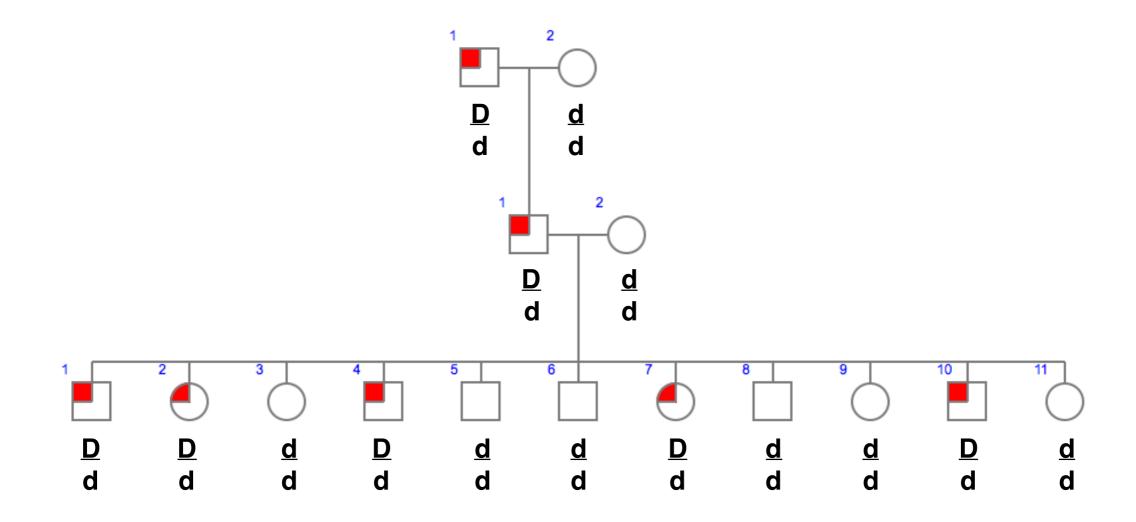
Incomplete penetrance

Non-complementation

Haploinsufficiency

Suppression and enhancement

We want to be able to find a marker linked with disease to identify the disease gene



Autosomal dominant

Genetic variants are used as markers to track disease

Single nucleotide variants (SNVs)

Reference ATGTGCAGACGTAGACGTA

Alternative ATGTGCAGACTTAGACGTA

Insertion-deletion variants (indels)

Reference ATGTGCAGACGTAGACGTA

Alternative ATGTGCAGACGTAGACGTA

Addition of 126 bp

Copy-number variants (CNVs)

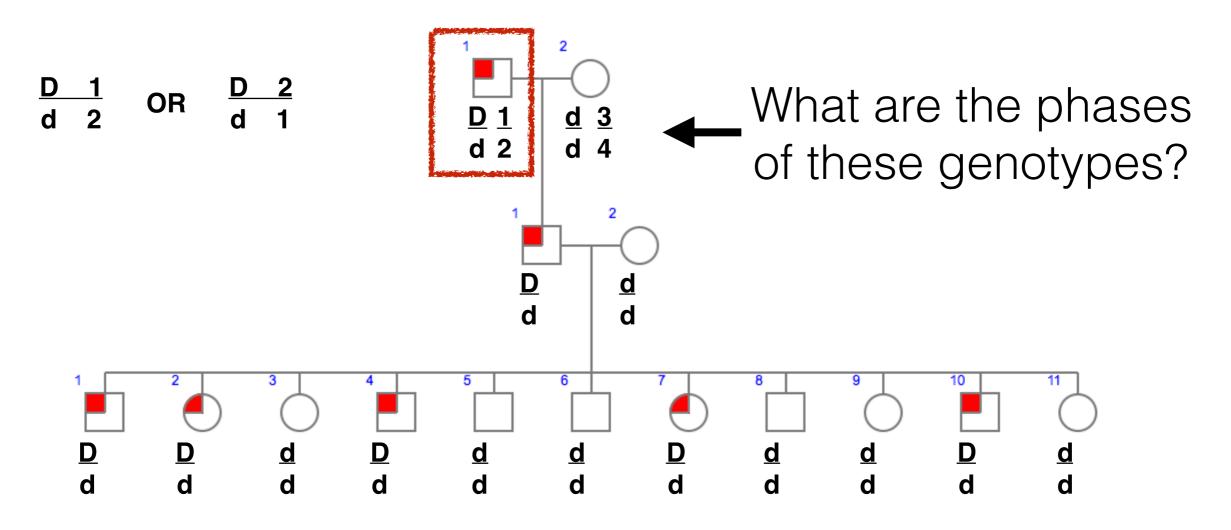
Reference Diploid (2 copies)

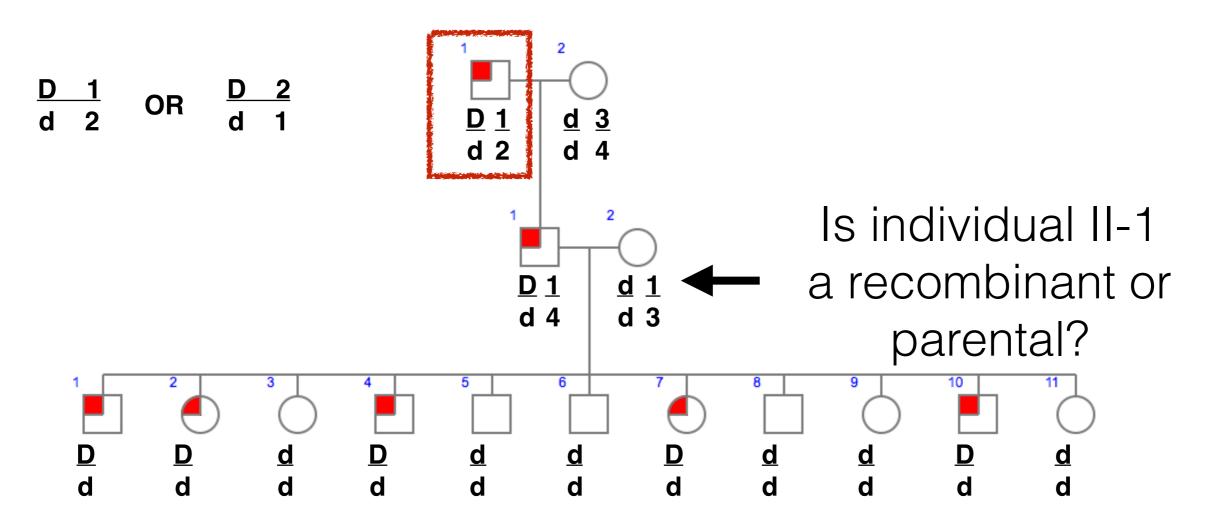
Alternative More (or fewer) than 2 copies

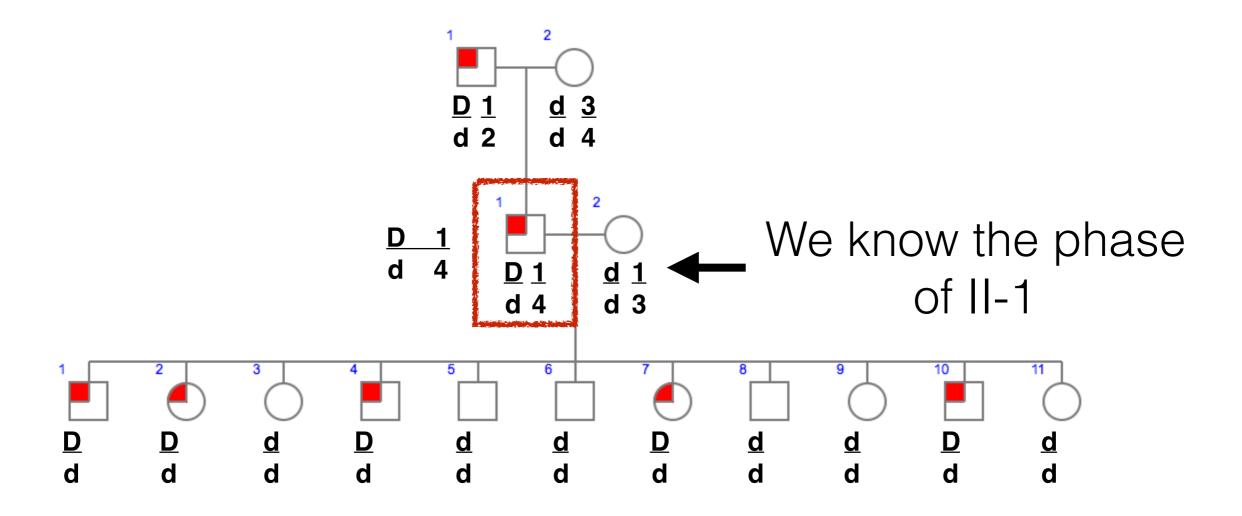
Microsatellites or short tandem repeats (STRs)

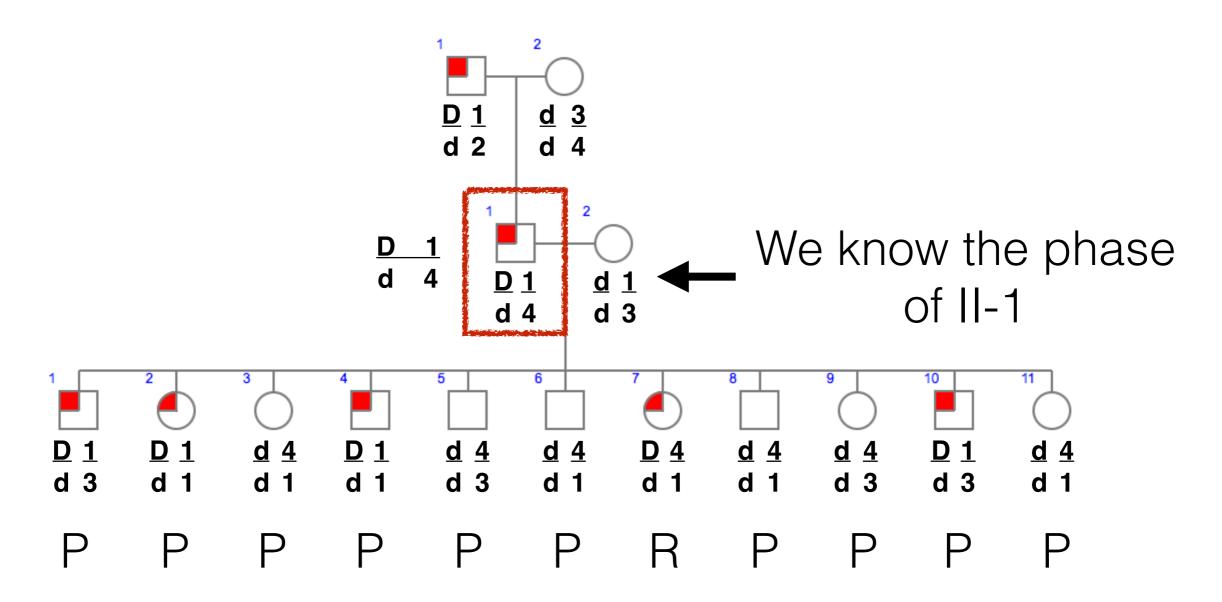
Reference ATGTGCAGCAGCAGCGTA

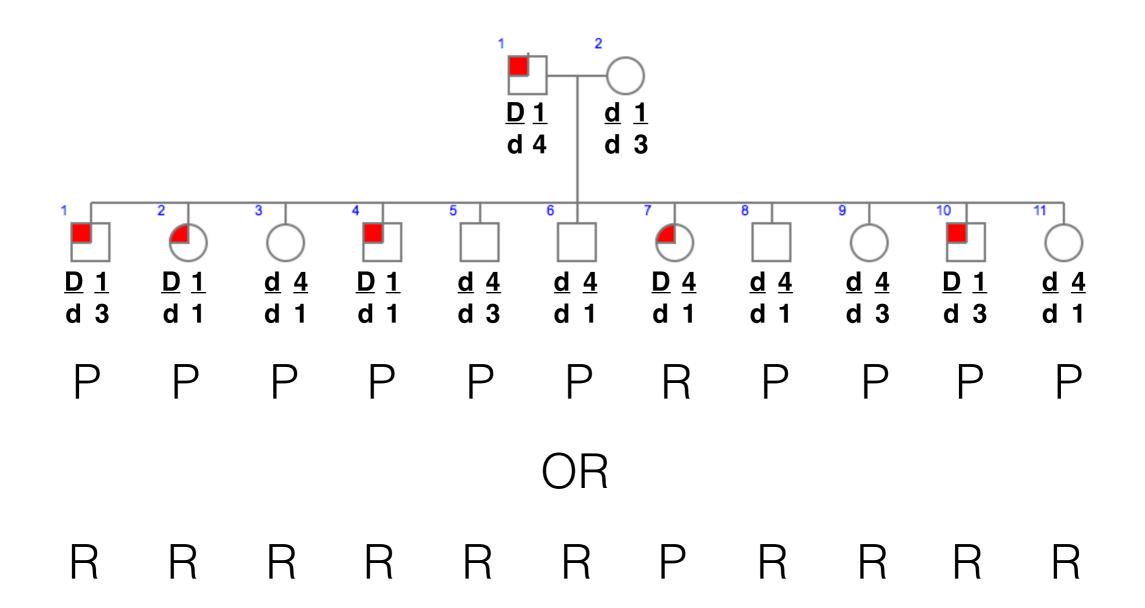
Alternative ATGTGCAGCAGCGTAGTGACT











Sometimes, we don't know the phase of the parent, and both possibilities of phase are equally likely