# Bioinformatics CS300 Chap 3 Computational Manipulation of DNA

Fall 2017
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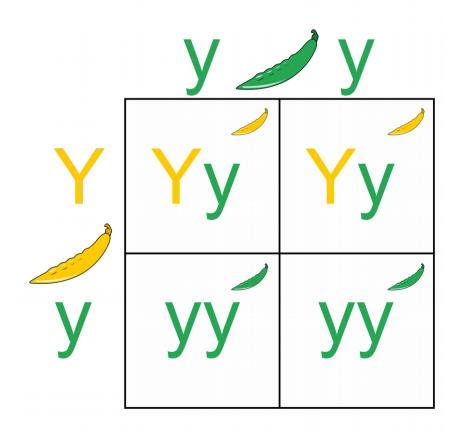


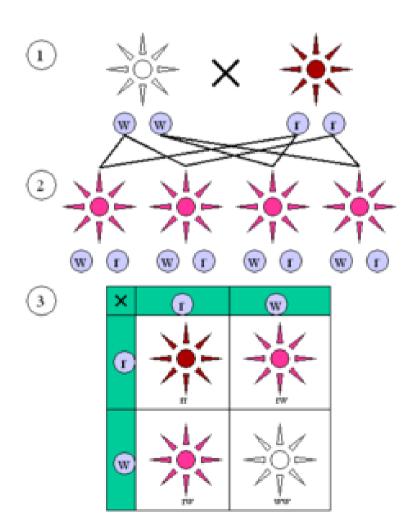
What is the difference between a gene and an allele?

Consider this...

Answer in the context of cystic fibrosis and the CFTR gene

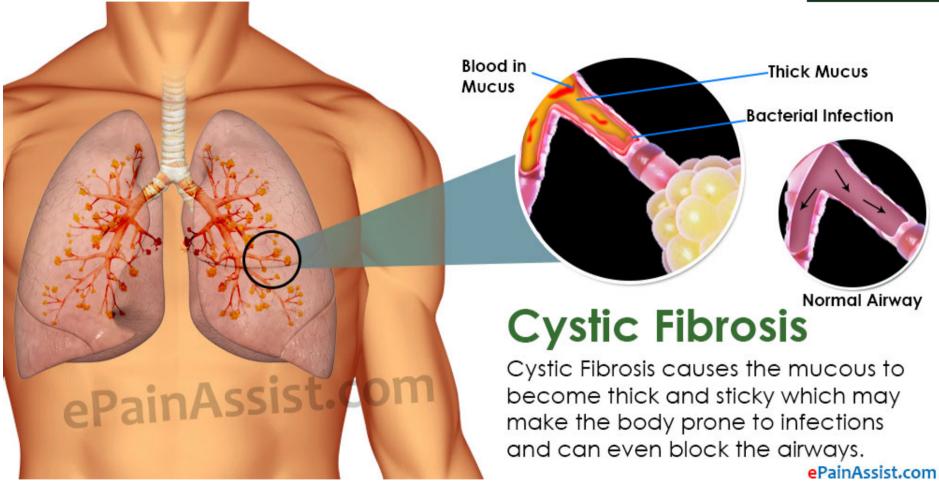
Hint: Think Mendelian Genetics







#### Cystic Fibrosis



 Inherited medical condition of the secretory glands (producers of mucous and sweat)



#### Cystic Fibrosis

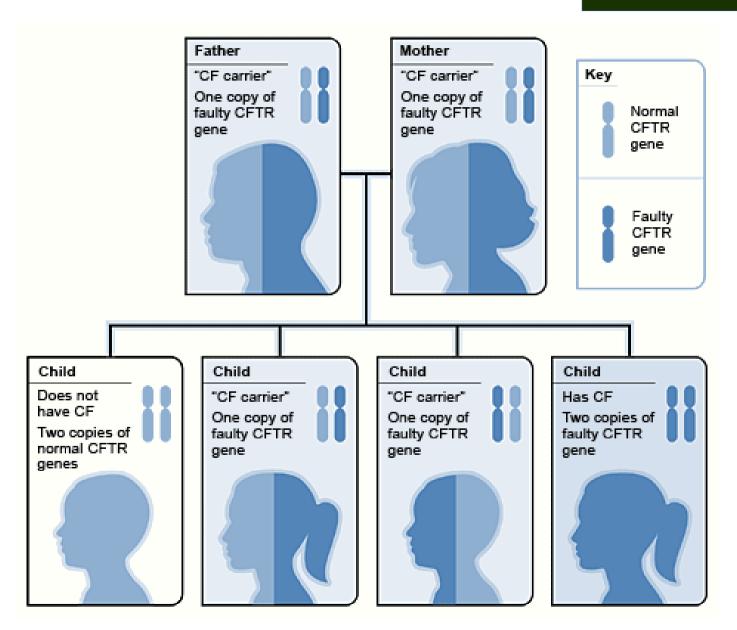


 Clubbed fingers: occurs in heart and lung diseases that reduce the amount of oxygen in the blood

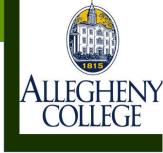


ALLEGHENY COLLEGE

- Autosomal recessive type condition: one faulty gene is inherited from both parents (together) in order for the offspring to get this condition
- Mendelian Genetic
- Impossible to know that someone is sure to get a condition.



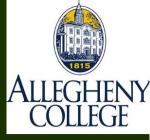


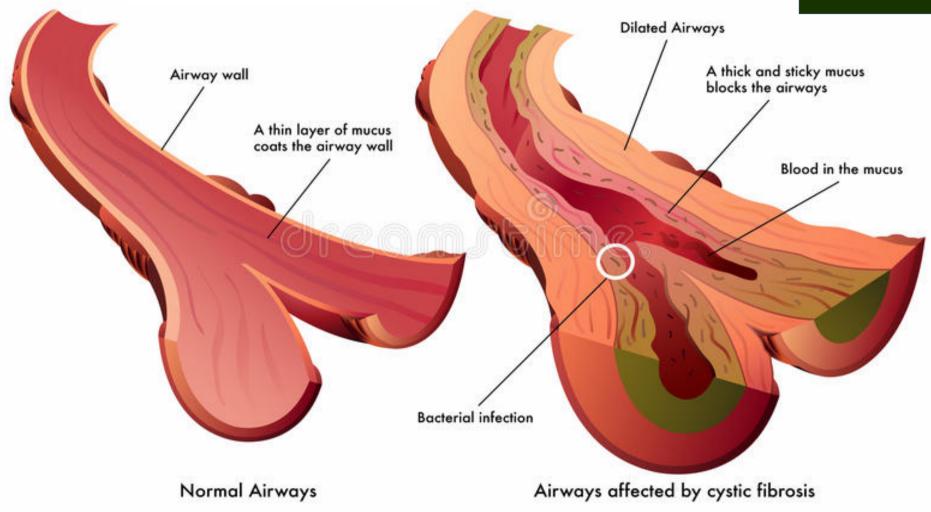


- Cystic Fibrosis Transmembrane conductance:
   CFTR
- Gene product is a bad regulator which fails to move water after displacing chloride ions in epithelial (thin tissue) cells
- Water follows chloride ions by osmosis.

 What if water regulation were not possible in the cells and organs?

#### **Cystic Fibrosis**





- Restricted flow in airways from mucous build-ups.
- Suffocation







• What if the the garbage collection crews in Paris went on strike (as they did in 2016)?

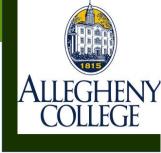
#### The Cystic Fibrosis Gene

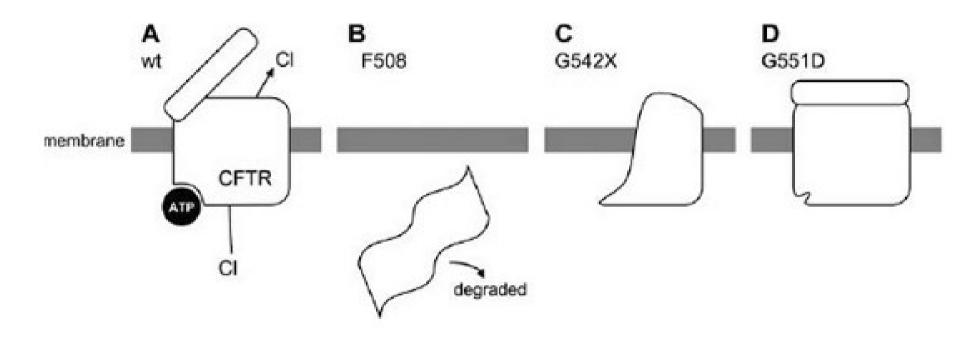


- Cystic Fibrosis Transmembrane conductance:
   CFTR
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- https://www.youtube.com/watch?v=EuLVCYrurok

 What if water regulation were not possible in the cells and organs?







**Figure 2.2** The wild-type allele (A) of the CFTR gene produces a chloride transport protein localized in the membrane; three different common CF alleles illustrated here result in variant proteins that are folded incorrectly (ΔF508; B), truncated (G542X; C), or unable to transport chloride (G551D; D).





 Gene codes for four different proteins: only one working type to move chloride ions and enable water displacement,

Healthy H₂0 Cystic Fibrosis Na

Mucous build-up





- Pam Can See The Man and Dog
- Frame shift by one letter!
- P amC anS eeT heM ana ndD og
- Frame shift by two letters!
- Pa mCa nSe eTh eMa nan dDo g
- Frame shift by three letters!
- Pam Can See The Man and Dog

Notice how the code changes depending on where you start reading?



### Open Reading Frames

Note: RF means reading frame, where you start reading the words.

Original: CAATGGCGAATCGACGTGTATAAA

RF1 - 5' - CAA TGG CGA ATC GAC GTG TAT AAA - 3'

RF2 - 5' - C AAT GGC GAA TCG ACG TGT ATA AA - 3'

RF 3 - 5' - CA ATG GCG AAT CGA CGT GTA TAA A - 3'

3' - CAA TGG CGA ATC GAC GTG TAT AAA - 5' - RF 4

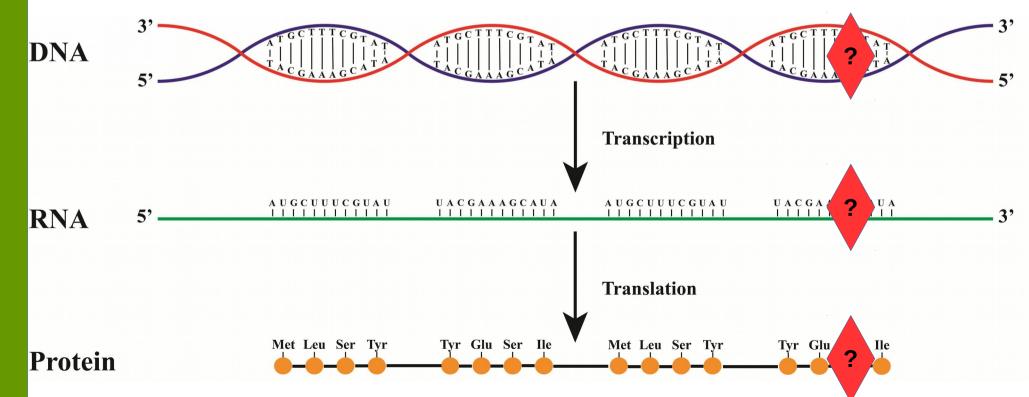
3' - C AAT GGC GAA TCG ACG TGT ATA AA - 5' - RF 5

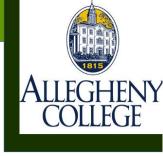
3' - CA ATG GCG AAT CGA CGT GTA TAA A - 5' - RF 6



#### Sequence is Carrier?

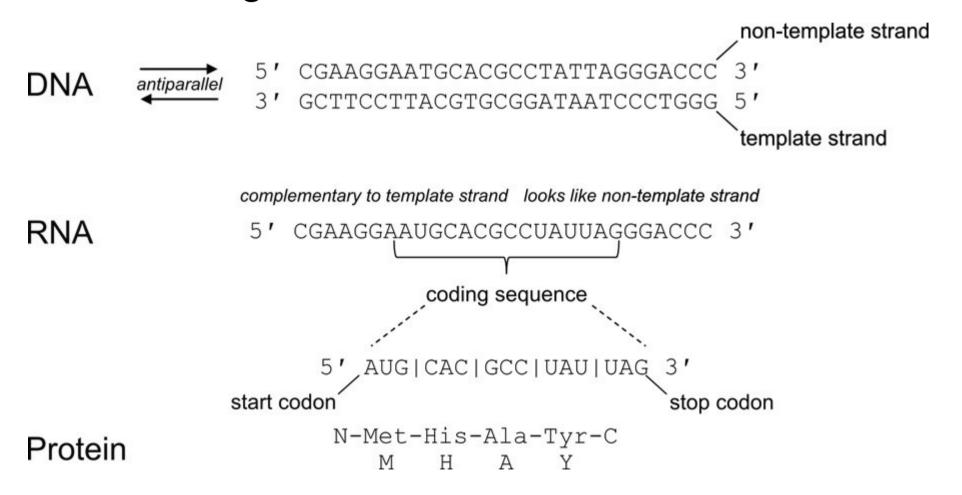
- How do we determine if a sequence carries the CF allele?
- Get DNA sample
- Translate DNA to protein: Compare this seq to seq of a "working protein"
- Is difference found between both proteins?





#### Analyze the Protein

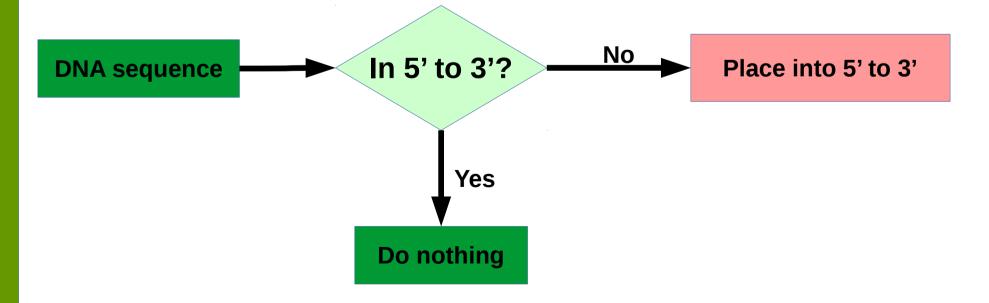
Translating DNA to find defects





#### The Unnamed Sequence

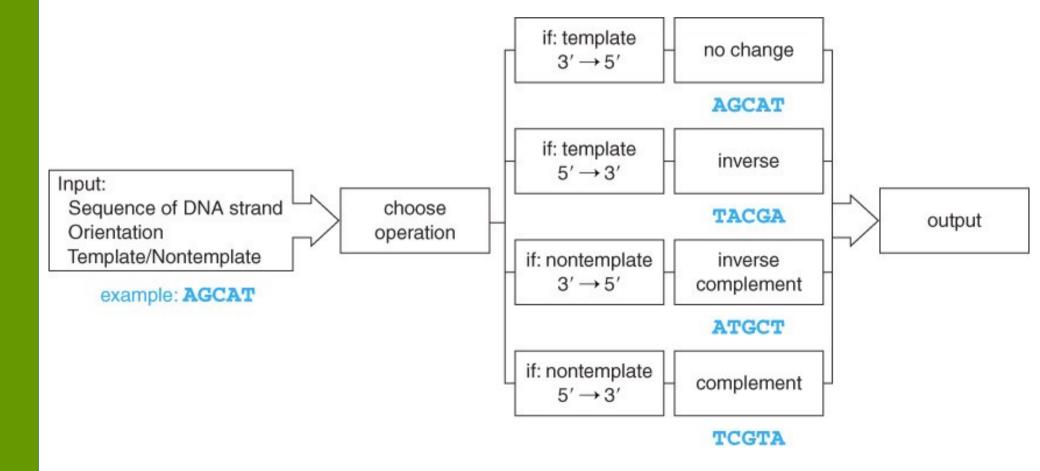
- Unlabeled strands of DNA are assumed to be in the 5' to 3', (left to right) direction.
- A new sequence is given to us for analysis.
- What are the steps to place this sequence into a format for use with bioinformatics tools?







A series of steps when handling DNA



#### The Algorithm in Words

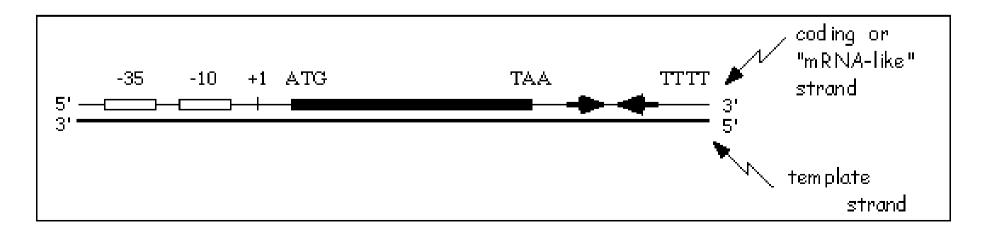


- Input a DNA sequence, including whether or it template or nontemplate strand and orientation
- Choose the appropriate operation:
  - If it is the template strand and oriented 3' -> 5', simply output the same sequence
  - If it is the template strand and oriented 5' -> 3', inverse the sequence (traverse the string from right to left and add each character to output string)
  - If it is the non-template strand and oriented 3' -> 5', generate the
    inverse complement sequence ((i.) traverse the string from right to
    left and (ii) for each character add the complement to the output string)
  - If it is the non-template strand and oriented 5' -> 3', generate the complement ((i.) traverse the string from left to right and (ii) for each character add the complement to the output string)
- Output the completed sequence, including 5' and 3' end labels

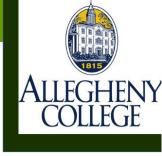




- Input:
  - DNA sequence AGCAT
  - Strand template (used to make mRNA) or non-template (the compliment of this strand that looks like mRNA)
  - Orientation 3' -> 5' or 5' -> 3'
- Output:
  - Template strand in 3' -> 5' orientation ready for transcription



## Codon Table to Translate the Protein Product



 DNA triplets read in groups of three called codons and represent an amino acid

Standard genetic code

1st	2nd base								3rd
base		Т		С		A		G	
т	TTT	(Phe/F) Phenylalanine	TCT	(Ser/S) Serine	TAT	(Tyr/Y) Tyrosine	TGT	(Cys/C) Cysteine	Т
	TTC		TCC		TAC		TGC	(Oyaro) Oyateme	С
	TTA	(Leu/L) Leucine	TCA		TAA <sup>[B]</sup>	Stop (Ochre)	TGA <sup>[B]</sup>	Stop (Opal)	A
	TTG		TCG		TAG <sup>[B]</sup>	Stop (Amber)	TGG	(Trp/W) Tryptophan	G
С	CTT		CCT	(Pro/P) Proline	CAT	(His/H) Histidine	CGT	(Arg/R) Arginine	Т
	CTC		CCC		CAC		CGC		С
	CTA		CCA		CAA	(Gln/Q) Glutamine	CGA		A
	CTG		CCG		CAG		CGG		G
A	ATT	(Ile/I) Isoleucine	ACT	(Thr/T) Threonine	AAT	(Asn/N) Asparagine	AGT	(Ser/S) Serine	Т
	ATC		ACC		AAC		AGC		С
	ATA		ACA		AAA	(Lys/K) Lysine	AGA	(Arg/R) Arginine	A
	ATG <sup>[A]</sup>		ACG		AAG		AGG		G
G	GTT	(Val/V) Valine	GCT	(Ala/A) Alanine	GAT	(Asp/D) Aspartic acid	GGT	(Gly/G) Glycine	Т
	GTC		GCC		GAC		GGC		С
	GTA		GCA		GAA	(Glu/E) Glutamic acid	GGA		Α
	GTG		GCG		GAG		GGG		G





- Biopython
- Translation functions
  - DNA → RNA
  - RNA → DNA
  - RNA → Protein
- Gives a protein sequence to compare to the wild type protein sequence

Follow along in class and save your notes in a text file!!

