

# **Bioinformatics**

**CS300**

**Chap 2**

**Computational Manipulation of DNA**

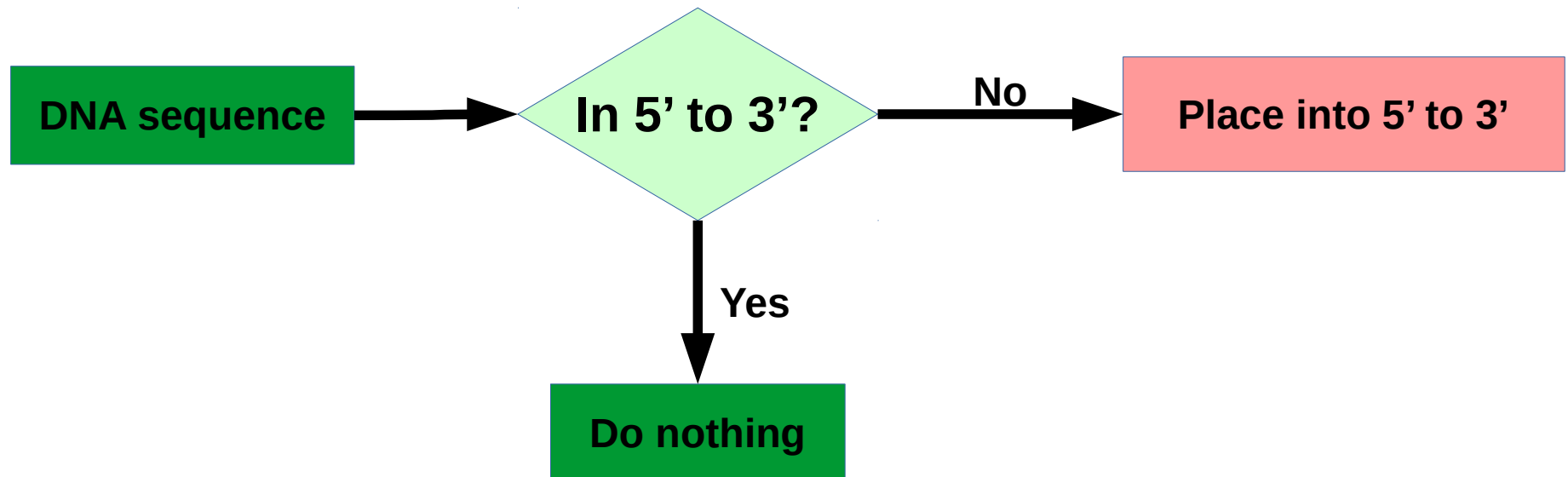
**Fall 2017**

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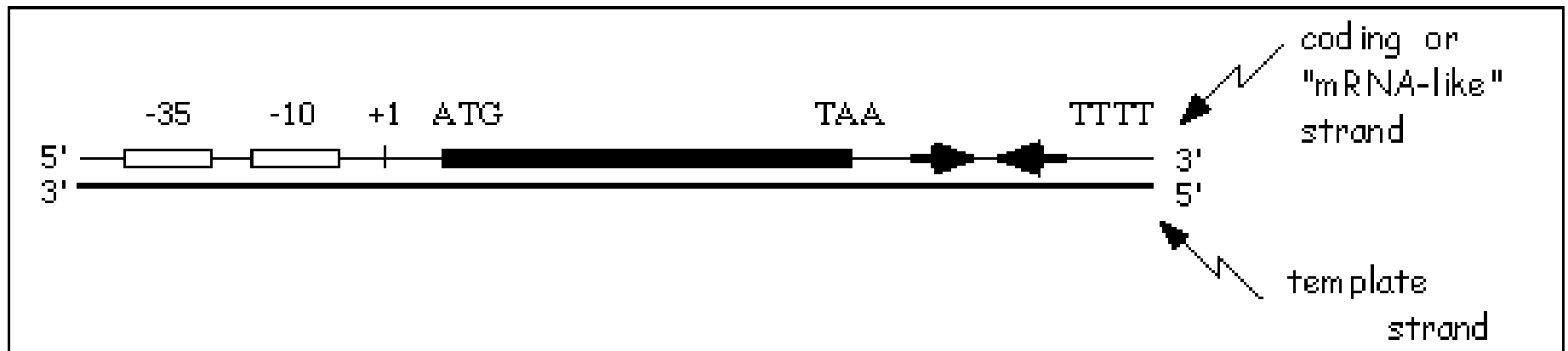
# The Unnamed Sequence

- 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?

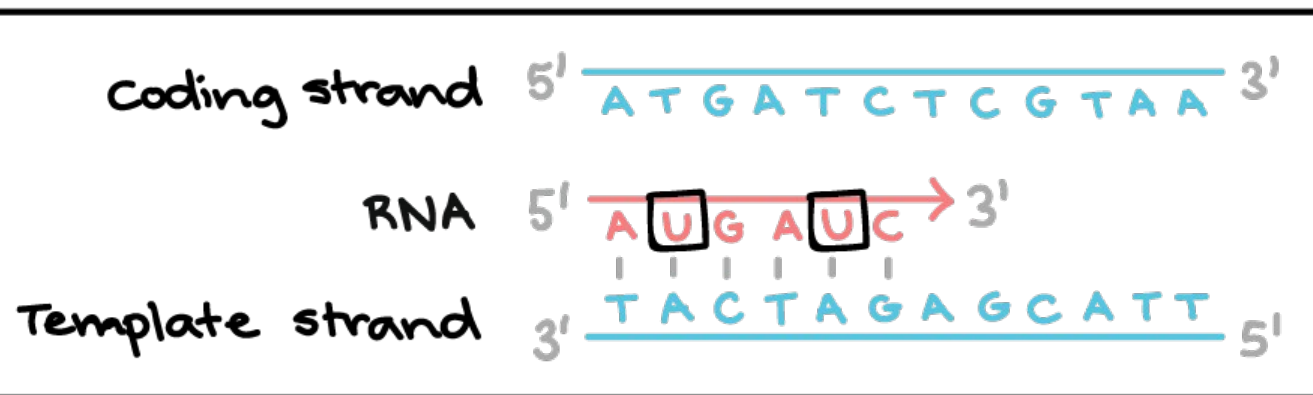
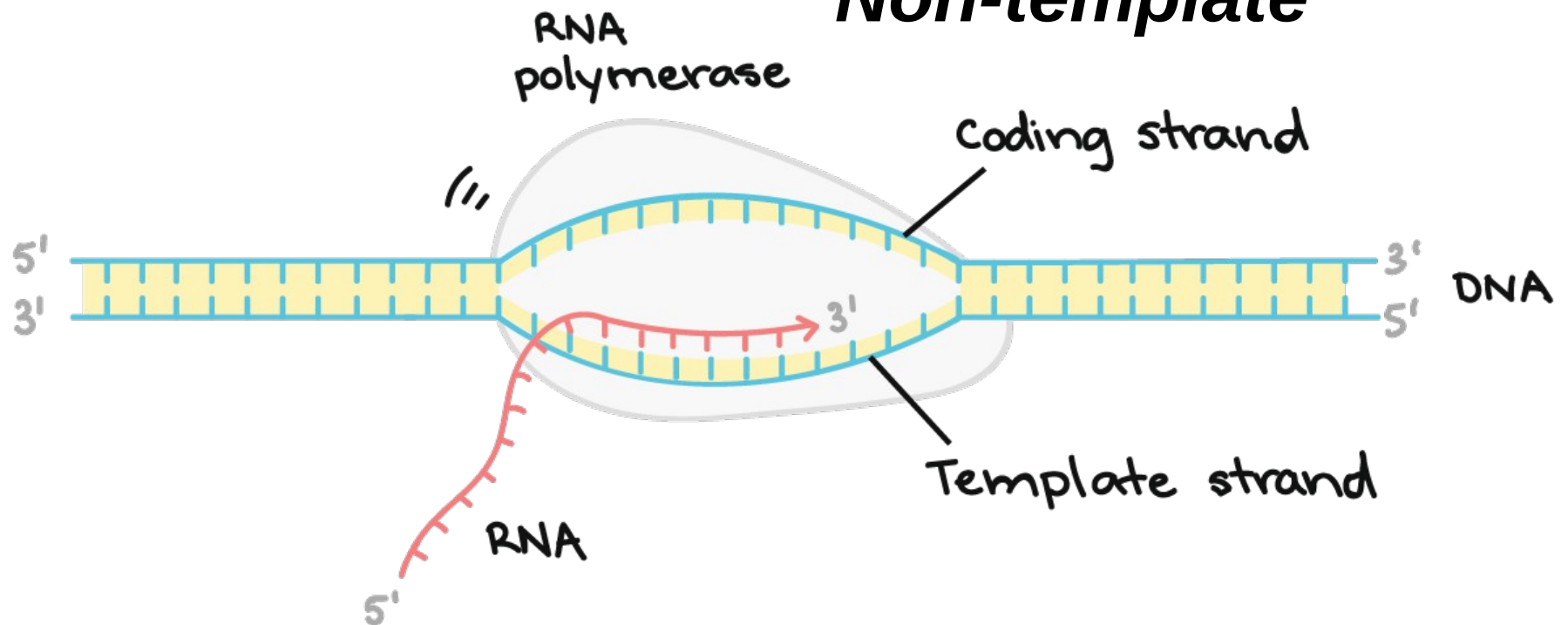


# Template vs nonTemplate

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

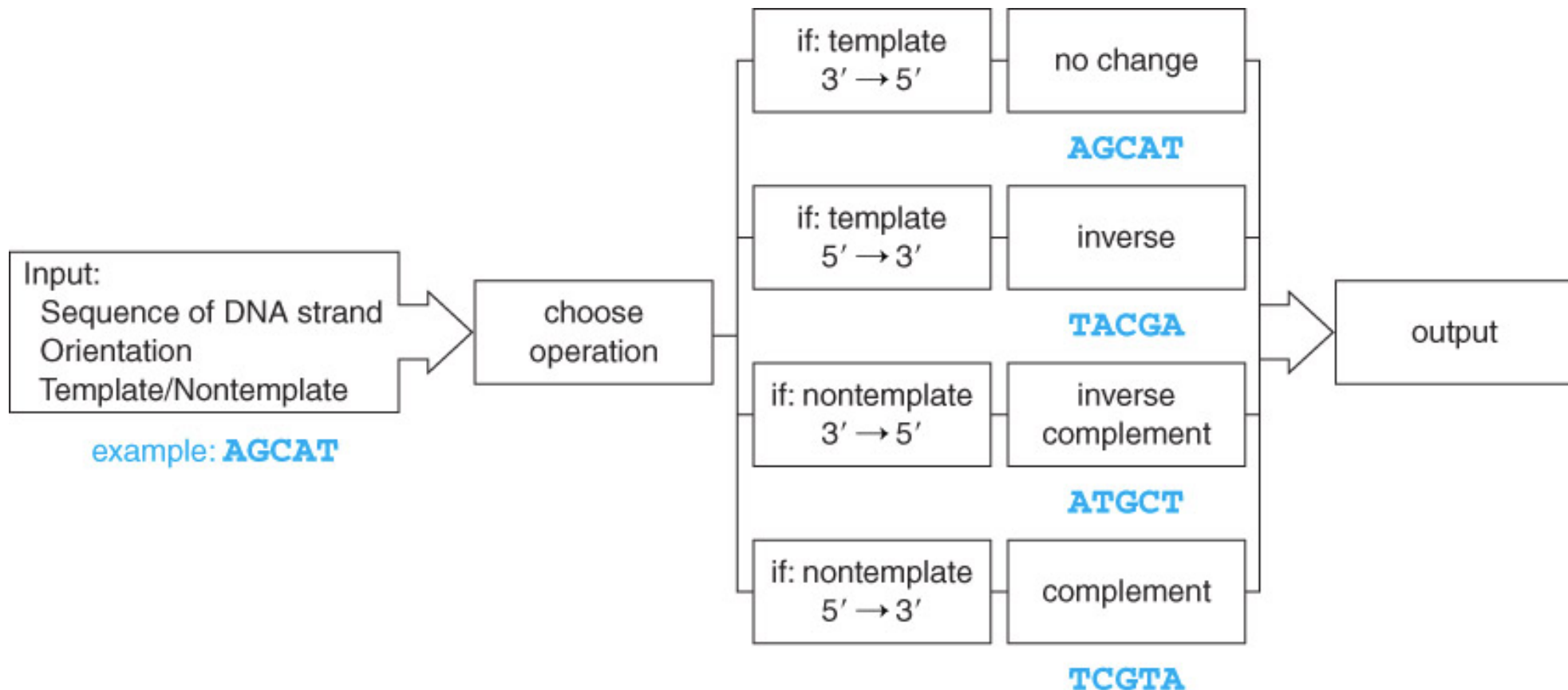


## Non-template



# DNA Manipulation Algorithm

- A series of steps when handling DNA



Output DNA in 3' to 5'



# The DNA Manipulation Algorithm

1. Input a DNA sequence, including details of being a template or non-template strand as well as its orientation
2. Convert to all uppercase
3. Choose the appropriate operation:
  1. If it is the **template** strand and oriented **3' -> 5'**, simply output the same sequence
  2. 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 the string)
  3. 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)
  4. 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)
4. Output the completed sequence, including 5' and 3' end labels



# Transcription Algorithm

- **Input:** **template** strand in the **3' → 5'** orientation
- **Output:** mRNA strand in the **5' → 3'** orientation
  - Traverse the string from left to right
    - add complementary base to the output string
    - (note T is now U)



# Alternative Transcription Algorithm

- **Input:** **non-template** strand in the **5' → 3'** orientation
- **Output:** mRNA strand in the **5' → 3'** orientation
  - Traverse the string from left to right
    - Replace all the T's with U's





# Translation Algorithm

- **Input:** mRNA strand in the **5' → 3'** orientation
- **Output:** amino acid sequence
  - Traverse the string looking at one codon at a time
  - Add one amino acid corresponding to the protein sequence.



# 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 base	2nd base								3rd base
	T		C		A		G		
T	TTT	(Phe/F) Phenylalanine	TCT	(Ser/S) Serine	TAT	(Tyr/Y) Tyrosine	TGT	(Cys/C) Cysteine	T
	TTC		TCC		TAC		TGC		C
	TTA		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
C	CTT	(Leu/L) Leucine	CCT	(Pro/P) Proline	CAT	(His/H) Histidine	CGT	(Arg/R) Arginine	T
	CTC		CCC		CAC		CGC		C
	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	T
	ATC		ACC		AAC		AGC		C
	ATA		ACA		AAA	(Lys/K) Lysine	AGA	(Arg/R) Arginine	A
	ATG <sup>[A]</sup>	(Met/M) Methionine	ACG		AAG		AGG		G
G	GTT	(Val/V) Valine	GCT	(Ala/A) Alanine	GAT	(Asp/D) Aspartic acid	GGT	(Gly/G) Glycine	T
	GTC		GCC		GAC		GGC		C
	GTA		GCA		GAA	(Glu/E) Glutamic acid	GGA		A
	GTG		GCG		GAG		GGG		G



# Python Programming

- Biopython
- DNA Manipulation Algorithm
- Translation functions
  - DNA → RNA
  - RNA → DNA
  - RNA → Protein

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



python