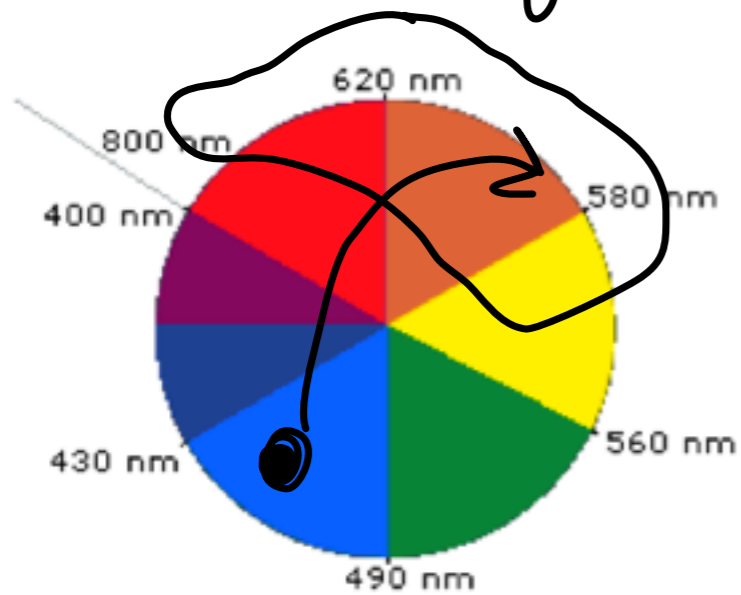


MID2: Diagnostic Primer Design

2/11/14

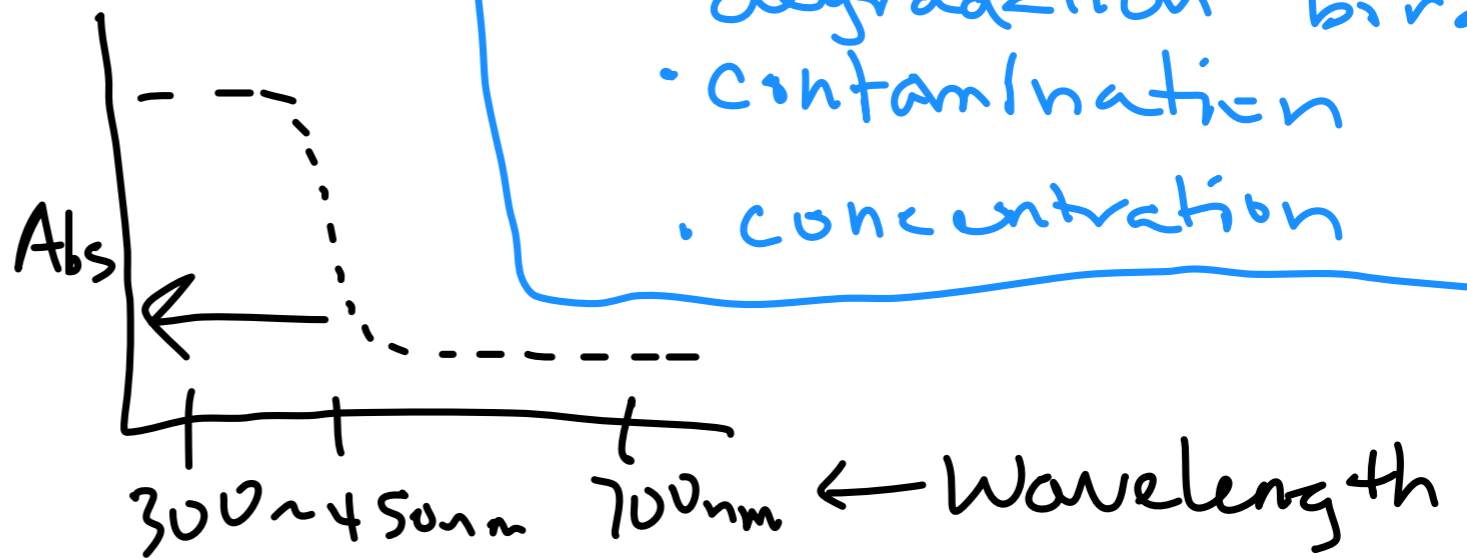
ROY
GBV



Announcements

Why coaxed samples?

- more info about
- degradation bird
- contamination
- concentration



$$V_T = 100 \text{ mL}$$

2% SDS

0.5 M NaOH

want. 0.2% SDS / 200 mM NaOH

$$C_1 V_1 = C_2 V_2$$

$$(2\%)(X) = (0.2\%)(100 \text{ mL})$$

$$X = 10 \text{ mL SDS}$$

$$C_3 V_3 = C_2 V_2$$

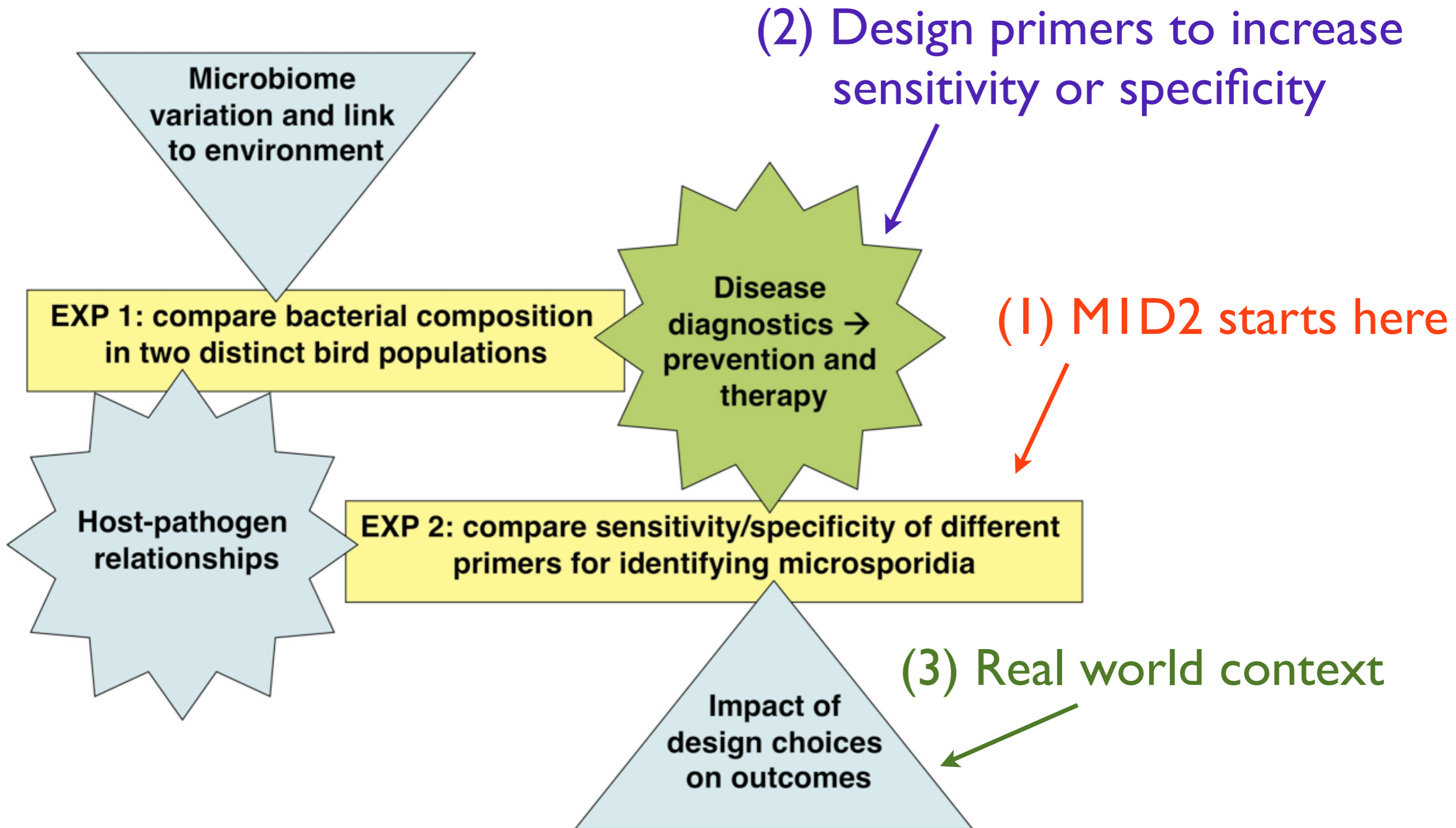
$$(0.5 \text{ M})(Y) = (0.2 \text{ M})(100 \text{ mL})$$

$$Y = 40 \text{ mL NaOH}$$

50 mL H₂O

$$(100 - 40 - 10) \uparrow$$

Module I Overview & Outline for lab today



(I) MID2 Starts Here 1957

< 3 Mbp
~ 2000 proteins

Microsporidia

No mitoch. | No home!
~2001 (genome seq.)

G = germinated spore
U = ungerminated spore
PT = polar tube

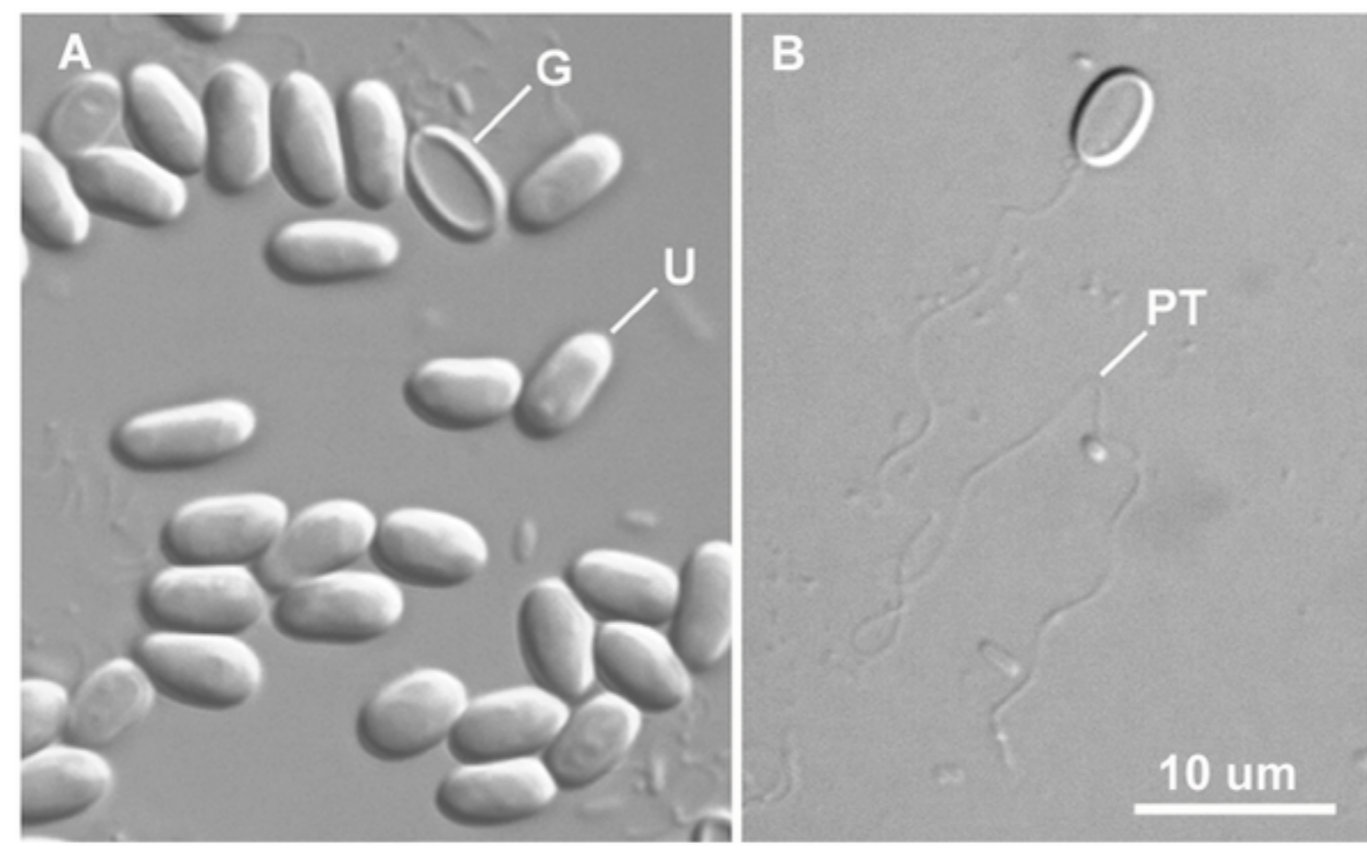


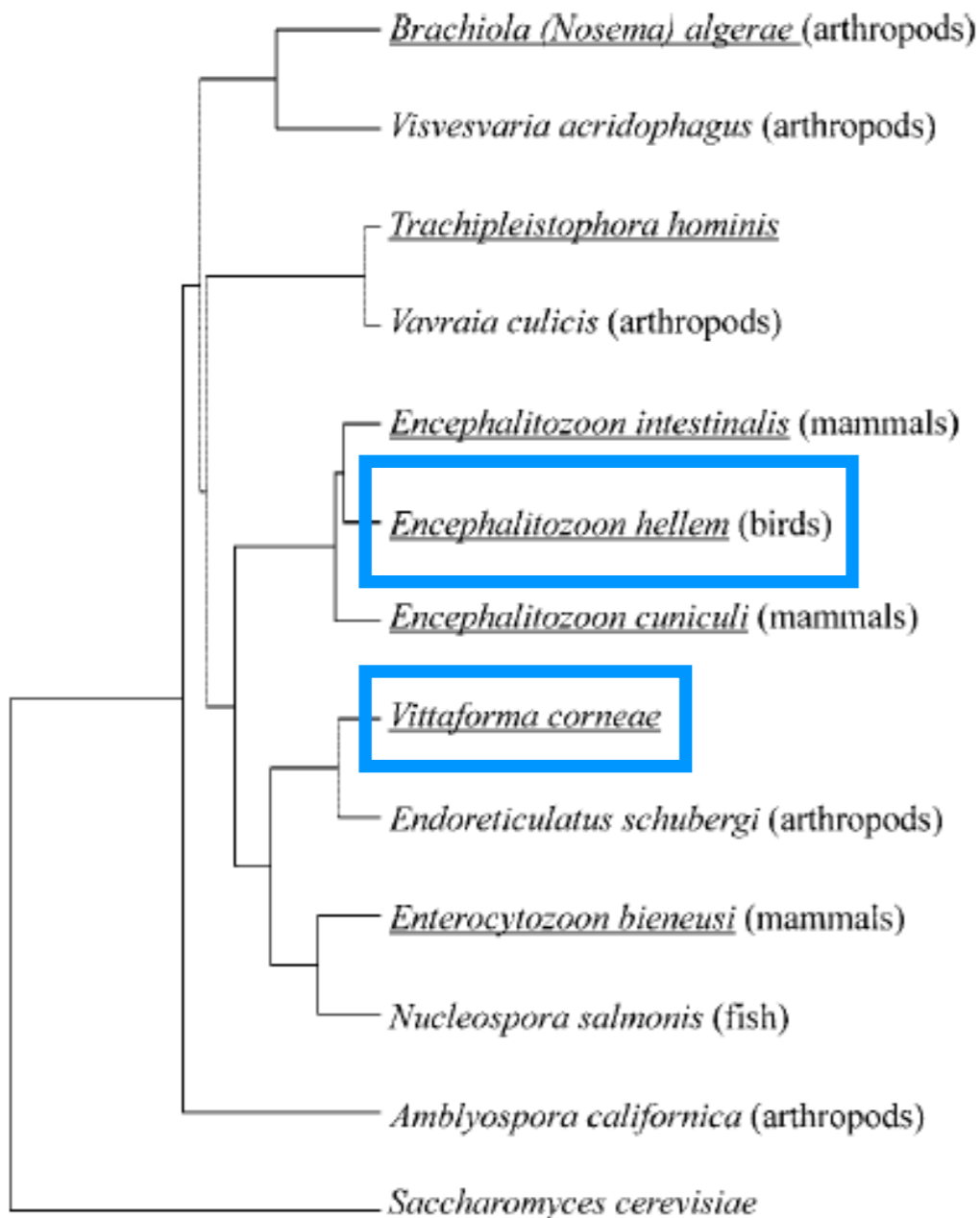
Image from: <http://www.plospathogens.org/article/info%3Adoi%2F10.1371%2Fjournal.ppat.1000489>

This is a free resource that has great information about microsporidia in a friendly format.

microsomes
HSP70
★ Fungus

We will work with DNA from two species of microsporidia:
Encephalitozoon hellem (or *E. hellem*)
Vittaforma corneae (or *V. corneae*)

(I) MID2 Starts Here



- ◆ μ sporidia are most closely related to fungus.
- ◆ μ sporidia are obligate intracellular meaning they require a host for survival. *organisms*
- ◆ That requirement allowed: *simplify their genome*
- ◆ What hosts?
 - ◆ See tree to the left -- common hosts for μ sporidia species are in brackets.
 - ◆ Those identified in human infections are underlined.

10 substitutions per 100 residues

FIG. 2. Dendrogram generated from the small subunit ribosomal RNA (ssrRNA) gene of microsporidian species identified in humans (underlined) and selected other species (Kimura's distance, unweighted pair group method of analysis). Known animal hosts are indicated in brackets; the brewer's yeast *Saccharomyces cerevisiae* serves as an outgroup. No corresponding gene sequences are known for the human-infecting microsporidian species *Pleistophora ronniae*, *Trachipleistophora anthropophthera*, *Brachiola* (formerly *Nosema*) *connori*, *B. vesicularum*, *Nosema ocularum*, *Microsporidium ceylonensis*, and *M. africanum* (Table 1).

Dendrogram generated from the ssrRNA gene of microsporidian species

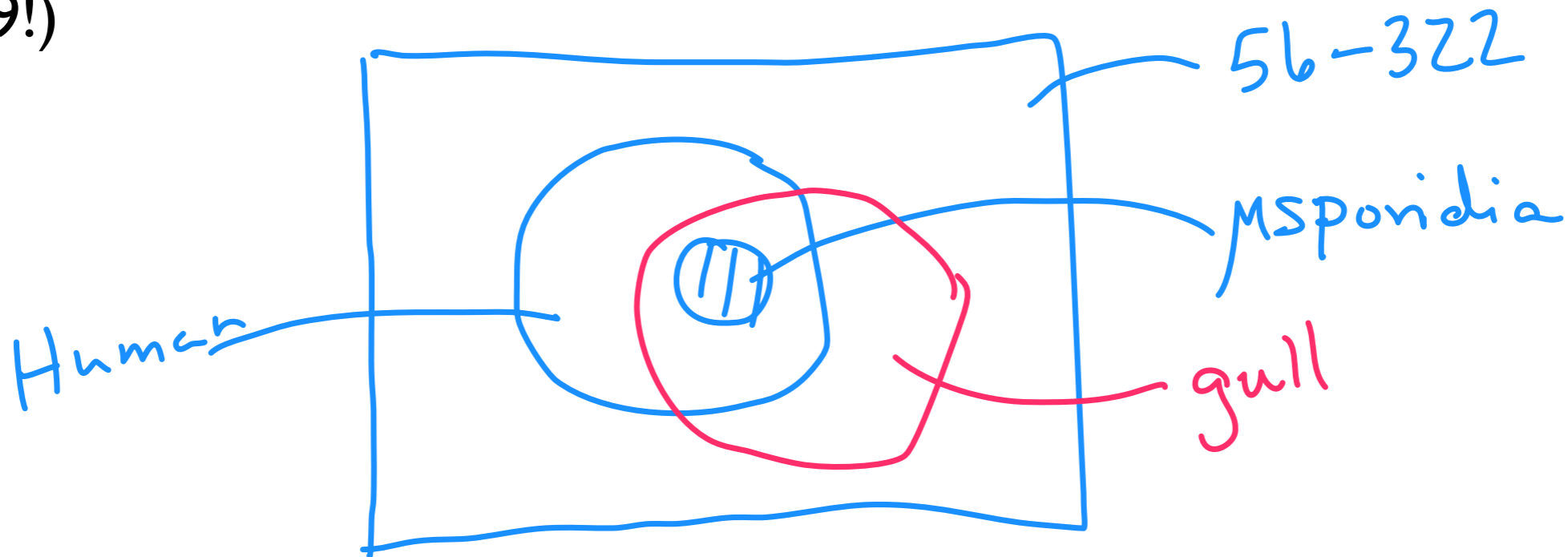
(3) Real World Context

◆ A couple more things about μ sporidia:

1. Humans infected with μ sporidia share a common trait -- weak immune systems

- ◆ HIV or other immunodeficiency diseases (lupus, RA, etc)
- ◆ Cancer patients undergoing treatment

2. μ sporidia are tricky to isolate -- the isolation has been done for you and you will work with purified DNA (this makes the analysis doable for 109!)



(2) Design primers to increase sensitivity or specificity

There are two design challenges for this part of Module 1

1. Selectivity

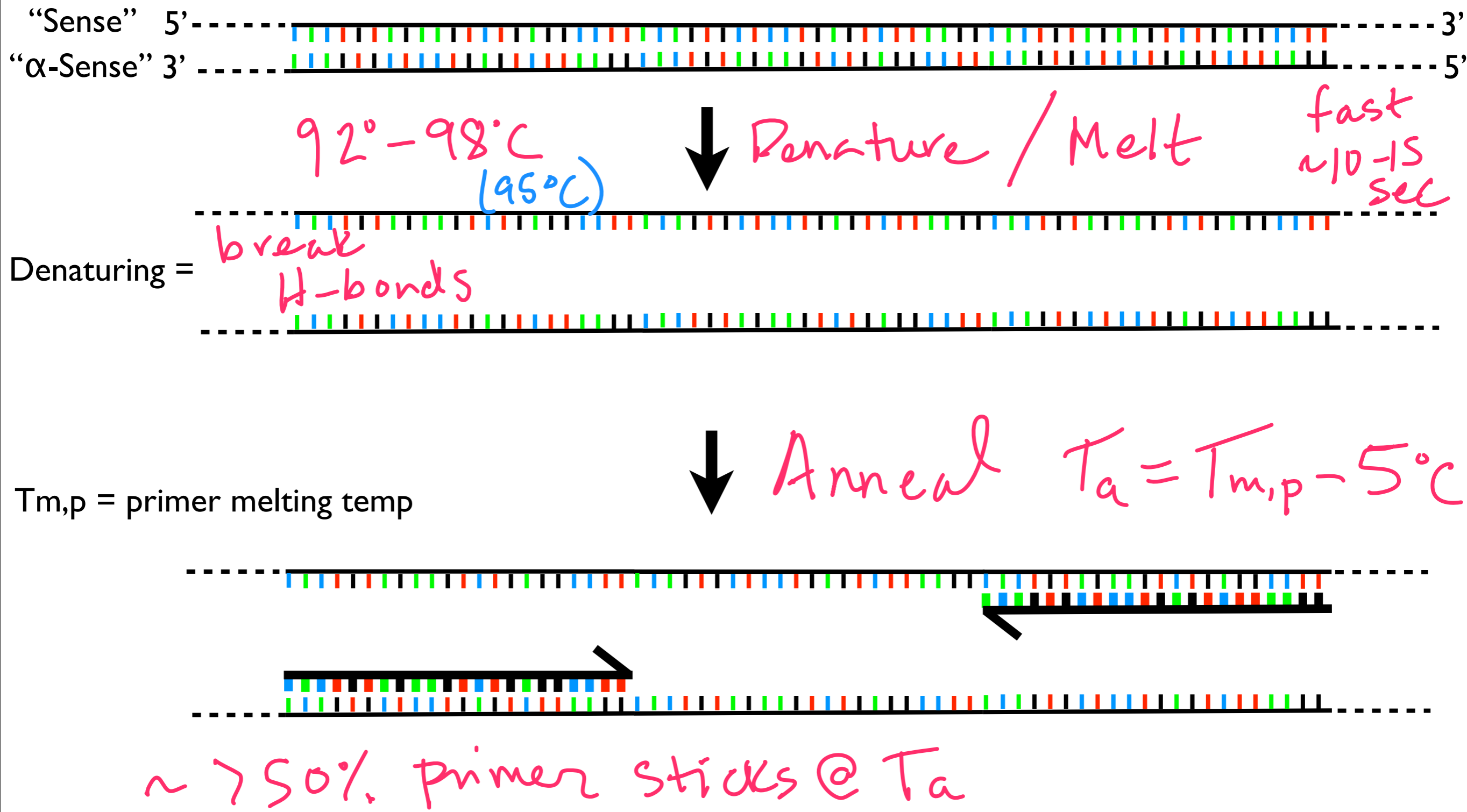
- ◆ Design PCR primers that can differentiate *E. helium* and *V. corneae*

2. Sensitivity

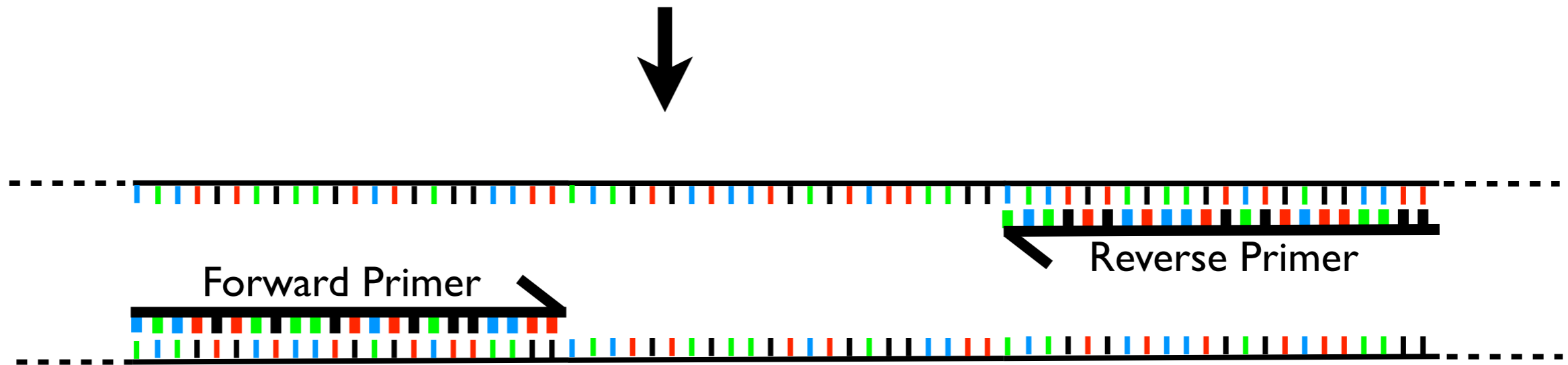
- ◆ Design PCR primers that can improve detection.
★ detect both species

Three teams per challenge. Sign up on the 'Talk' page of MID2.

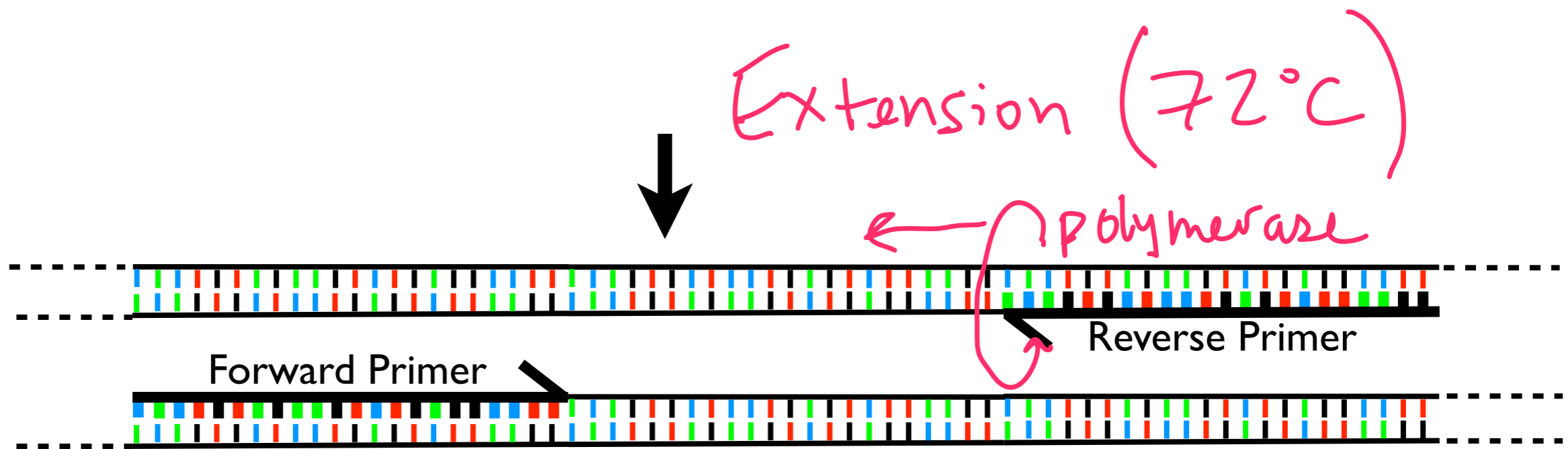
(2) Design primers to increase sensitivity or specificity



Ta < Tm,p
Why?



Extension
temp is:



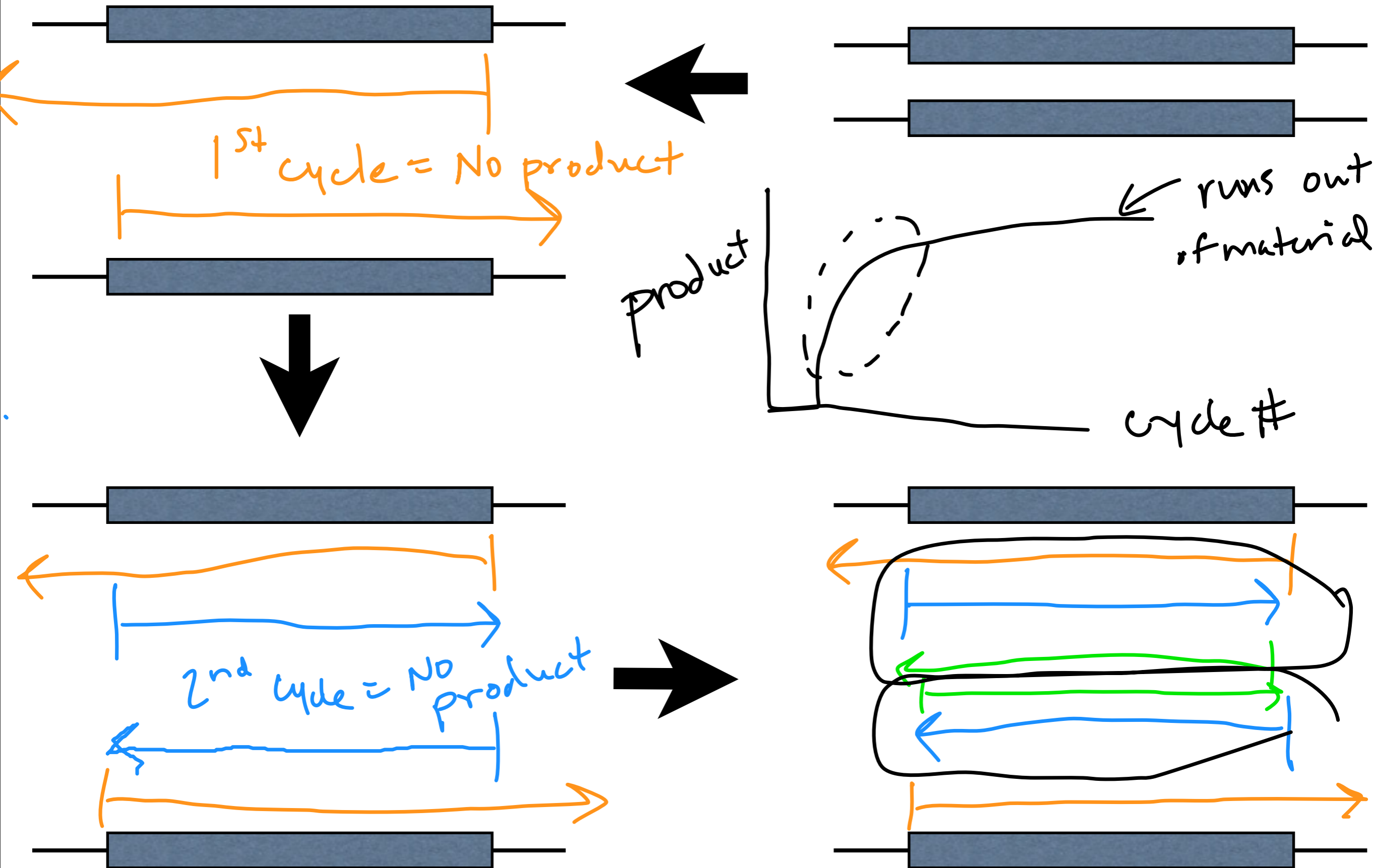
Extension (72°C)

← polymerase

1 min / 1000 bp

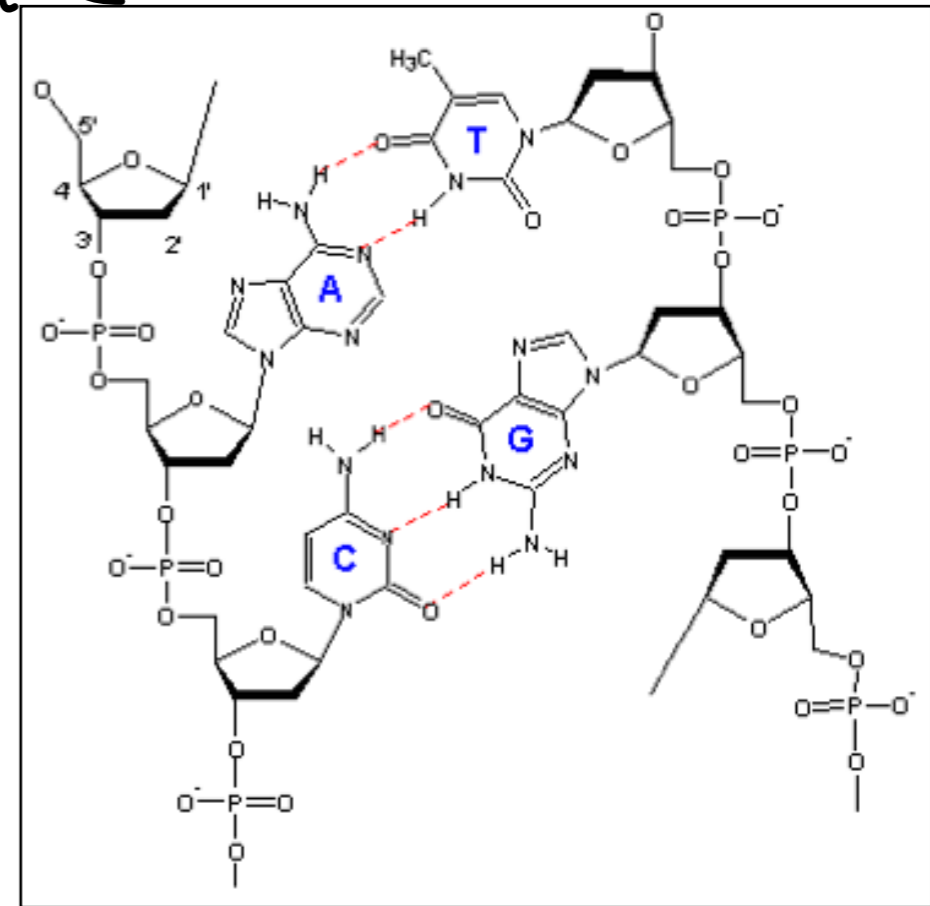
< 500 bp

(2) Design primers to increase sensitivity or specificity: First three rounds of PCR



(2) Design primers to increase sensitivity or specificity: Primer Design Basics

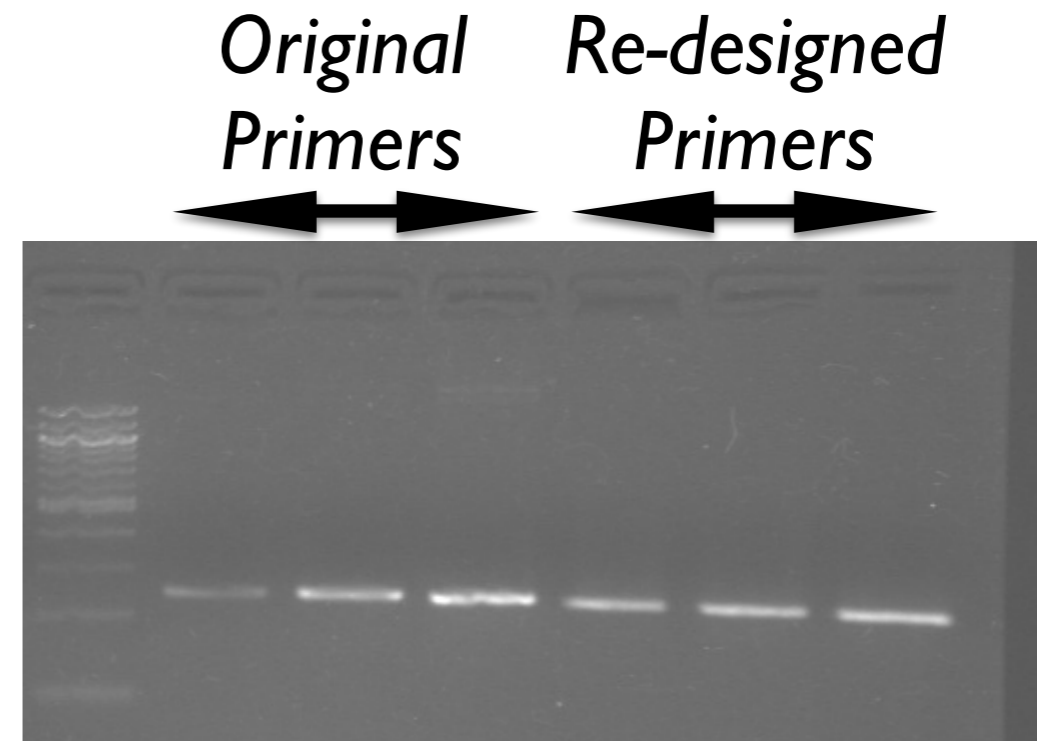
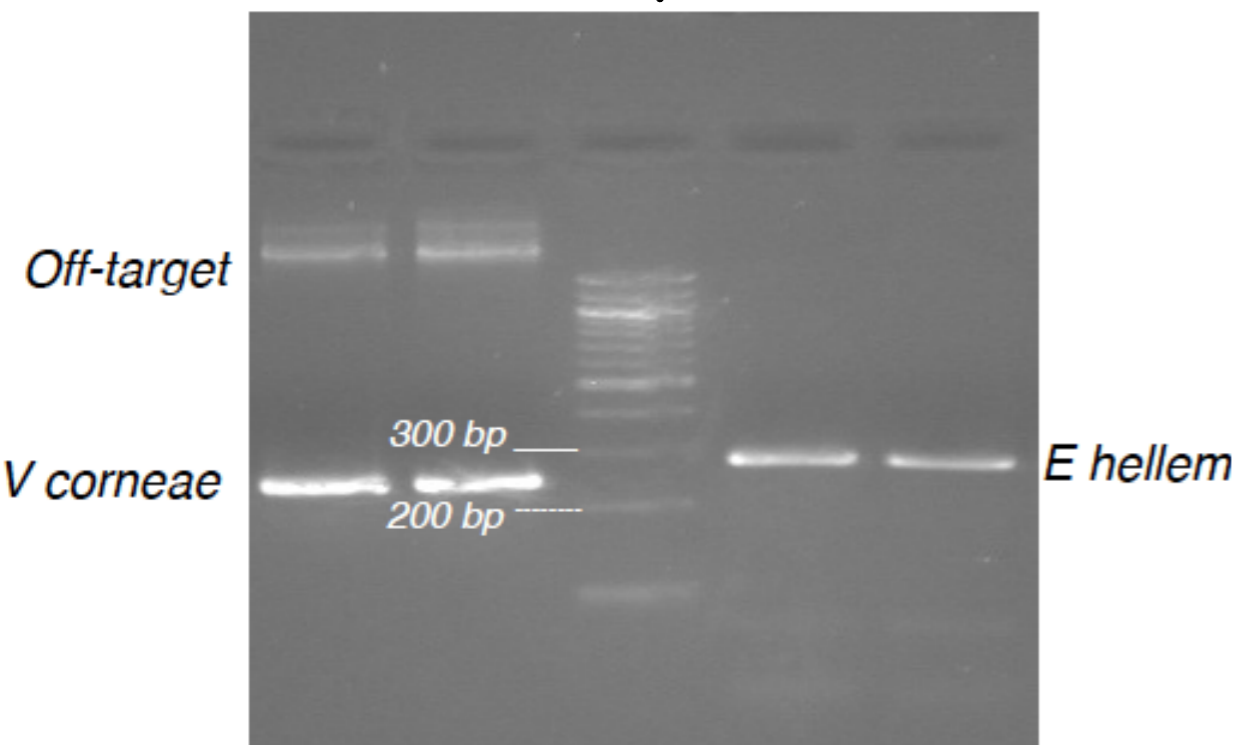
- Length (17-28 bp) $\sim 3 \times 10^9$ bp
primer 10 bp
- Melting Temp $\left\{ \begin{array}{l} \text{G/C} \\ \text{content} \end{array} \right. \sim 4^{10} \sim 10^6$ bp
- TATATATA $\left\{ \begin{array}{l} \text{thermodynamics} \\ \text{secondary structure} \end{array} \right.$
- $\left\{ \begin{array}{l} \text{low M} \\ \text{"off-target"} \end{array} \right.$
- CAGT \sim ACTG $\left\{ \begin{array}{l} \text{priming} \\ \text{hairpin} \end{array} \right.$
- G/C clamp 3' \rightarrow promote polymerization



(2) Design primers to increase sensitivity or specificity: What we'll do next

You design → We order → You prep primers (D5) →
We run PCR → You analyze via electrophoresis (D7)

current primer set



*Note: Sensitivity challenge must detect both
Species

MID2 Part I explanation

OligoAnalyzer 3.1

Instructions | Definitions | Feedback

Sequence # Bases 21
5'-CCTCTCCGGAACCAAACCCTG

Target Type DNA

Oligo Conc 0.25 μ M

Na⁺ Conc 50 mM

Mg⁺⁺ Conc 0 mM

Analyze

Hairpin

Self-Dimer

Hetero-Dimer

NCBI Blast

TM Mismatch

Clear Sequence

Results

5' mods

Internal Mods

3'

HOMO-DIMER ANALYSIS ?

Dimer Sequence

5' - CCTCTCCGGAACCAAACCCTG -3'

Maximum Delta G -43.97 kcal/mole

Delta G -12.9 kcal/mole

Base Pairs 6

IDT Website: "You can also compare the value of the maximum delta g (the delta g for a perfect duplex) to that of each individual self dimer. If the values are within 10% of each other, you should redesign. Heterodimer analysis works the same way."

Lab Quizzes

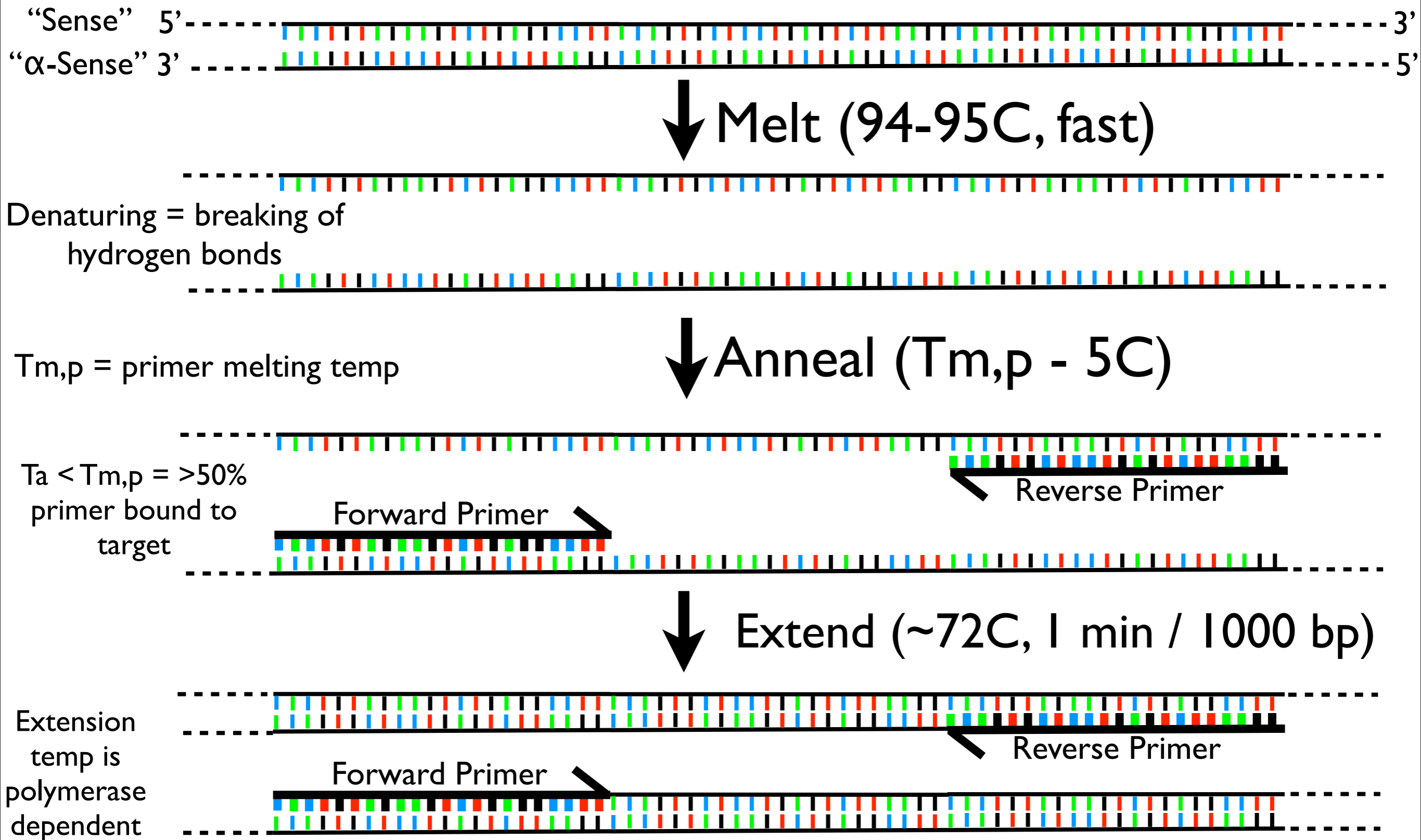
- ◆ Purpose: Continuity and accountability
 1. 10 points
 2. 10 min
 3. Start at 1:05pm
- ◆ First quiz covers MIDI & 2 lecture and lab content
- ◆ See wiki for information on quiz schedule

Today in Lab

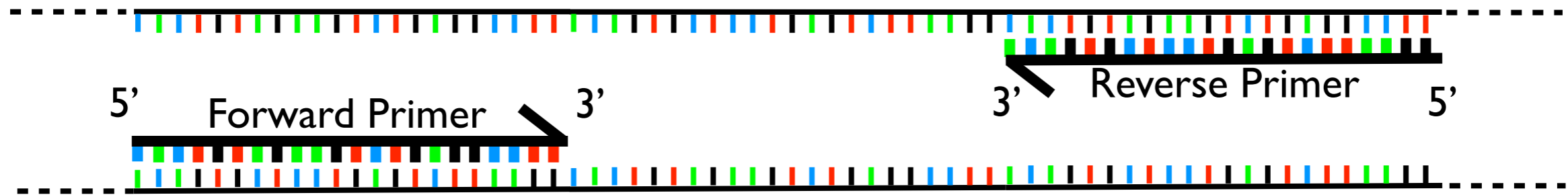
- ◆ Explore existing microsporidia primers
- ◆ Design new primers
 - ◆ Specificity or Sensitivity challenge — sign up on Talk page
- ◆ Start keeping your notebook today!
 - ◆ You should add your design criteria and results to your lab notebook
 - ◆ Primer design information will be used to prepare a *Memo* as part of the written assignment for Mod I (5% of total grade)

For Next Time: Koenig et al PNAS paper discussion + slide preparation/presentation practice + WAC visit

(2) Design primers to increase sensitivity or specificity: A PCR Cycle

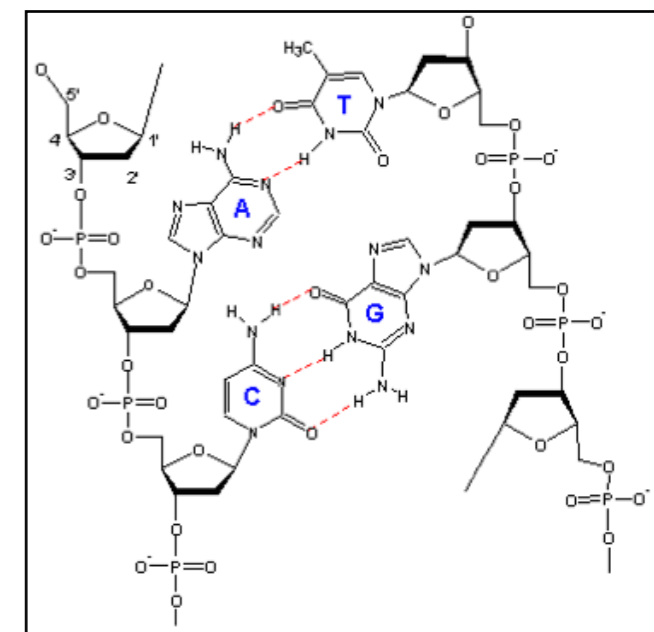


(2) Design primers to increase sensitivity or specificity: Primer Design



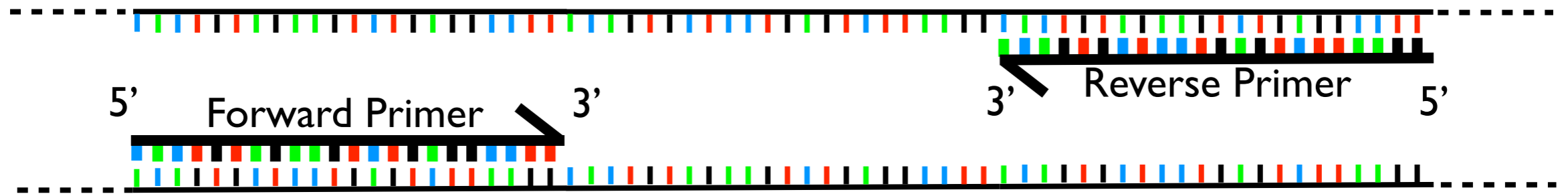
1. The forward primer binds to the α -sense strand (or the 'Template') and 'reads' in an intuitive direction from 5' to 3'. Look at the reverse primer and consider its orientation.
3. Primer length is important to decrease the chances of off-target binding:
 - Consider that the human genome is $\sim 3 \times 10^9$ bp. If we designed primers that were only 10 bp long, we might expect to find that 10bp sequence once in every $4^{10} \approx 10^6$ bp -- a very risky gamble for off target binding.
 - The optimal primer length is > 16 bp for specificity. Think about why.
3. Primer melting temperature should optimally be kept between 55-60 C.
 - $T_{m,p}$ is the temp $\sim 50\%$ of the primer is double vs. single stranded.
 - The melting temperature will be higher with increased G/C content.Why? Look at the diagram of bp hydrogen bonding to the right -- which pair requires more energy to denature? *Also explains why optimal primer design calls for only 40-50% of the bp to be G/C.*

The $T_{m,p}$ is kept between 55-60C so that the annealing (hybridization) step is optimally efficient.



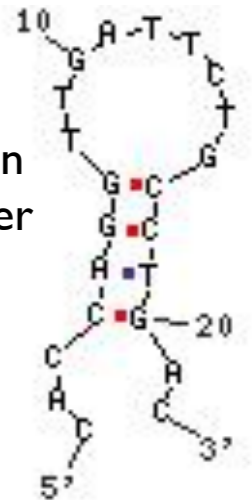
Thermodynamics of DNA Duplex, New Mexico State University

(2) Design primers to increase sensitivity or specificity: Primer Design



4. Avoid long repeats of one type of bp (ex. ATATATA) or one bp individually -- especially TTTT -- remember the polyA tail on pre-mRNA? This can lead to non-specific priming.
5. Consider secondary structure of your primer.
 - Does the primer have an internal sequence that can bind itself? If so, you can end up with a hairpin structure that will prefer (energetically speaking) to bind to itself and not your target sequence.

Making a hairpin with your primer is bad.



In fact, this behavior of DNA has been harvested to make higher order structures: DNA Origami is an active area of research.

DNA Origami is cool.

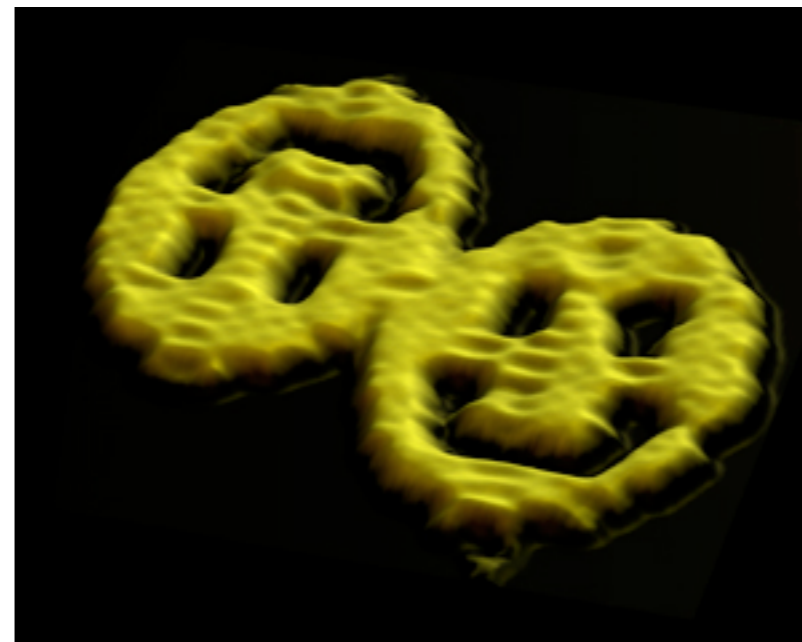
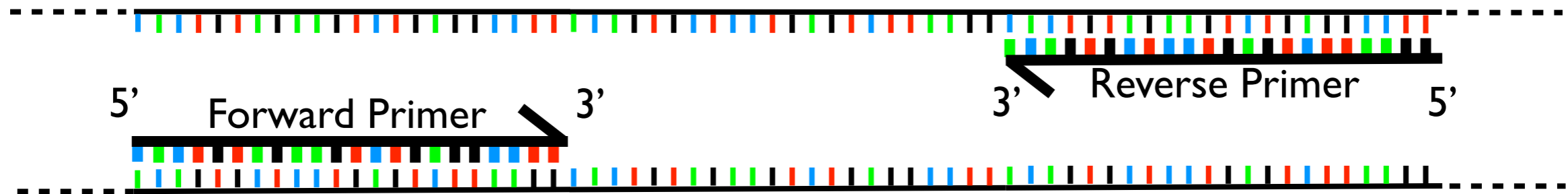


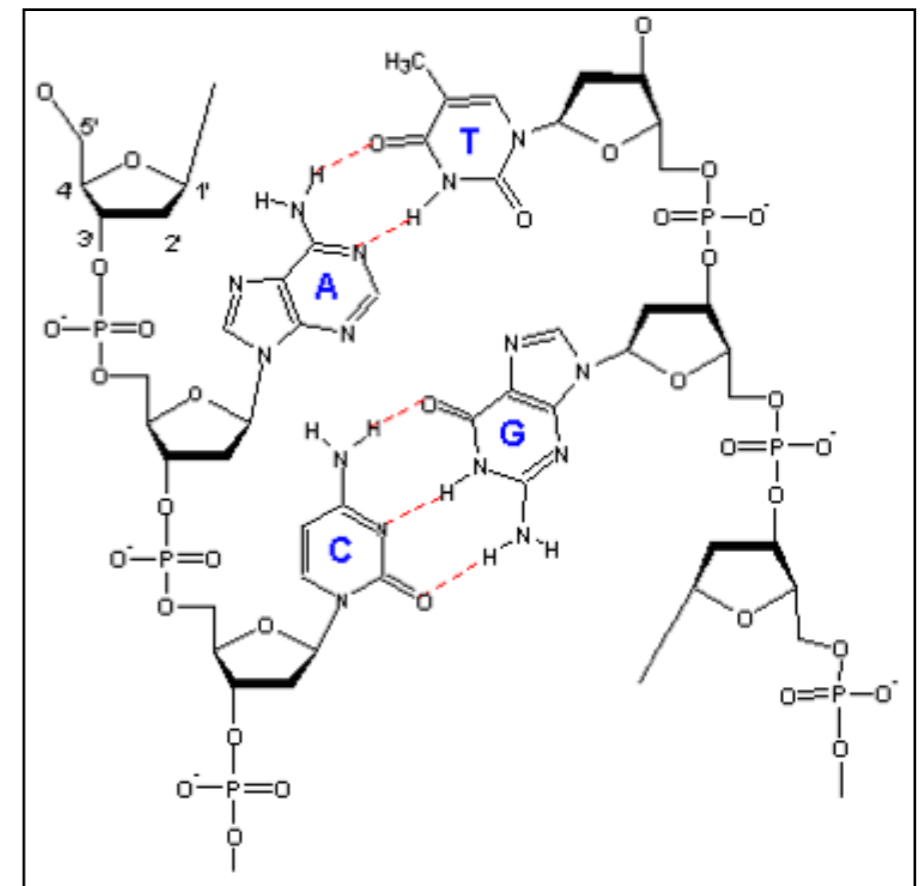
Image from: <http://www.dna.caltech.edu/~pwkr/>

(2) Design primers to increase sensitivity or specificity: Primer Design



6. Tip the deck in your favor: Add a GC clamp to the 3' end if possible.
- Consider again the image below. G/C binding is more stable and can help to increase efficiency of polymerase binding at the 3' end to promote extension.
 - But don't go overboard! > 5 G/C pairs won't help you.

I have also found this website useful: http://www.premierbiosoft.com/tech_notes/PCR_Primer_Design.html



Thermodynamics of DNA Duplex, New Mexico State University