

## DNA

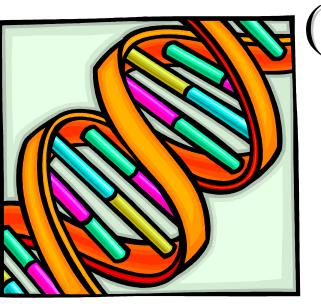
# Computing

#### **Sources**

Richard Spillman, Prateek Tandon, Lars Schäfer, Julian Miller, Thierry Metais, Westcott, Sanders Chong, Craig Jacobs, Daniel McFarlin, Russell Deaton, Charlie Moad, W. Joel Strait, Junghuei Chen, Byoung-Tak Zhang, Anton Lopatinsky, Nicholas Carter.

# Biological Computing Biochemical Computation

Computation Using DNA Molecules



(Bio)Molecular Computing

**DNA Computing** 

### **Outline**

- What Is Biological and what is Molecular Computing?
- What is DNA?
- DNA Computing Operators
- DNA Computing
- Examples
  - Hamiltonian Path of Adleman
  - Traveling Salesman
  - Molecular Theorem Proving
  - Molecular Optimization
- DNA versus Silicon
- The Difficulties of DNA Computers
- Applications of DNA Computing
- Future of DNA computing
- Conclusions
- Information Sources and Exam Problems

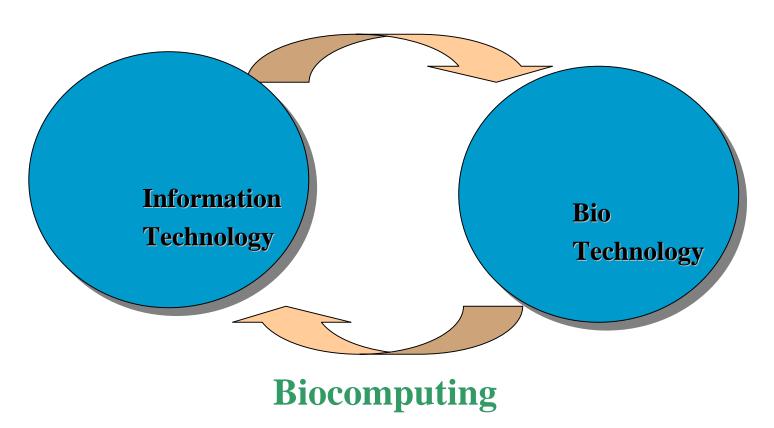


## Whatis

# Molecular Computing?

### Biocomputing vs. Bioinformatics

#### **Bioinformatics**



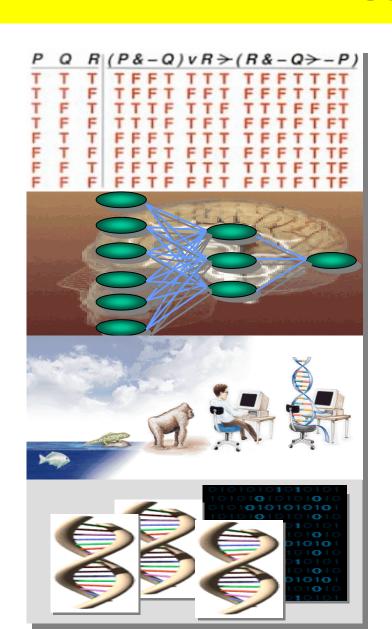
### Artificial Intelligence (AI) and Biology

Symbolic AI
Rule-Based Systems

**Connectionist AI Neural Networks** 

**Evolutionary AI Genetic Algorithms** 

Molecular AI:
DNA Computing

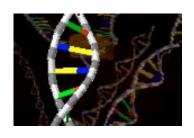


## Nanotechnology

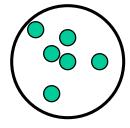
We are at the point of connecting machines to individual cells



Atoms <1 nm



**DNA** ~2.5 nm



Cells thousands of nm

# Introduction to Molecular Biology

- In order to sustain life, biological systems have developed the ability to:
  - to build three-dimensional molecules that assist in the critical functions of life (proteins, RNA).
  - to compress the information about how (and when) to build these molecules in a linear code (DNA).

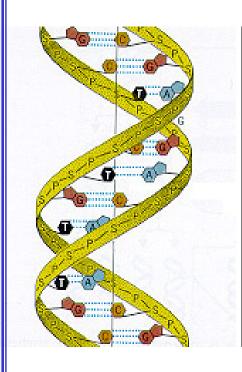
# Broad Generalization: Proteins versus DNA

#### • Protein molecules:

- do the work,
- their 3D structure is critical.

#### DNA molecules:

- store the information,
- don't do much work,
- their 3D structure is incidental.



### Protein Molecules

- Protein molecules are made up of linked subunits
  - These subunits are amino acids (also called protein residues for historical reasons).
- There are 20 different amino acids with different physical and chemical properties.
- The interaction of these properties allows a chain of the amino acids (upto 1000's long) to <u>fold into a unique</u>, reproducible 3D shape.

### DNA Action

- The sequence of amino acids is determined by DNA
- DNA uses an alphabet of 4 letters (A,T,C,G), more commonly called bases.
  - Although the 4 letters have interesting chemical structure, for our purposes they are just information carriers.
- Long sequences of these 4 letters are linked together to create GENES and CONTROL INFORMATION.

### Enzymes

- Enzymes are biochemical catalysts
- Enzymes can:
  - cut,
  - copy,
  - paste,
  - error-check **DNA** (c.f. AND, OR, NOT, XOR, Rotate, Compare...?)
- Parallelism:
  - Enzyme molecules <u>do not act sequentially</u>
    - many enzyme molecules <u>act on many</u> DNA molecules at the same time

# Mass Parallel operation of Enzymes

- Enzymes can work on many DNA nucleotides at once.
- The problem of replicating speeds up exponentially, and is a quite reliable process.

### Genetic Code

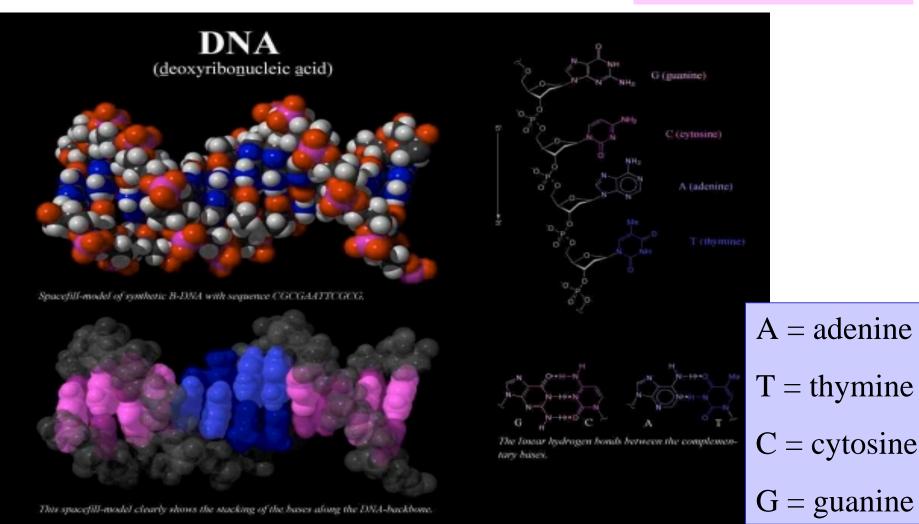
- Each of the twenty protein amino acids can be specified by 3 consecutive DNA bases.
- A cellular apparatus can:
  - "read" a sequence of DNA bases (three at a time) and
  - create the corresponding protein chain—which folds itself based on the amino acid properties.
- The 64 mappings of 3 bases to 1 amino acid is called the GENETIC CODE
- This code is universal (on earth...).
- Present in nearly all living organisms
  - Some bacteria and viruses use RNA

### Cells (and DNA) as Computers and Memories

#### Cells process and store information

- **DNA** stores the information for the construction of proteins
- This information is preserved and past on to other generations
- DNA serves as memory:
  - RNA performs a memory access,
  - ribosomes serve as processors

• The life's molecule:



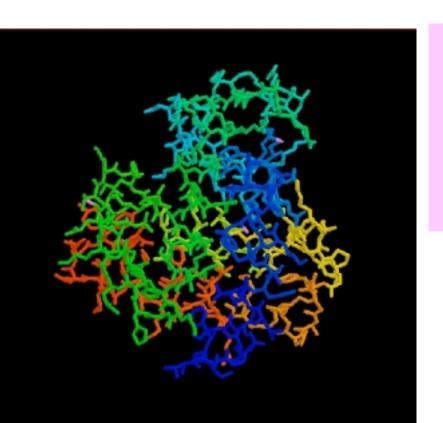
#### Gene for Myoglobin

### Myoglobin Gene

ctgcagataa ctaactaaag gagaacaaca acaatggtte tgtetgaaggtgaatggcag etggttetge atgtttggge taaagttgaa getgaegteg etggteatgg teaggaeate ttgattegae
tgttcaaate teateeggaa actetggaaa aattegateg tttcaaacat etgaaaactg aagetgaaat gaaagettet gaagatetga aaaaacatgg tgttaeegtg ttaaetgee taggtgetat
cettaagaaa aaagggeate atgaagetga geteaaaceg ettgegeaat egeatgetae taaacataag ateeegatea aataeetgga atteatetet gaagegatea teeatgttet geattetaga
cateeaggta aetteggtge tgaegeteag ggtgetatga acaaagetet egagetgtte egtaaagata tegetgetaa etgggttaee agggttaatg aggtaee

#### - BASE COUNT 155 a 108 c 115 g 129 t

- Myoglobin Protein sequence
  - MVLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEM KASEDLKKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHV LHSRHPGNFGADAQGAMNKALELFRKDIAAKYKELGYQG



# Myoglobin Protein

A = adenine

T = thymine

C = cytosine

G = guanine

### What is Biological Computing?

- Using biological processes to perform computation
  - Most efforts focus on DNA-based reactions

- Tremendous parallelism
- Slow cycle times
  - Biological gates may operate at mili-Hertz frequencies
- Leverage <u>ability of biological processes</u> to manipulate matter at the molecular level
- Biological Computing is also an Interface with an organism that is studied and/or manipulated

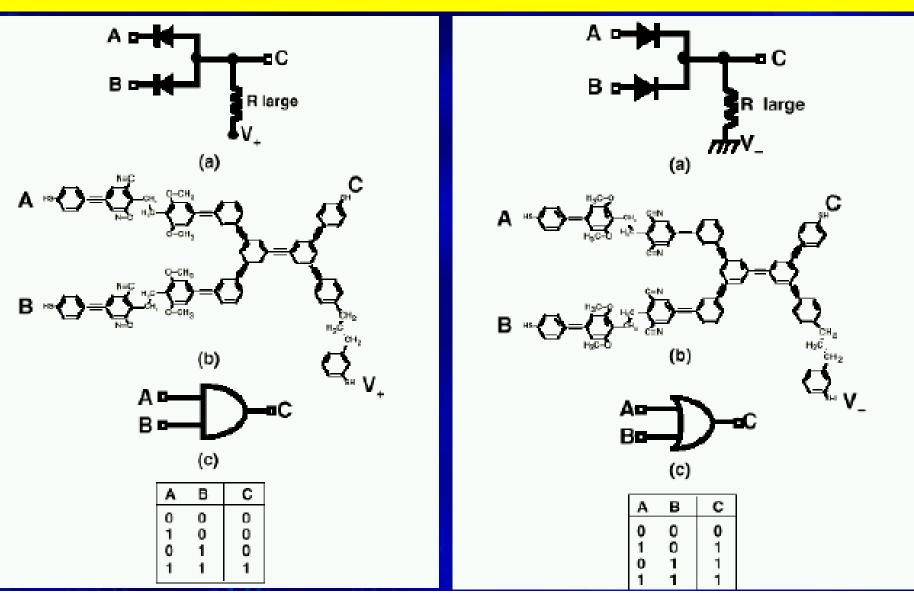
# Approach 1: Construct Logic Gates Within Cells

• Basic question: Can we use biological processes within cells to implement logic gate-like functions?

#### • Things to consider:

- What to use to carry signals?
  - Need to be able to generate
  - Need to be able to use as input
  - Need underlying process with high gain for 0-1 mapping
- How to input signals to the system?
- How to read outputs?

### Molecular Electronics: AND Gate, OR Gate



• Picture form MITRE Corp

### First Approach: Results

- Use <u>levels</u> of specific <u>proteins as signals</u>
  - Have minimum and maximum concentrations
  - Can "program" cells to produce them
  - Relatively independent multiple signals within a cell
- Chemical reactions give good **inverter-like** response
  - High gain
  - Saturation at 0 and 1
  - Relative insensitivity to operating conditions
  - Use different dimers to control "gain"

#### Issues

- Slow (mili-Hertz)
- No demonstratiof actual implementation
- Application
  - Use of cells to fabricate nanotech-scale devices

# Approach 2: Use DNA to Perform Computations

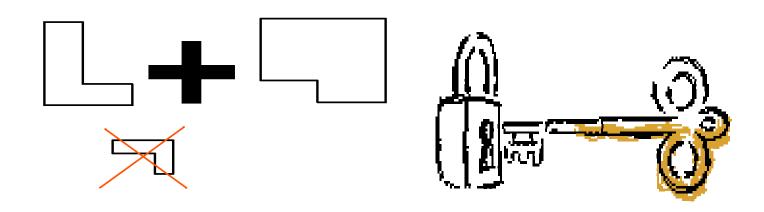
- This is what people generally talk about when they talk about biological computing
- Basic Idea:
  - Encode all possible inputs to an operation as strands of DNA,
  - then sort out input strands that match a particular criterion
    - Useful for "search" problems, which tend to be NP-complete
    - Vast parallelism many strands of DNA/tube
    - Relatively slow -- ~15 minutes/step

# What is Molecular Computing?

The use of biological molecules, primarily DNA, DNA analogs, and RNA, for computation purpose.

### What is Molecular Computing?

- **Answer:** Systems in which **macromolecules** mediate information-processing: *e.g. biological organisms*
- Macromolecules are mostly <u>proteins</u>, <u>DNA</u>
- Underlying principle: Macromolecules can <u>recognize</u> <u>specific molecules</u> using physiochemical content (*lock-key* model)



### What is DNA computing?

- History of DNA computing.
  - Around 1950 first idea (precursor Feynman)
  - First important experiment 1994: Leonard Adleman
  - Massive Parallelism through simultaneous biochemical reactions
    - The concept of base used for computing
    - In a liter of water, with only 5 grams of DNA we get around  $10^{21}$  bases!
    - Each DNA strand represents a processor!
  - In Vitro Selection and Evolution
  - Satisfiability and Hamiltonian Path as examples

### What is DNA computing?

- Molecular level (just greater than 10<sup>-9</sup> meter)
- DNA can perform computations
  - Huge information <u>storage density</u>
    - Stores information (up to 10<sup>8</sup> TByte in 1 liter)
  - Allows manipulation
- DNA is tiny and "fast"
  - New computing paradigm:
    - Try all possible solutions (parallel)
    - Remove wrong solutions

### DNA Computing is A Different Approach

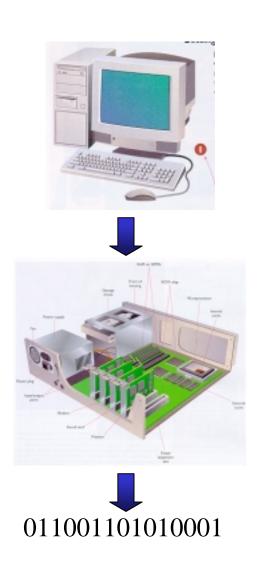
#### What DNA computing is:

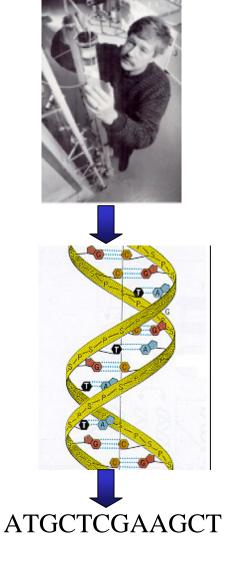
- a completely new method among a few others
   (e.g., quantum computing) of general computation alternative to electronic/semiconductor technology
- uses biochemical processes based on DNA

#### What DNA computing isn't:

not to confuse with <u>bio-computing</u>
 which applies biological laws (evolution, selection)
 to computer algorithm design.

### **DNA Computing**





# DNA Computing: What are the Advantages?

- 1. Computes in parallel
- 2. Compact information storage
- 3. Low energy consumption

....it is possible thanks to......

- Great advances in molecular biology and laboratory techniques:
  - PCR (Polymerase Chain Reaction)
  - DNA Microarrays
  - New enzymes and proteins
  - Better understanding of biological molecules
- Ability to produce massive numbers of DNA molecules with specified sequence and size
- DNA molecules interact through template matching reactions

# What is

# DIVA?

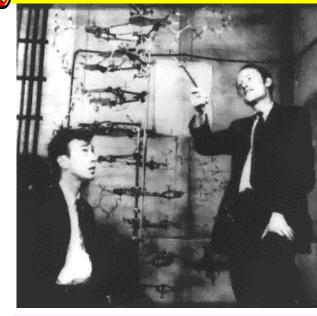
### What is DNA?

- DNA contains the basic information used to replicate cells and proteins
- Protein manufacture is a two-step process:
  - 1. Information in DNA is copied into RNA
  - 2. RNA copy then used to make proteins
- The most common control point is the <u>DNA->RNA</u>
   <u>copying</u>
  - Protein binding to particular sites within DNA interferes with copying of adjacent information into RNA
- Proteins are continually degraded within cells
  - To maintain a given protein concentration, cell has to keep producing it

# Various People that are of interest to DNA study



- Rosalind Franklin
- Maurice Wilkins
- Linus and Peter Pauling
- Probably others



- James D. Watson
- Francis H. C. Crick

There are **complementarities** between bases (Watson-Crick).  $(A) \leftarrow \rightarrow (T)$ 

### The Double Helix

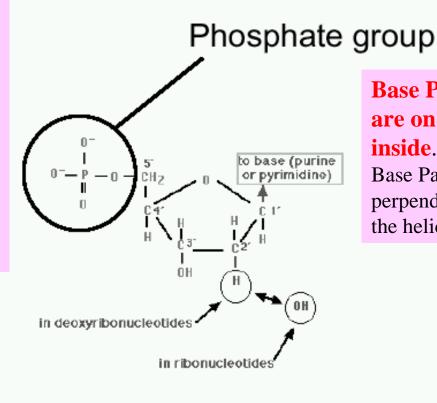
Base Pairs

Minor Groove

Major Groove

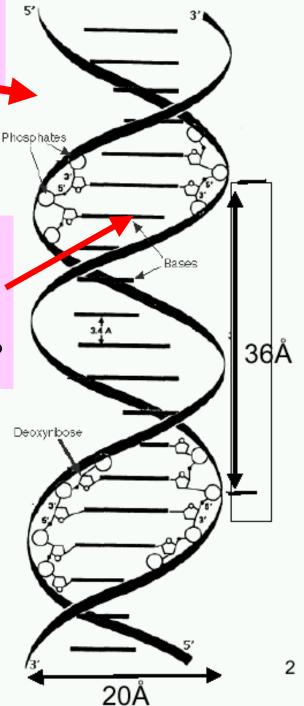
Sugar/Phosphate Backbone DNA is the hereditary molecule in every biological cell. Its shape is like a twisted rubber ladder (i.e. a double helix).

The rungs of the ladder consist of two bonded molecules called bases, of 4 possible types, labeled G, C, **A**, **T**.



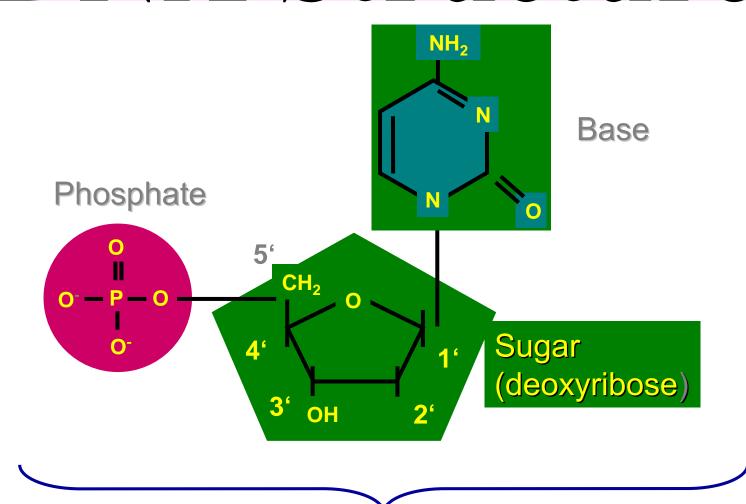
**Base Pairs** are on the inside.

Base Pairs are perpendicular to the helical axis



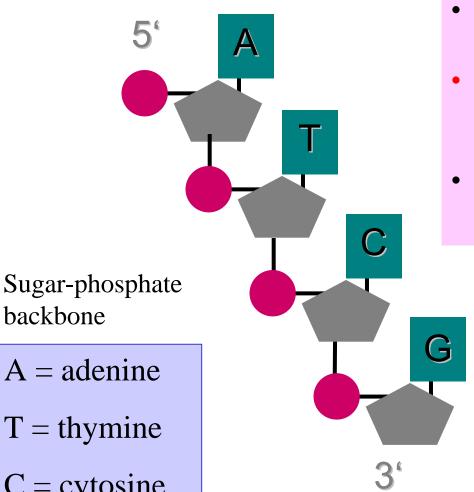
### Double Helix

### DNA Structure



Nucleotide (DeoxyriboNucleic Acid)

### **DNA Structure - Single Strand**



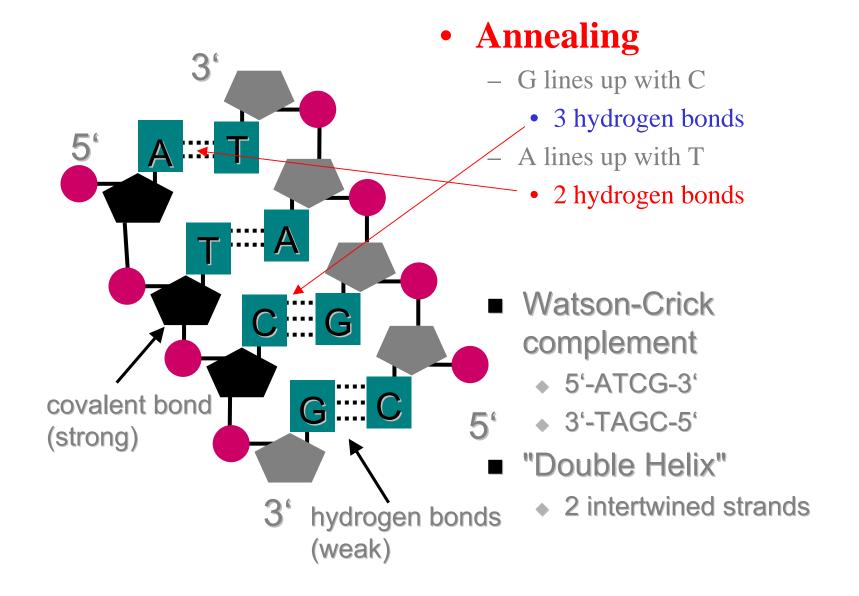
- 4 bases (A, T, C, G) 4 states
- Bases sequenced in different orders to represent different information
- Double strands are *complementary*:
  - **A** and **T**,
  - G and C (Base pairs)
- Complementarity serves purpose of error checking
  - Distinctive ends
    - ◆ 5' (5-prime) end
    - 3' end
  - Sequence
    - ◆ 5'-ATCG-3'

C = cytosine

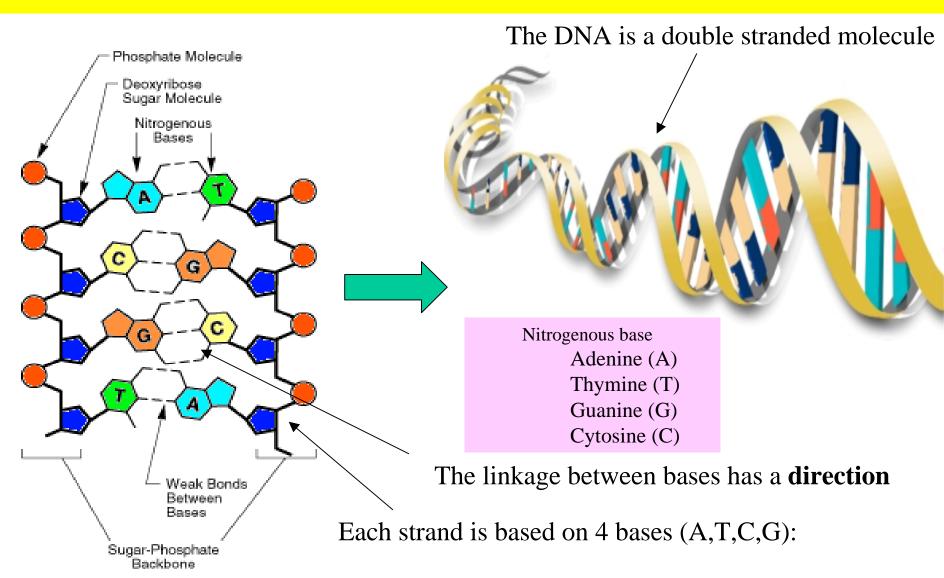
backbone

G = guanine

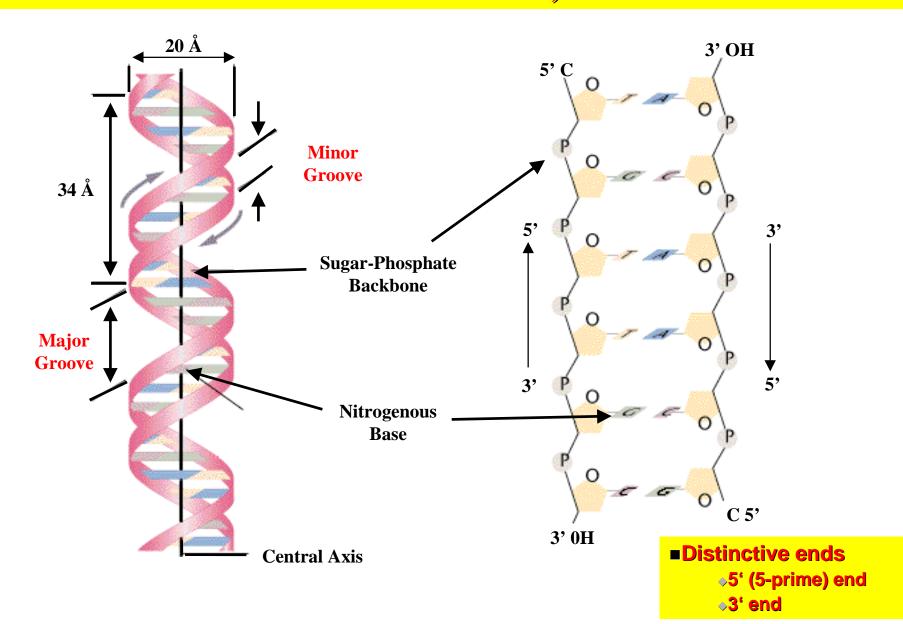
### DNA Structure - Double Strand



#### What is DNA? Conclusion



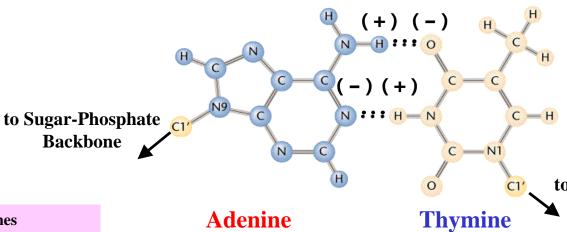
#### More detailed look at Physical Structure of DNA and distinctive ends 5', 3'



### Nitrogenous Bases

- Two Types
  - Pyrimidines
    - six-membered ring
    - Cytosine and Thymine
  - Purines
    - five and six-membered rings sharing a side
    - Guanine and Adenine

#### INTER-STRAND HYDROGEN BOND



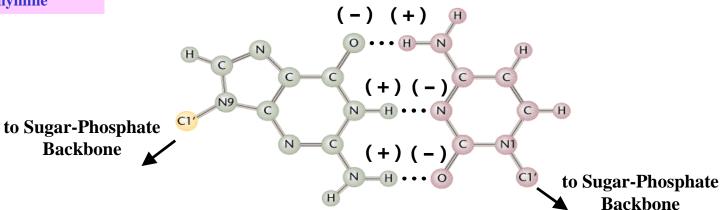
- Chargaff's Rule
  - Amount of A=T and amount of C=G
  - **Purine:Pyrimidine = 1**
  - Purines always pair with pyrimidines
    - A always pairs with T
    - G always pairs with C

to Sugar-Phosphate **Backbone** 

#### **Pyrimidines**

**Cytosine and Thymine** 

#### **Adenine**



Guanine

**Cytosine** 

#### DNA as a Data Structure

- DNA is base 4 (G, T, C, A)
- Nucleotides are spaced every 0.35nm.
- 18 Mbits/inch and over 1 million Gbits/in<sup>2</sup>.
- A factor of 100,000 times smaller than a typical hard drive.

- Quarternary data structure
- Billions of bases (≈bits)
- 100,000 times higher data density that traditional storage media
- Lots of "agents". (strands)
- Tools provided by nature.
   (enzymes)
- How can we use all this?

- If we want to use DNA as an information bulk, we must be able to manipulate it.
- However we are talking of handling molecules...

## Using Enzymes for DNA manipulations:

- **ENZYMES** = Natural **CATALYSERS**.
- So instead of using physical processes, we would have to *use natural ones*, more effective:
  - for lengthening: polymerases…
  - for cutting: nucleases (exo/endo-nucleases)...
  - for linking: ligases…
- *Serialization:* 1985: Kary Mullis → PCR

Thanks to this reaction we get millions of identical strands, and we are allowed to think of massive parallel computing.

## **Conclusion:** DNA Computing Takes Advantage of these:

- 1. Our ability to produce massive numbers of DNA molecules with specific properties (size, sequence)
- 2. The natural proclivity of specific DNA molecules to chemically interact according to defined rules to produce new molecules
- 3. Laboratory techniques that allow the isolation/identification of product molecules with specific properties
  - PCR Polymerase Chain Reaction,
  - Ligation,
  - Gel Electrophoresis,
  - etc.

## DIVA

## operations

## Computation with DNA: operations

- Construct a DNA molecule for each potential solution:
  - 1. Generate candidate solutions in parallel
  - 2. Use molecular operations to <u>eliminate invalid solutions</u>
- Five basic "mathematical" operations:
  - Extract: separates DNA containing a particular substring
  - *Merge*: mixes two tubes of DNA to label solutions
  - Detect: checks if there are any labeled DNA strands
  - *Copy*: amplifies the labeled strands
  - Append: Attaches a string to the end of every molecule in a tube

#### **DNA Computer: Physical Operations**

 Storage: DNA/RNA strands – more information/molecule (efficient packing)

- Amplification (PCR),
- Cutting (Enzymes),
- Adjoining (Hybridization/ligation),
- Filtering (biotin-avidin beads)
- Reading: Sequencing, Gel-Electrophoresis

• Input: DNA strand creation, solution mixing

## The bio-lab technology: DNA processes

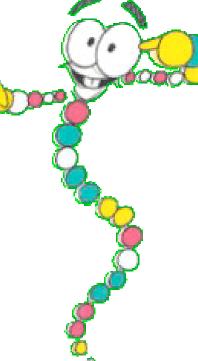
- -1. Hybridization
- -2. Ligation
- -3. Polymerase Chain Reaction (PCR)
- —4. Gel electrophoresis
- -5. Affinity separation (Bead)
- **−6.** Enzymes: restriction enzyme...

### **Operations:** P1. Separating **DNA** strands (denaturation)

### DNA operations:

- P2. Binding together DNA strands
  - (renaturation or annealing)
- P3. Completing sticky ends
- P4. Synthesizing DNA molecules

....what are sticky ends?.....



#### P3. Completing Sticky Ends

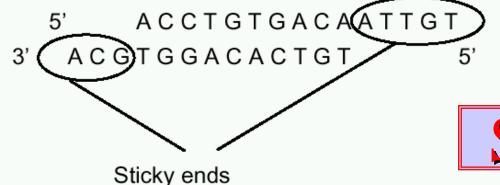
If a single **strand** (**string**) of DNA is placed in a solution with isolated bases of A, G, C, T, then those bases will **pair off** with the bases in the string, and form a complementary string, e.g.

GATTCAGAGATTAT CTAAGTCT CT

5' ACCTGTGAC 3'

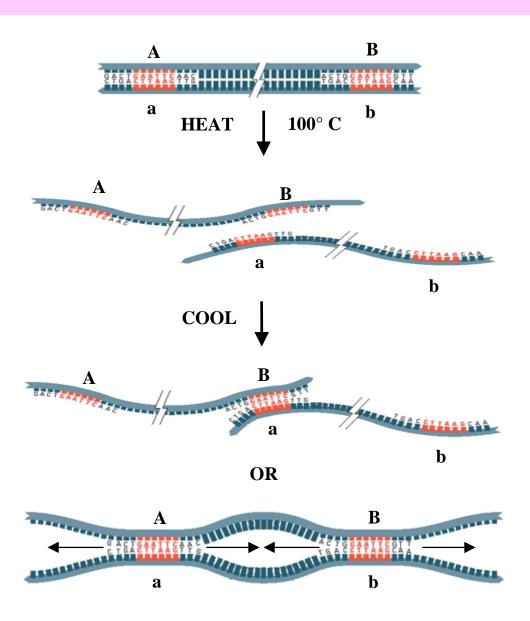
3' TGGACACTG 5'

#### **DNA** Code



Sticky Ends

#### 1. STRAND HYBRIDIZATION



### DNA operations

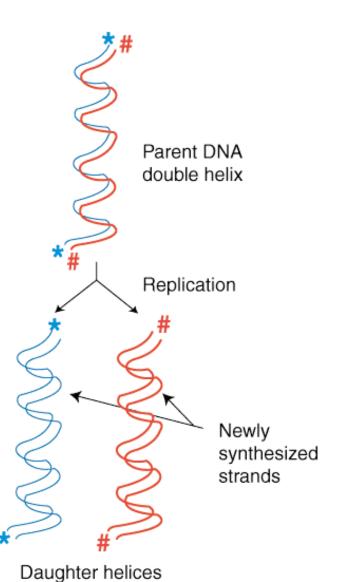
- O1. Linking DNA molecules
- O2. Inserting or deleting short subsequences
- **O3. Multiplying** (*replicating*) DNA molecules

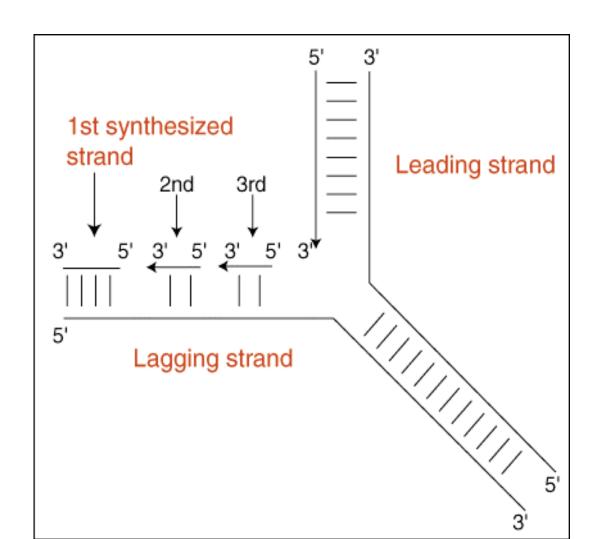
## O3. DNA Replication

- DNA replication is "semiconservative"
  - 2 daughter strands each contain half the parent strand
- Many enzymes are involved
  - Polymerase(s), Ligase, Helicase
- Enzymes operate in parallel

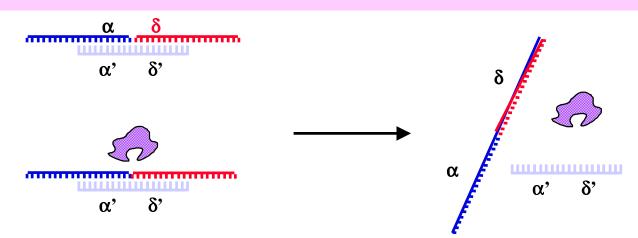


### DNA Replication





### 2. DNA LIGATION



Ligase Joins 5' phosphate to 3' hydroxyl

anneal = bind together

- Enzyme T4 DNA ligase
  - Anneal:
    - **♦** Overhanging complementary ends (sticky ends)
    - **♦** Hydrogen bonds
  - Ligate a biochemical process of ligation:
    - ♦ Covalently bond 3' and 5' ends

## 3. PCR: Polymerase Chain Reaction

- Process by which DNA is amplified
- Uses controlled biological processes similar to those which occur in the cell
- Can be done selectively
  - Using primers

**Replication of DNA** 

Original Double Stranded DNA

ATTCGTCTAAACTTAGACCTAGATAC TAAGCAGATTTGAATCTGGATCTATG

Strands Separated by Heat & Primers Added

ATTCGTCTAAACTTAGACCTAGATAC

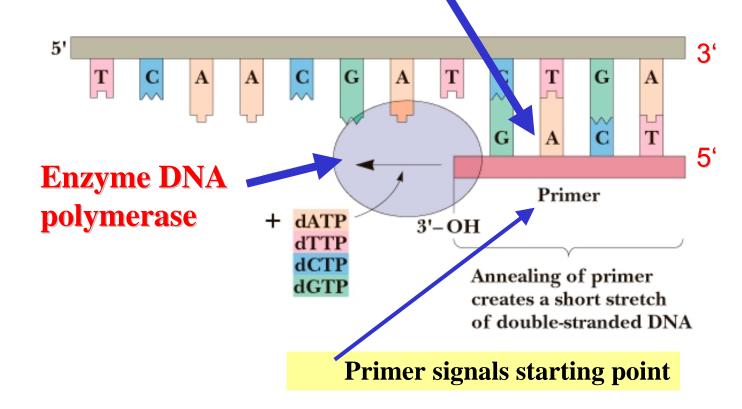
TAAGCAG ...

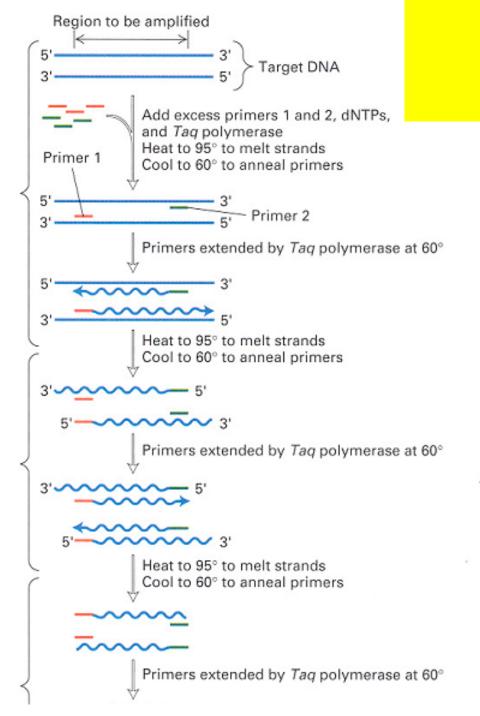
...TAGATAC
TAAGCAGATTTGAATCTGGATCTATG

#### DNA Polymerase: using primers

**Complementary copy of template** strand

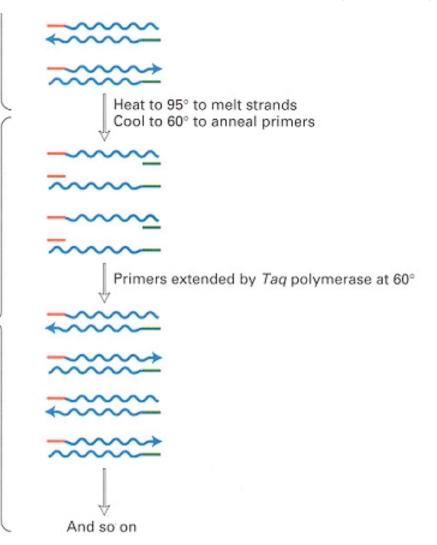
Singlestranded DNA



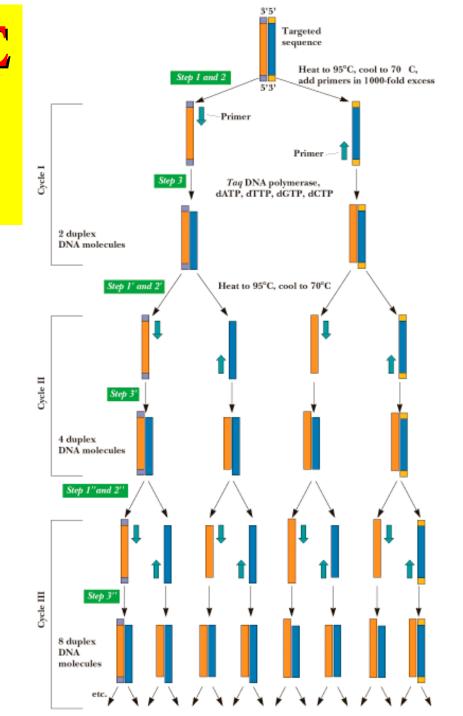


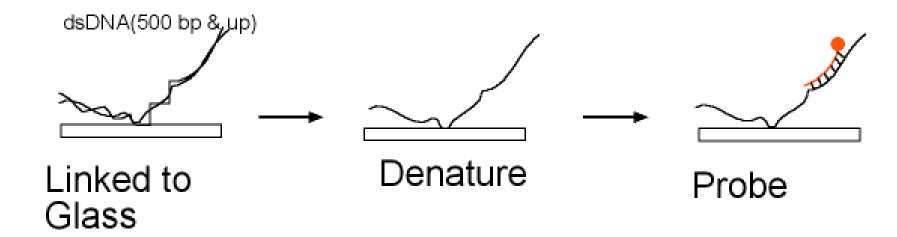
### Complete PCR process

Primers, heating, cooling,



## POLYMERASE CHAIN REACTION



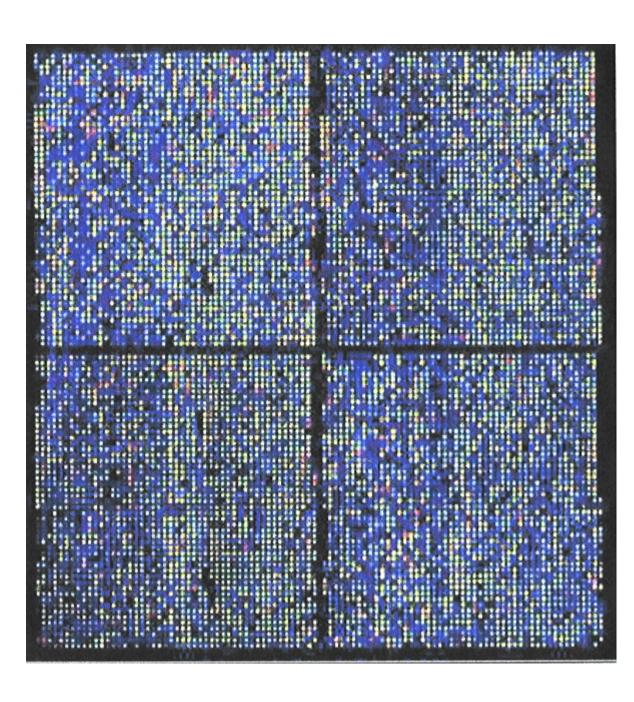


ssDNA(less than 100-mer)

irect synthesis Probe

(direct synthesis or covalently linked)

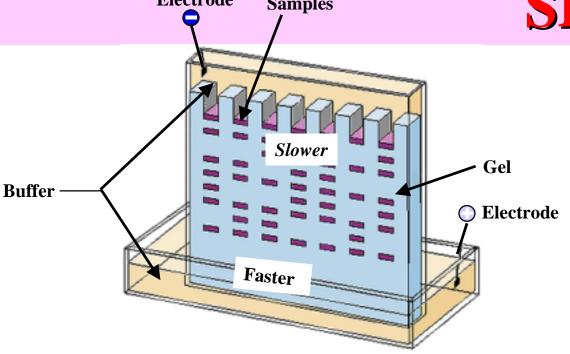
bp = base pair



# DNA operations: <u>filtering, separation by</u> <u>length, reading</u>

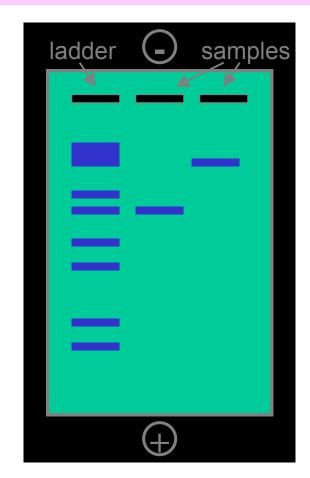
- Filtering
- Separation by length
- Reading

## 4. GEL ELECTROPHORESIS Electrode Samples SIZE SORTING

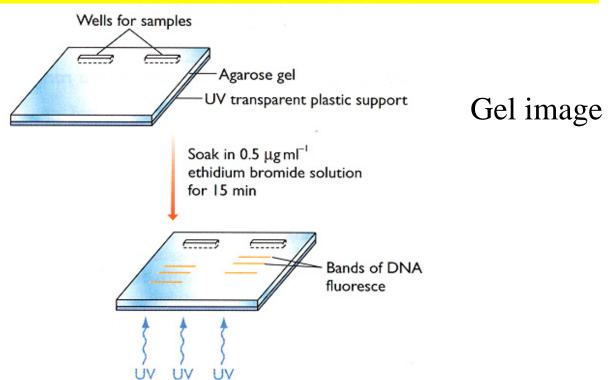




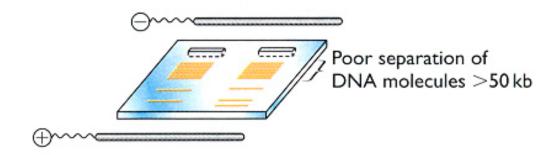
- Size
- Electrical charge
- Fill with agarose gel (0.5 5%)
- Load slots with samples and ladder
- Apply current
- Identify and extract

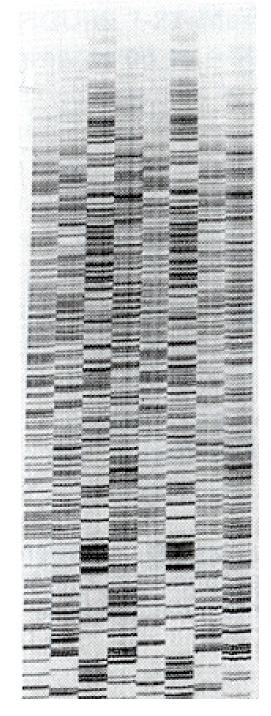


#### Gel Electrophoresis

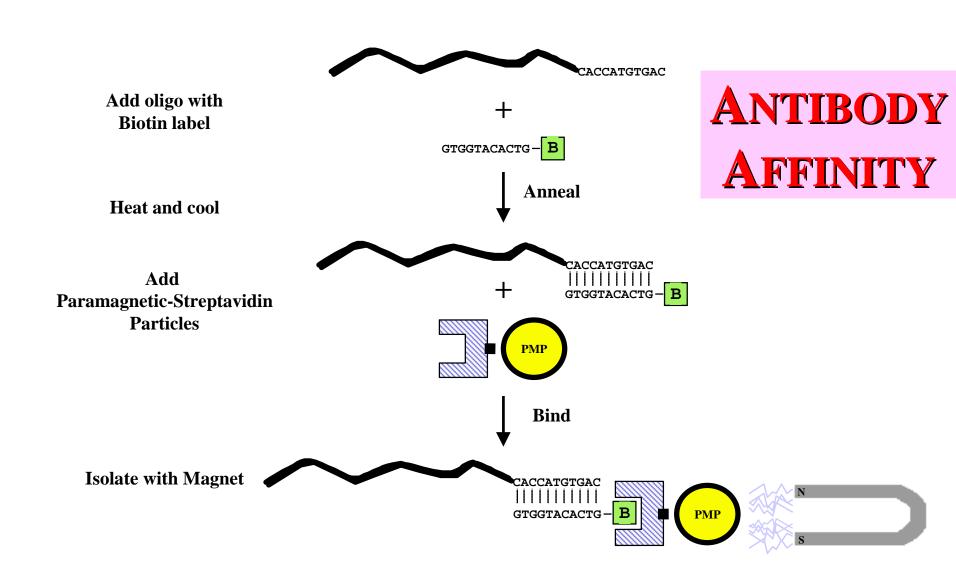


(A) Standard agarose gel electrophoresis

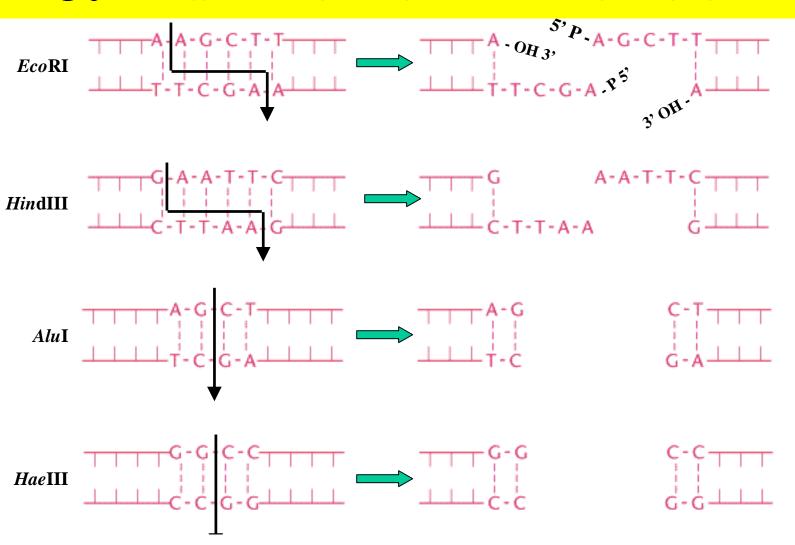




#### 5. AFFINITY SEPARATION



#### 6. RESTRICTION ENDONUCLEASES



DNA operations: Shortening and Cutting DNA molecules

