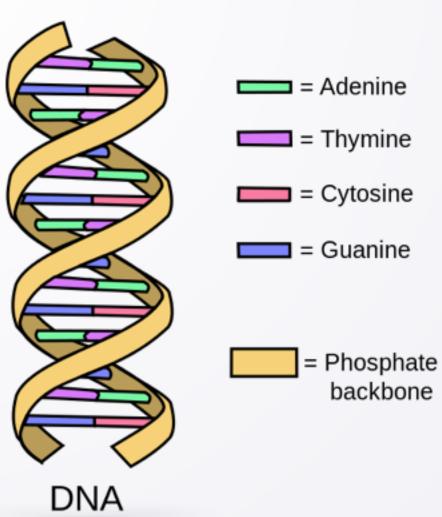
StorageResource Class

Methods for Finding and Storing



Finding and Processing Data

- You've seen code for finding start and stop codons: simple extension to finding genes
 - What if genes must have 50+ nucleotides?
 - What if genes must have CG content > 60%?
 - How do we process all the genes





Finding and Processing Data

- You've seen code for finding start and stop codons: simple extension to finding genes
 - What if genes must have 50+ nucleotides?
 - What if genes must have CG content > 60%?
 - How do we process all the genes
- Simple extension to web crawling
 - How do we find links in a web page
 - Search for href=".." instead of ATG..TAA



Finding All Genes

- Printing all genes found in DNA
 - findStopIndex() discussed in earlier lesson

```
public void printAll(String dna){
        int start = 0;
        while (true){
            int tag = dna.index0f("atg",start);
            if (tag == -1) {
               break;
            int end = findStopIndex(dna,tag+3);
            if (end != dna.length()) {
                System.out.println(dna.substring(tag,end+3));
                start = end+3;
            else {
                start = start + 3;
```



Finding All Genes

- Printing all genes found in DNA
 - findStopIndex() discussed in earlier lesson

```
public void printAll(String dna){
int tag = dna.index0f("atg",start);
if (tag == -1) {
     break;
          if (end != dna.length()) {
              System.out.println(dna.substring(tag,end+3));
              start = end+3;
          else {
             start = start + 3;
```



Finding All Genes

- Printing all genes found in DNA
 - findStopIndex() discussed in earlier lesson

```
public void printAll(String dna){
      int start = 0;
      while (true){
         int tag = dna.index0f("atg",start);
         if (tag == -1) {
int end = findStopIndex(dna,tag+3);
if (end != dna.length()) {
    System.out.println(dna.substring(tag,end+3));
    start = end+3;
    start = start + 3;
```



Storing Strings: Post-Processing

- Modifying the gene finding/printing code
 - To find/print genes that are long
 - To find/print genes that are good
 - Combines finding and printing, separating hard
- StorageResource class helps here
 - Can add strings with .add(str)
 - Can ask for count of added with .size()
 - Can use as iterable with .data()



Post-Processing Example

- If we had stored all genes in a
 StorageResource object we could ...
 - Print those long enough

```
public void printGenes(StorageResource sr){
    for(String gene : sr.data()){
        if (gene.length() > 60) {
            System.out.println(gene.length()+"\t"+gene);
        }
    }
}
```



Post-Processing Example

- If we had stored all genes in a
 StorageResource object we could ...
 - Print those long enough
 - Print those rich enough in CG content

```
public void printGenes(StorageResource sr){
    for(String gene : sr.data()){
        if (cgRatio(gene) > 0.35) {
            System.out.println(gene.length()+"\t"+gene);
        }
    }
}
```



Adding to a StorageResource

- Adding words to StorageResource object
 - Simply call .add() to add String to collection
 - Suppose tracking only words not seen before?

```
public StorageResource getWords(){
   FileResource fr = new FileResource("/data/confucius.txt");
   StorageResource store = new StorageResource();
   for(String w : fr.words()){
      if (! store.contains(w)){
         store.add(w);
      }
   }
  return store;
}
```

