Interfaces: improving Shotgun

- **We don't want to use a String to represent a DNA strand/sequence**
  - Probably not efficient for merging two strands
  - Strands can't have annotations: names, features,..
  - Doesn't mirror what's done in BioJava library

- **We want to use a class to represent a sequence, but we don't want to force client code into using a specific class**
  - Doesn't allow for future improvements
  - Doesn't allow for idiosyncratic coding requirements
  - Doesn't adhere to good engineering principles

- **What are our options?**
Toward Interfaces

- **What's an iterator?**
  - A `java.util` interface for doing ...
  - Has a few methods: `hasNext()`, `next()`, ...
  - What does it iterate over?

- **Interface** specifies a collection of related methods and constants
  - Classes *implement* the interface, providing implementations of the methods specified in the interface

- **Allows client code to conform to a specification rather than an implementation**
  - How do I drive a car? Operate a CD-player?
How do I work an MP3 player?

- What's the common interface for a windows-based MP3-player?

- Do I need to understand different buttons to use this?
The Comparable interface

- To compare two objects, e.g., for sorting, they must implement the `java.lang.Comparable` interface
  - Consider the implementation below from Card class

```java
public int compareTo(Object o) {
    ICard other = (ICard) o;
    int rdiff = getRank() - other.getRank();
    if (rdiff == 0) {
        return getSuit() - other.getSuit();
    } else {
        return rdiff;
    }
}
```