#### True positive rate (Sensitivity)

true positive rate = 
$$\frac{\text{# of true positives}}{\text{# of known positives}}$$

(Proportion of actual positives that are correctly identified)

#### True negative rate (Specificity)

true negative rate = 
$$\frac{\text{# of true negatives}}{\text{# of known negatives}}$$

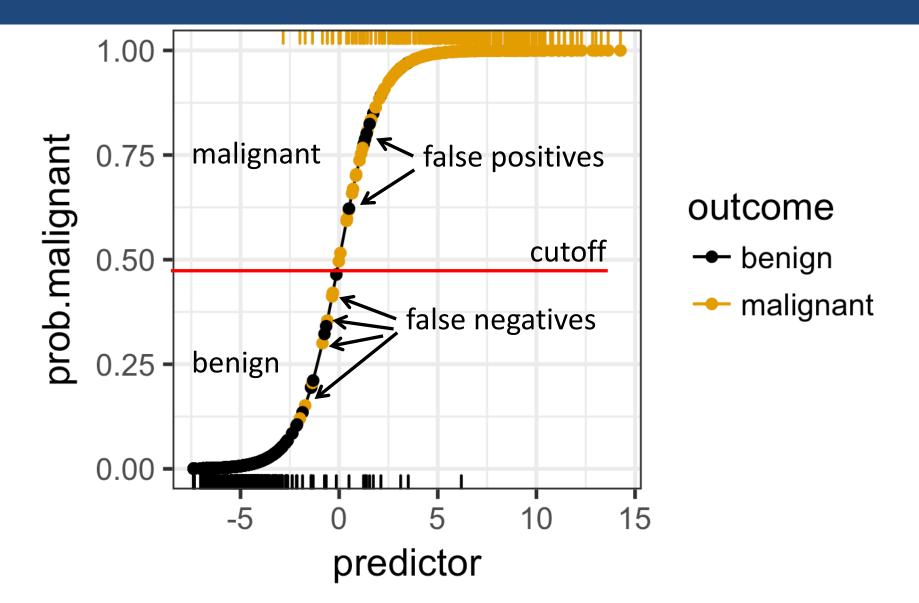
(Proportion of actual negatives that are correctly identified)

### False positive rate (1 – Specificity)

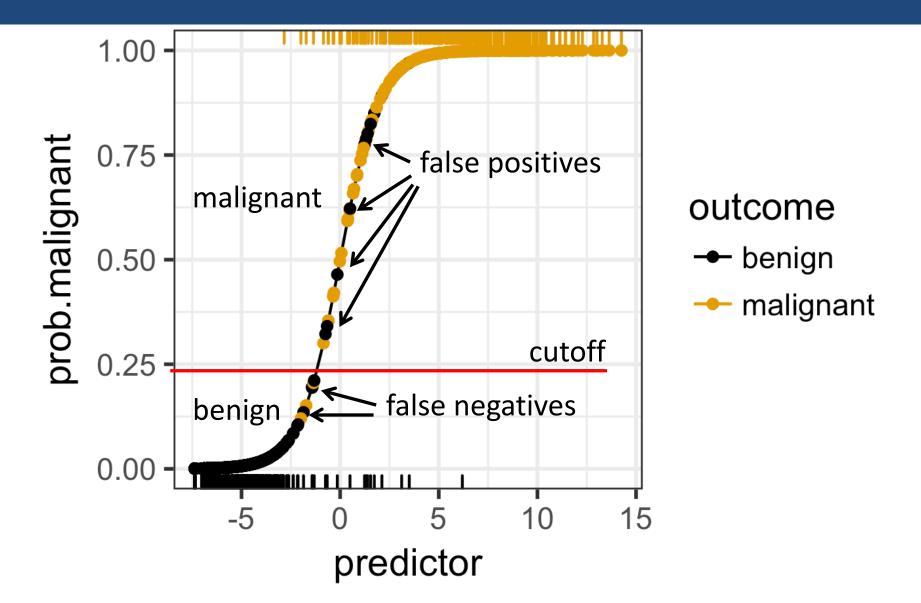
false positive rate = 
$$\frac{\text{# of false positives}}{\text{# of known negatives}}$$

(Proportion of actual negatives that are incorrectly identified)

### Sensitivity and specificity depend on a chosen cutoff

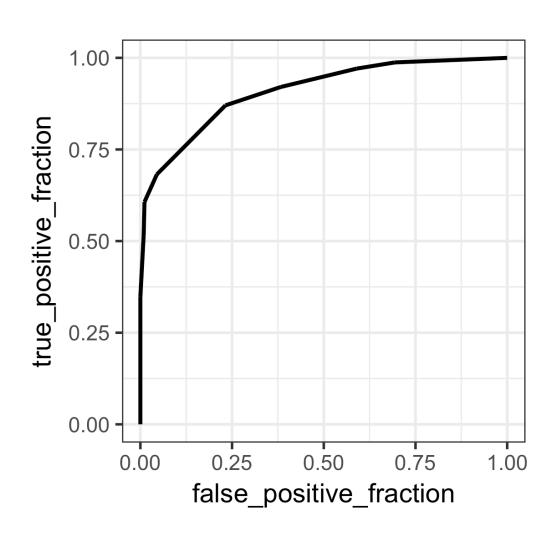


### Sensitivity and specificity depend on a chosen cutoff



#### Do Part 1 of the worksheet now

### We usually plot the true pos. rate vs. the false pos. rate for all possible cutoffs



#### **ROC** curve

Receiver
Operating
Characteristic
curve

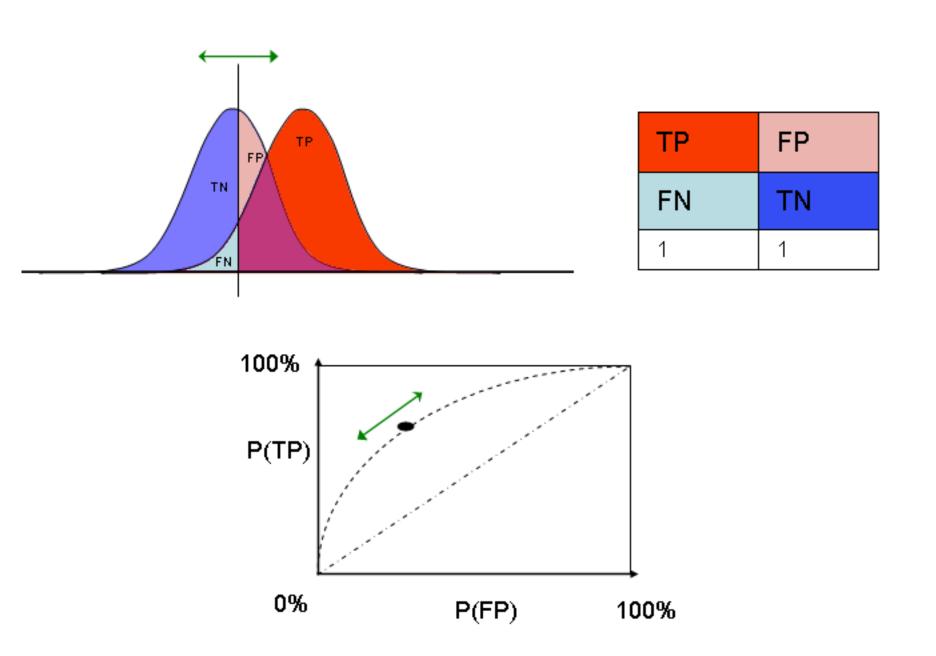
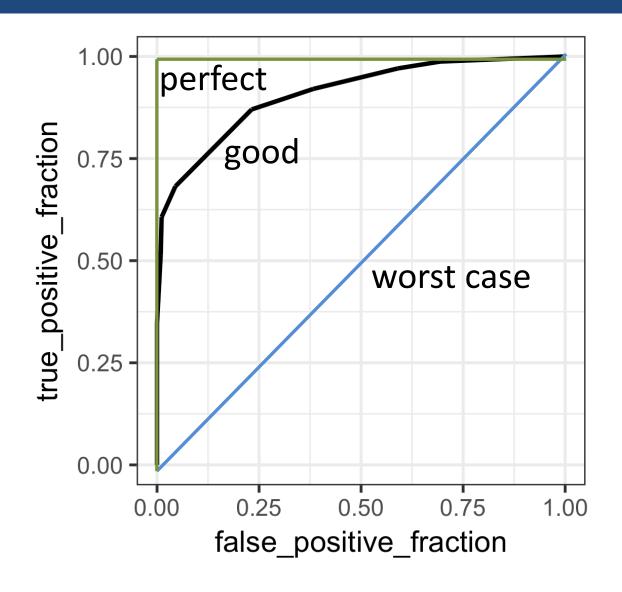
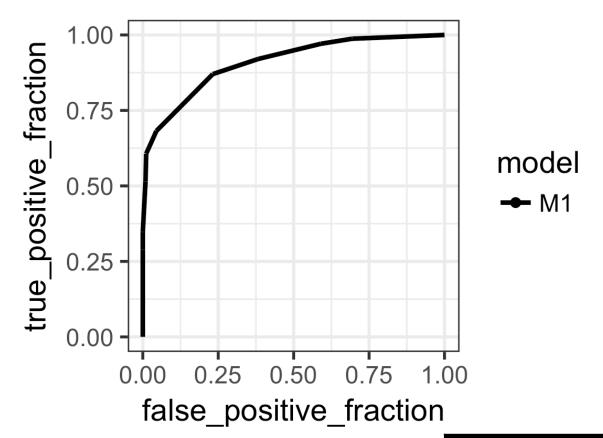


Image from: http://en.wikipedia.org/wiki/Receiver\_operating\_characteristic

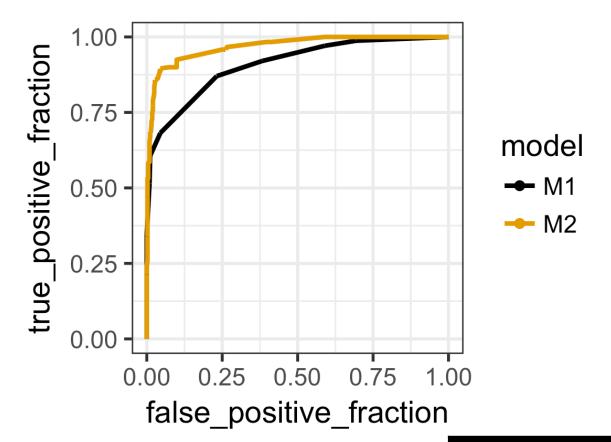
### The area under the curve tells us how good a model's predictions are



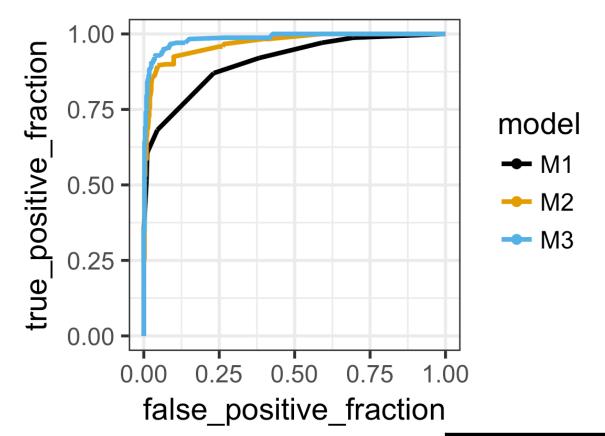
## Let's look at the performance of several different models for the biopsy data set



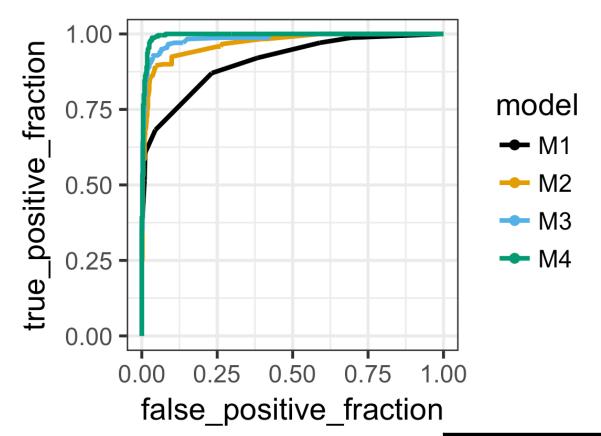
Predictor	M1	
clump_thickness	<b>✓</b>	
normal_nucleoli		
marg_adhesion		
bare_nuclei		
uniform_cell_shape		
bland_chromatin		



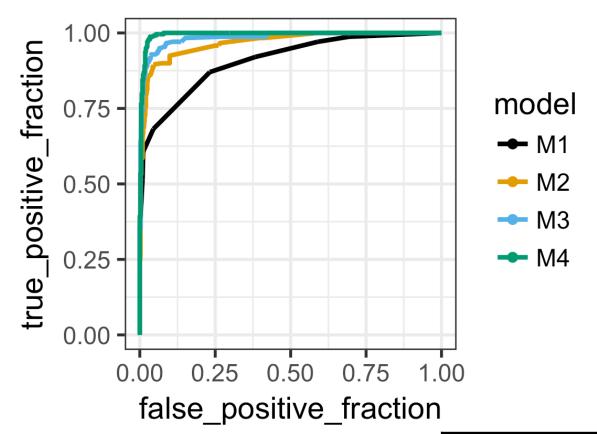
Predictor	<b>M1</b>	M2	
clump_thickness	<b>✓</b>	<b>✓</b>	
normal_nucleoli		<b>✓</b>	
marg_adhesion			
bare_nuclei			
uniform_cell_shape			
bland_chromatin			



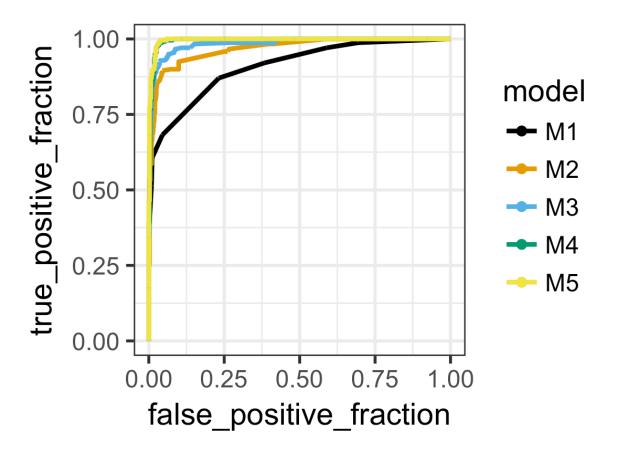
Predictor	M1	M2	<b>M</b> 3	
clump_thickness	<b>✓</b>	<b>✓</b>	<b>✓</b>	
normal_nucleoli		<b>✓</b>	<b>✓</b>	
marg_adhesion			<b>✓</b>	
bare_nuclei				
uniform_cell_shape				
bland_chromatin				



Predictor	M1	M2	<b>M3</b>	M4	
clump_thickness	<b>✓</b>	<b>✓</b>	<b>✓</b>	<b>✓</b>	
normal_nucleoli		<b>✓</b>	<b>✓</b>	<b>✓</b>	
marg_adhesion			<b>✓</b>	<b>✓</b>	
bare_nuclei				<b>✓</b>	
uniform_cell_shape					
bland_chromatin					

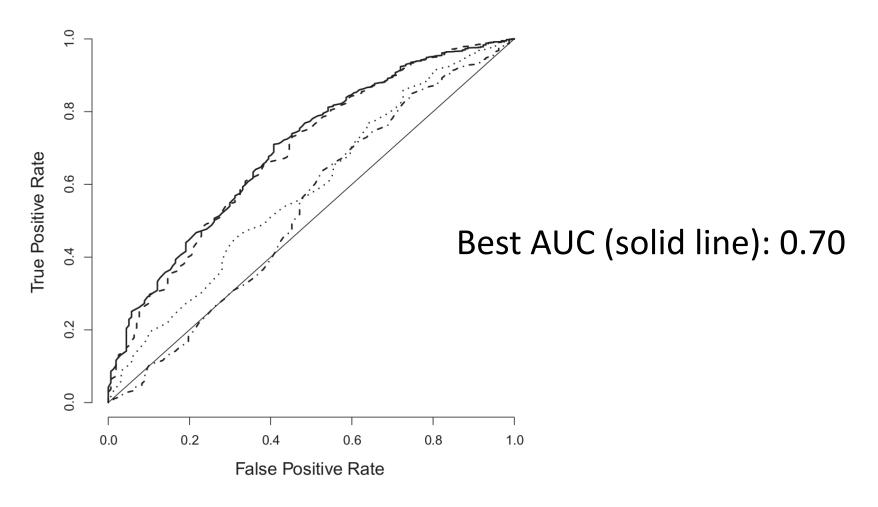


Predictor	M1	M2	M3	M4	M5
clump_thickness	<b>✓</b>	<b>✓</b>	<b>✓</b>	<b>✓</b>	<b>✓</b>
normal_nucleoli		<b>✓</b>	<b>✓</b>	<b>✓</b>	<b>✓</b>
marg_adhesion			<b>✓</b>	<b>✓</b>	<b>/</b>
bare_nuclei				<b>✓</b>	<b>✓</b>
uniform_cell_shape					<b>/</b>
bland_chromatin					<b>/</b>



Model	Area Under Curve (AUC)
M1	0.909
M2	0.968
M3	0.985
M4	0.995
M5	0.996

### Things usually look much worse in real life



Keller, Mis, Jia, Wilke. Genome Biol. Evol. 4:80-88, 2012

### Calculating ROC curves in R

```
# fit a logistic regression model
glm.out <- glm(outcome ~ clump thickness,
               data=biopsy, family=binomial)
# prepare data for ROC plotting
df <- data.frame(probabilities = predict(glm.out, biopsy),</pre>
                 known truth = biopsy$outcome,
                 model = 'M1')
# the aesthetic names are not the most intuitive
# `d` (disease) holds the known truth
# `m` (marker) holds the predictor values
p <- ggplot(df, aes(d = known.truth, m = predictor)) +
       geom roc(n.cuts = 0) + coord fixed()
p # make plot
```

#### Calculating the area under the curve (AUC)

#### Do Part 2 of the worksheet now