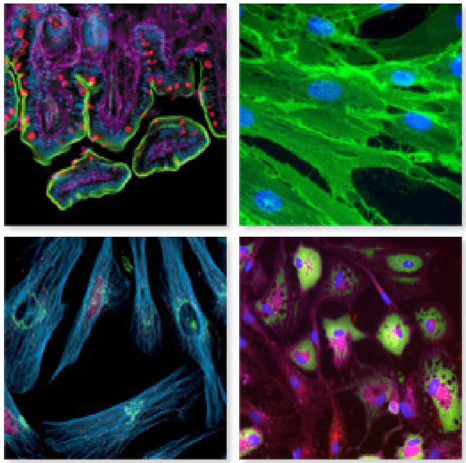

Bayesian Estimation Example Using PyMC

SciPy 2010 Lightning Talk

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What is PyMC?

PyMC is a Python module that provides tools for Bayesian analysis.

- NOTE: I am not a contributer to this project--just an enthusiastic user!

Motivation

- Suppose we have a series of short DNA sequences, each known to cause one of two experimental outcomes:

Sequence	Outcome
CGTCGGAGGTACATGATTGGAAGAAAACCT	Y
GCGCCTTTGCACATCTCTTAATCTCAGTCA	X
TTAAAATAGCAGAGACACTTCTACTGATAC	Y
CCAAGAGCCTCGTAATTAAGTATTGCAATA	Y
TTATGACGTCGTTTCGAGTGGATTTGTCTT	X
...	...

- We want to train a statistical model to predict the outcome from any arbitrary sequence.

Motivation (continued)

- A common strategy looks for motifs in the sequences and correlates them to outcomes.
  - Simple example: Nucleotide “A” may follow nucleotide “T” in the sequences more frequently for outcome X than for outcome Y,

$$P(A \mid T, X) > P(A \mid T, Y)$$

- If you know such probabilities, you can create a variety of scoring models for arbitrary input sequences to help predict experiment outcome.

But how do we get the probabilities?

- Option #1 - Maximum Likelihood Method (Frequentist Approach)
  - Derive probabilities from a large experimental set with measured outcomes.
- Option #2 - Maximum *a Posteriori* (MAP) Estimation (Bayesian Approach)
  - Use Bayes’ theorem to combine researcher intuition with a small experimental dataset to estimate probabilities.
  - *PyMC makes this easy!*

Python Bayesian Estimation Workflow

- Start with Bayes' theorem:

D = observed data
θ = scoring model parameters

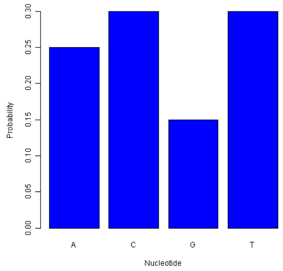
$$P(\theta \mid D) = \frac{P(D \mid \theta) \cdot P(\theta)}{P(D)}$$

Python Bayesian Estimation Workflow

- Specify the prior distribution:

```
import numpy as np
from pymc import Dirichlet  # conjugate prior
alpha = np.array([30.0,25.0,20.0,25.0])
prob_dist = Dirichlet(‘prob_dist', alpha)
```

Prior Distribution of the Nucleotides



$$P(\theta \mid D) = \frac{P(D \mid \theta) \cdot \boxed{P(\theta)}}{P(D)}$$

Python Bayesian Estimation Workflow

- Specify the experimental data:

```
exp_data = np.array([1, 1, 3, 2, 2, 1, 0, …])
```

Experimental Data

Observation #	Nucleotide
1	1
2	1
3	3
4	2
5	2
6	1
7	0

$$P(\theta \mid D) = \frac{P(\boxed{D} \mid \theta) \cdot P(\theta)}{P(D)}$$

Python Bayesian Estimation Workflow

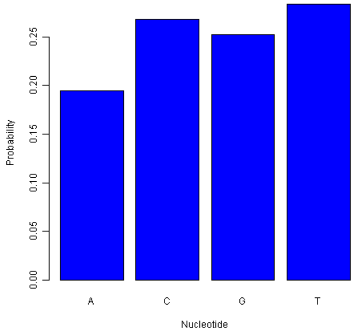
- Specify the value to maximize using numerical simulation, as well as the expected form of the posterior distribution:

```
from pymc import Categorical
f_x = Categorical('cat', prob_dist, value=exp_data, observed=True)
```

$$P(\theta \mid D) = \frac{\boxed{P(D \mid \theta) \cdot P(\theta)}}{P(D)}$$

Python Bayesian Estimation Workflow

Posterior Distribution of the Nucleotides



- Compute maximum *a posteriori* estimates of the probabilities:

```
from pymc import MAP, Model
model = Model({'f_x' : f_x, 'prob_dist' :
  prob_dist})
M = MAP(model)
M.fit()   # Nelder-Mead Optimization
```

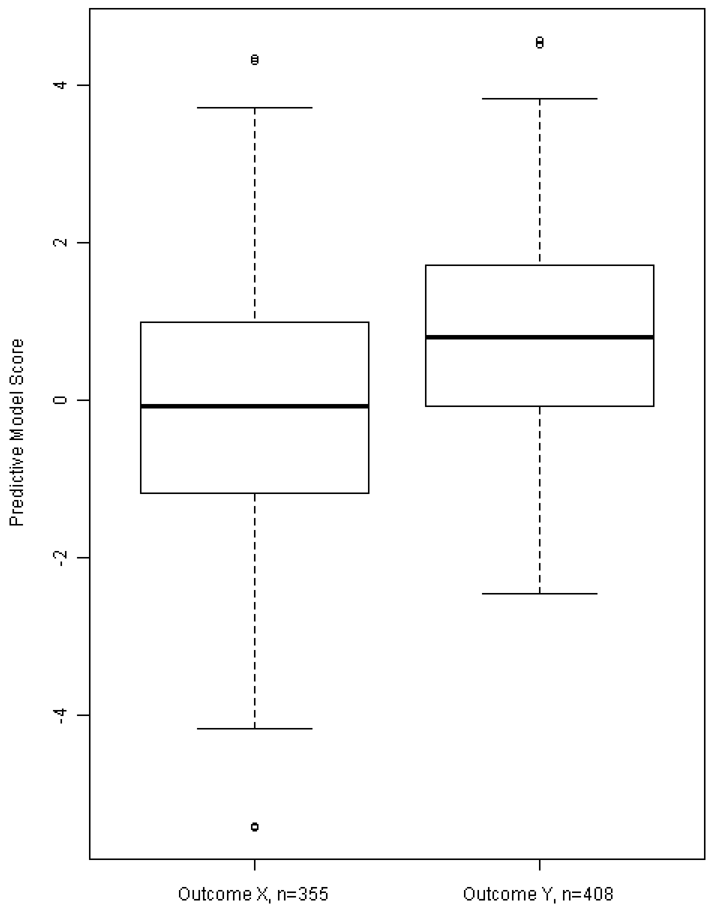
- The MAP estimates are now contained in the M.prob_dist value:

```
>>> print M.prob_dist.value
[ 0.19472259  0.26842748  0.25265728]
```

$$\boxed{P(\theta \mid D)} = \frac{P(D \mid \theta) \cdot P(\theta)}{P(D)}$$

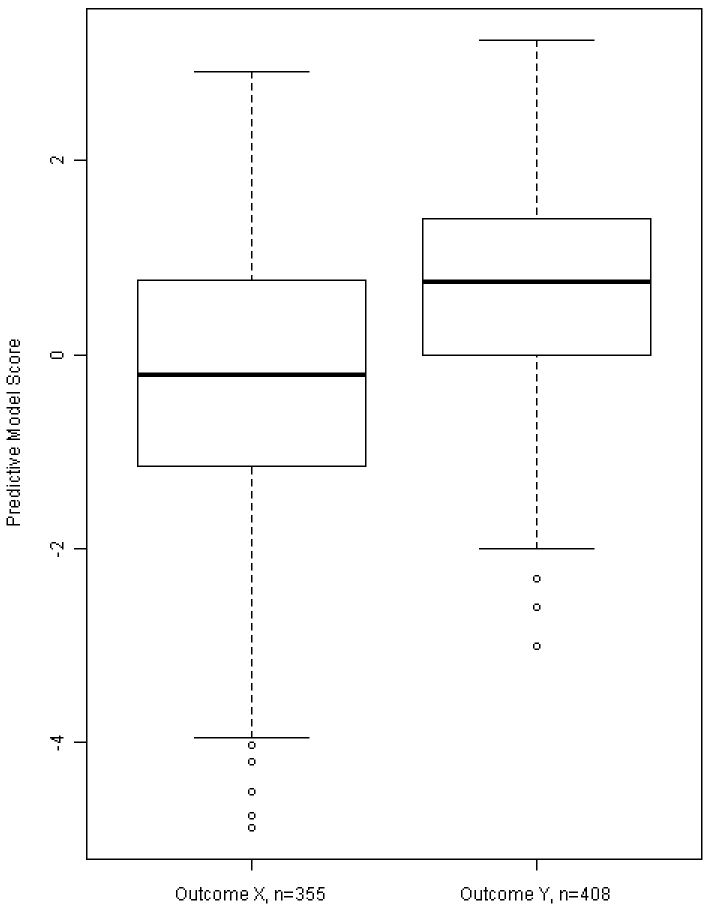
Testing Set Results: A Predictive Model Parameterized by Informed Priors vs. the Same Model Parameterized by MAP Estimates

Predictive Model Built Using Informed Priors Only



Test Set, p=2.0e-15 (Mann-Whitney)

Predictive Model Built Using MAP Estimation



Test Set, p=1.7e-17 (Mann-Whitney)

Thank you!