# pomegranate

fast and flexible probabilistic modeling in python

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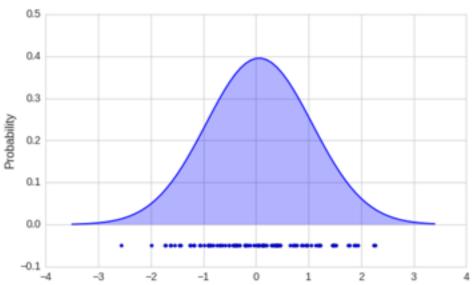


## Follow along with the Jupyter tutorial

# goo.gl/cbE7rs

### What is probabilistic modeling?





### Tasks:

- Sample from a distribution.
- Learn parameters of a distribution from data.
- Predict which distribution generated a data example.



### When should you use pomegranate?

# Use scipy or scikit-learn

- logistic regression
- sample from a Gaussian distribution
- speed is not important

Use pomegranate

# Use custom packages (in R or stand-alone)

 distributions not implemented in pomegranate

complex

problem-specific inference algorithms

simple



complexity of probabilistic modeling task



### When should you use pomegranate?



- Scientific computing: Use numpy, scipy
- Non-probabilistic supervised learning (SVMs, neural networks): Use scikit-learn
- Visualizing probabilistic models: Use matplotlib
- Bayesian statistics: Check out PyMC3

Use pomegranate



### Overview: this talk

### Overview

Major Models/Model Stacks

- 1. General Mixture Models
- 2. Hidden Markov Models
- 3. Bayesian Networks
- 4. Bayes Classifiers

Finale: Train a mixture of HMMs in parallel



### The API is common to all models

model.log\_probability(X) / model.probability(X)

model.sample()

model.fit(X, weights, inertia)

model.summarize(X, weights)

model.from summaries(inertia)

model.predict(X)

model.predict\_proba(X)

model.predict\_log\_proba(X)

Model.from\_samples(X, weights)

All models have these methods!

All models composed of distributions (like GMM, HMM...) have these methods too!



### Overview: supported models

### Six Main Models:

- 1. Probability Distributions
- 2. General Mixture Models
- 3. Markov Chains
- 4. Hidden Markov Models
- 5. Bayes Classifiers / Naive Bayes
- 6. Bayesian Networks

### Two Helper Models:

- 1. k-means++/kmeans||
- 2. Factor Graphs

### pomegranate supports many distributions

### Univariate Distributions

- 1. UniformDistribution
- 2. BernoulliDistribution
- 3. NormalDistribution
- 4. LogNormalDistribution
- 5. Exponential Distribution
- BetaDistribution
- 7. GammaDistribution
- 8. DiscreteDistribution
- 9. PoissonDistribution

### **Kernel Densities**

- 1. GaussianKernelDensity
- 2. UniformKernelDensity
- 3. TriangleKernelDensity

### **Multivariate Distributions**

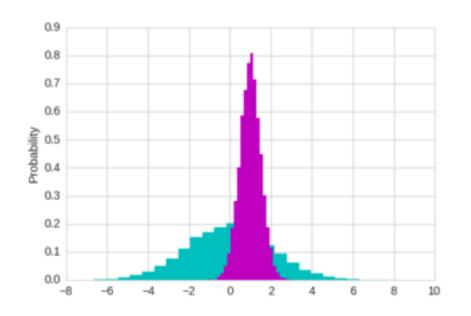
- IndependentComponentsDistribution
- 2. MultivariateGaussianDistribution
- DirichletDistribution
- 4. ConditionalProbabilityTable
- JointProbabilityTable

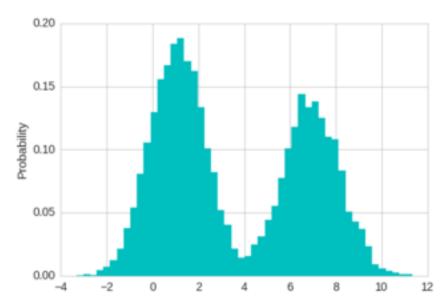
### Models can be created from known values



mu, sig = 0, 2a = NormalDistribution(mu, sig) a = GaussianKernelDensity(X)

X = [0, 1, 1, 2, 1.5, 6, 7, 8, 7]



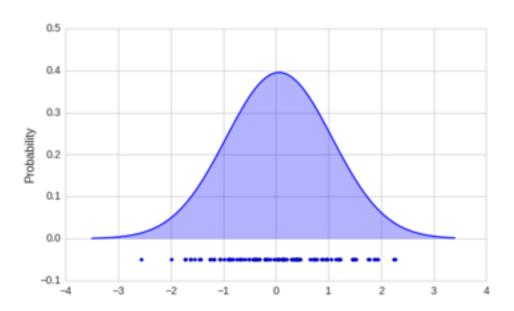




### Models can be learned from data

```
X = numpy.random.normal(0, 1, 100)
```

a = NormalDistribution.from\_samples(X)



# Sub-model

### Overview: model stacking in pomegranate

**Distributions** 

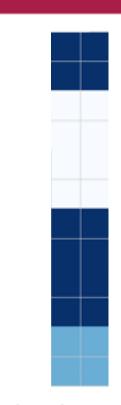
**Bayes Classifiers** 

**Markov Chains** 

**General Mixture Models** 

Hidden Markov Models

Bayesian Networks



Wrapper model

# Sub-model

### Overview: model stacking in pomegranate

**Distributions** 

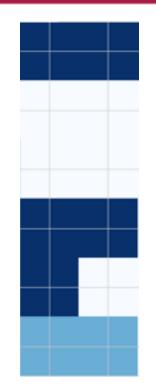
**Bayes Classifiers** 

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**General Mixture Models** 

Hidden Markov Models

Bayesian Networks



D BC MC GMM HMM BN Wrapper model

# Sub-model

### Overview: model stacking in pomegranate

**Distributions** 

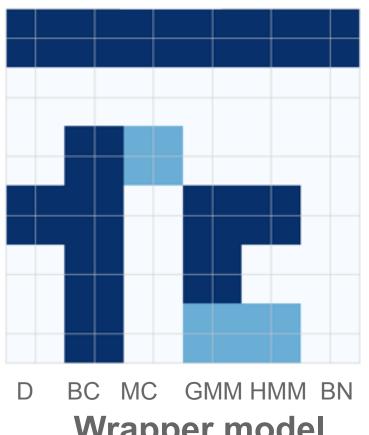
**Bayes Classifiers** 

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**General Mixture Models** 

Hidden Markov Models

Bayesian Networks



Wrapper model

### Overview: model stacking in pomegranate

**Distributions** 

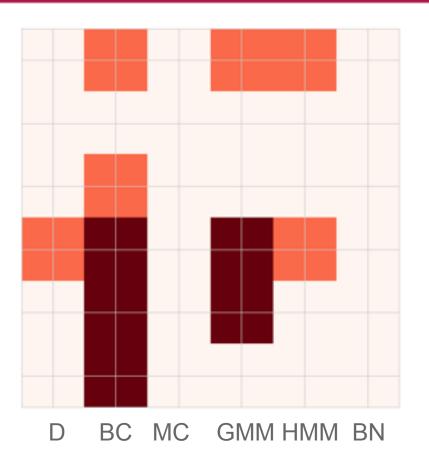
**Bayes Classifiers** 

Markov Chains

**General Mixture Models** 

Hidden Markov Models

Bayesian Networks





### pomegranate can be faster than numpy

Fitting a Normal Distribution to 1,000 samples

```
data = numpy.random.randn(1000)
print "numpy time:"
%timeit -n 100 data.mean(), data.std()
print
print "pomegranate time:"
%timeit -n 100 NormalDistribution.from samples(data)
numpy time:
100 loops, best of 3: 46.6 μs per loop
pomegranate time:
100 loops, best of 3: 22.2 μs per loop
```



### pomegranate can be faster than numpy

Fitting Multivariate Gaussian to 10,000,000 samples of 10 dimensions

```
data = numpy.random.randn(10000000, 10)
print "numpy time:"
%timeit -n 10 data.mean(), numpy.cov(data.T)
print
print "pomegranate time:"
%timeit -n 10 MultivariateGaussianDistribution.from_samples(data)
numpy time:
10 loops, best of 3: [1.02 s per loop
pomegranate time:
10 loops, best of 3: 799 ms per loop
```



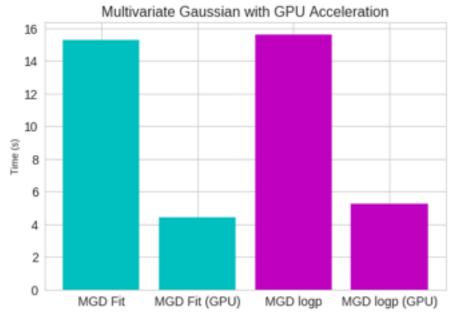
### pomegranate uses BLAS internally

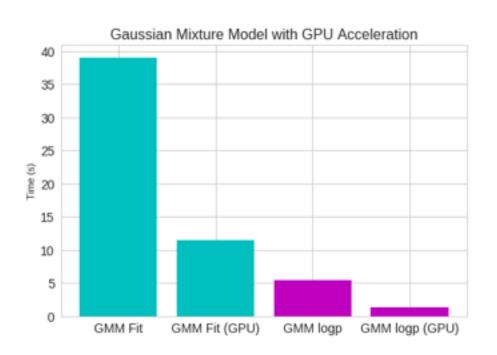
### from scipy.linalg.cython\_blas cimport dgemm

```
dgemm('N', 'T', &d, &d, &n, &alpha, y, &d, X, &d, &beta, pair_sum, &d)
```

### pomegranate just merged GPU support









### pomegranate uses additive summarization

pomegranate reduces data to sufficient statistics for updates and so only has to go datasets once (for all models).

Here is an example of the Normal Distribution sufficient statistics

$$\sum_{i=1}^{n} w_i \qquad \sum_{i=1}^{n} w_i x_i \qquad \sum_{i=1}^{n} w_i x_i^2. \longrightarrow$$

$$\mu = \frac{1}{\sum_{i=1}^{n} w_i}$$

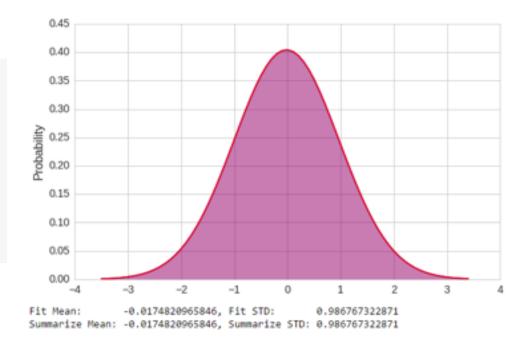
$$\sigma^2 = \frac{\sum_{i=1}^{n} w_i x_i^2}{\sum_{i=1}^{n} w_i} - \frac{\left(\sum_{i=1}^{n} w_i x_i\right)^2}{\left(\sum_{i=1}^{n} w_i\right)^2}$$



### pomegranate supports out-of-core learning

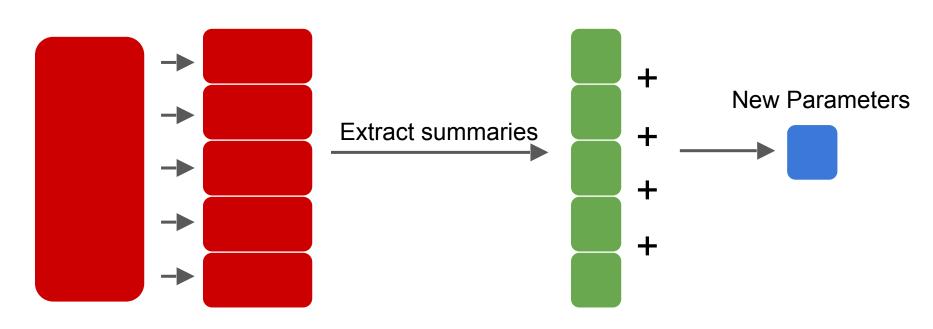
Batches from a dataset can be reduced to additive summary statistics, enabling exact updates from data that can't fit in memory.

```
a.fit(data)
b.summarize(data[:1000])
b.summarize(data[1000:2000])
b.summarize(data[2000:3000])
b.summarize(data[3000:4000])
b.summarize(data[4000:])
b.from_summaries()
```





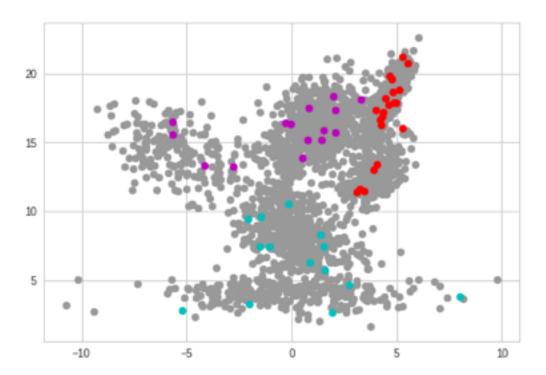
# Parallelization exploits additive summaries





## pomegranate supports semisupervised learning

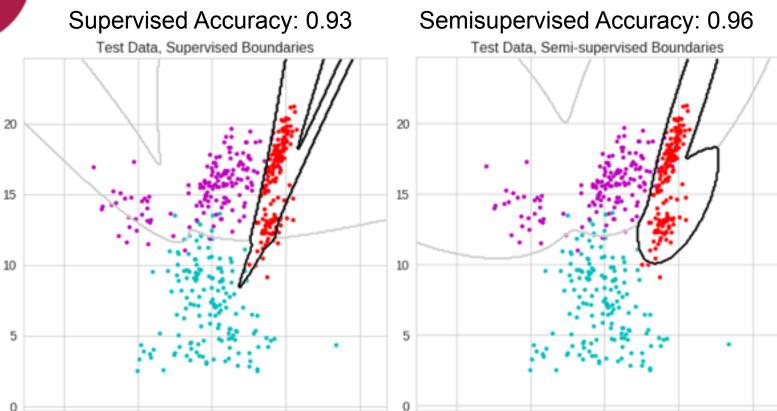
Summary statistics from supervised models can be added to summary statistics from unsupervised models to train a single model on a mixture of labeled and unlabeled data.





-10

### pomegranate supports semisupervised learning



-10



### pomegranate can be faster than scipy

```
mu, cov = numpy.random.randn(2000), numpy.eye(2000)
d = MultivariateGaussianDistribution(mu, cov)
X = numpy.random.randn(2000, 2000)
print "scipy time: ",
%timeit multivariate normal.logpdf(X, mu, cov)
print "pomegranate time: ",
%timeit MultivariateGaussianDistribution(mu, cov).log probability(X)
print "pomegranate time (w/ precreated object): ",
%timeit d.log probability(X)
scipy time: 1 loop, best of 3: 1.67 s per loop
pomegranate time: 1 loop, best of 3: 801 ms per loop
pomegranate time (w/ precreated object): 1 loop, best of 3: 216 ms per loop
```



### pomegranate uses aggressive caching

$$P(X|\mu,\sigma) = \frac{1}{\sqrt{2\pi}\sigma} exp\left(-\frac{(x-\mu)^2}{2\sigma^2}\right)$$
$$log P(X|\mu,\sigma) = -\log\left(\sqrt{2\pi}\sigma\right) - \frac{(x-\mu)^2}{2\sigma^2}$$
$$log P(X|\mu,\sigma) = \alpha - \frac{(x-\mu)^2}{\beta}$$





### Example 'blast' from Gossip Girl

Spotted: Lonely Boy. Can't believe the love of his life has returned. If only she knew who he was. But everyone knows Serena. And everyone is talking. Wonder what Blair Waldorf thinks. Sure, they're BFF's, but we always thought Blair's boyfriend Nate had a thing for Serena.



### How do we encode these 'blasts'?

Better lock it down with Nate, B. Clock's ticking.

- +1 Nate
- -1 Blair



### How do we encode these 'blasts'?

This just in: S and B committing a crime of fashion. Who doesn't love a five-finger discount. Especially if it's the middle one.

- -1 Blair
- -1 Serena

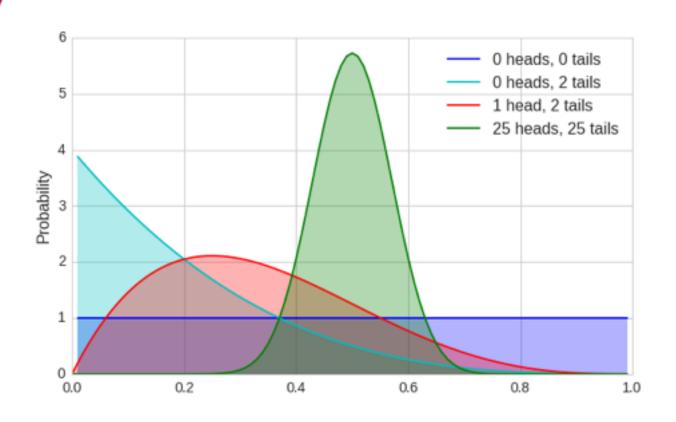


### Simple summations don't work well



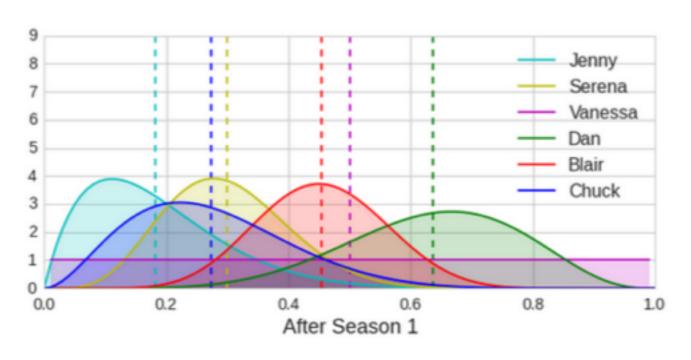


## Beta distributions can model uncertainty

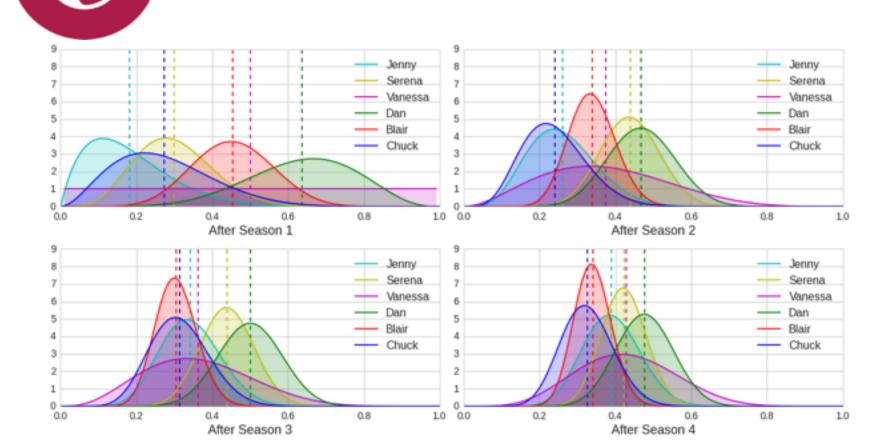




## Beta distributions can model uncertainty



### Beta distributions can model uncertainty





#### Overview: this talk

#### Overview

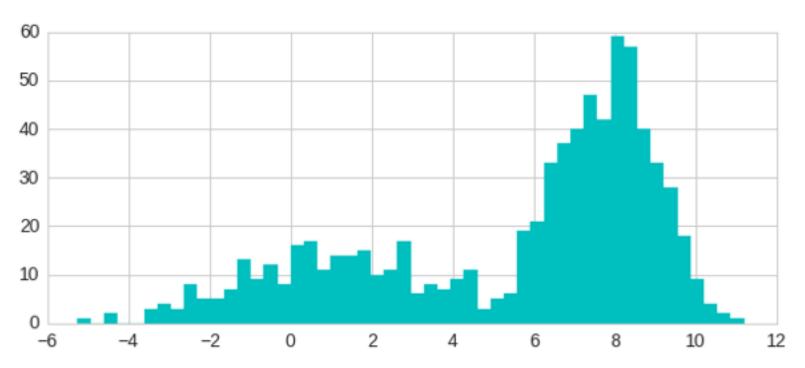
#### Major Models/Model Stacks

- 1. General Mixture Models
- 2. Hidden Markov Models
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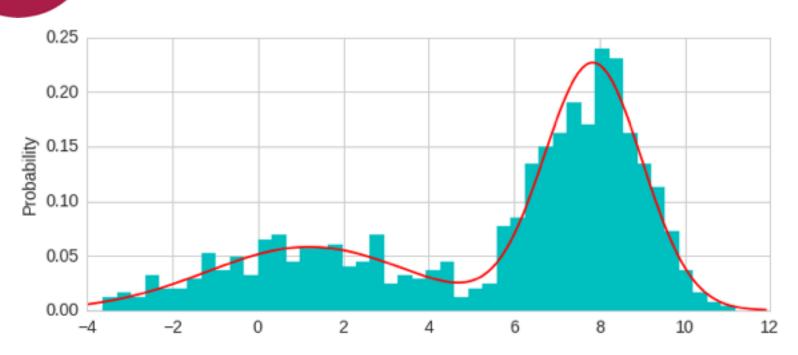
Finale: Train a mixture of HMMs in parallel



# GMMs can model complex distributions



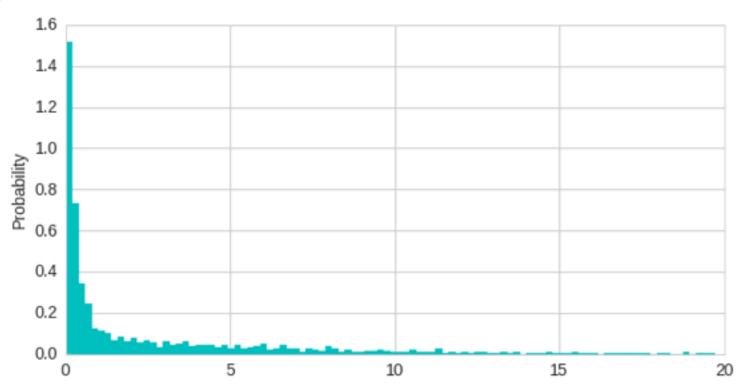
# GMMs can model complex distributions



model = GeneralMixtureModel.from\_samples(NormalDistribution, 2, X)

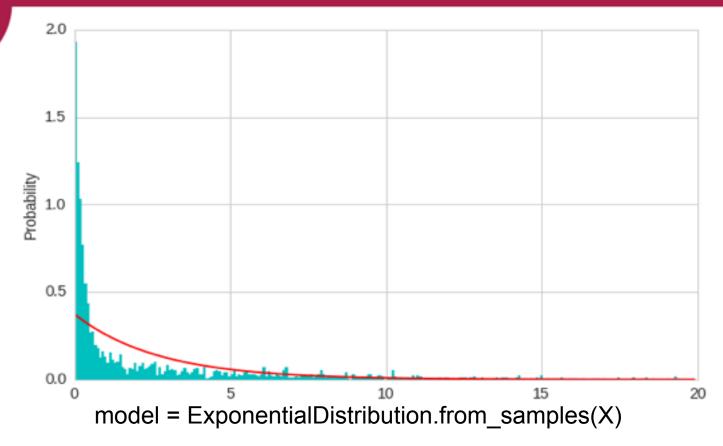


### GMMs can model complex distributions



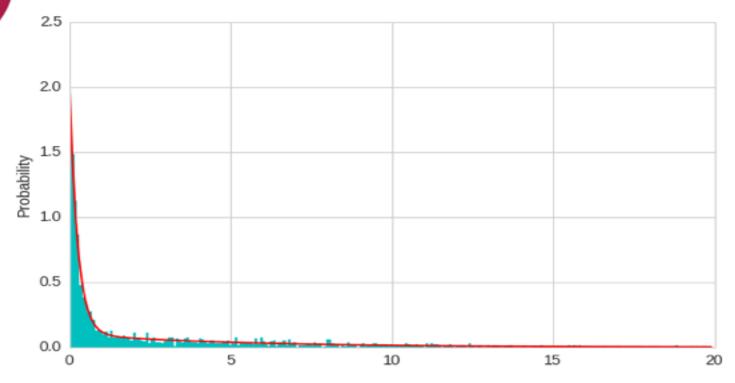


### An exponential distribution is not right





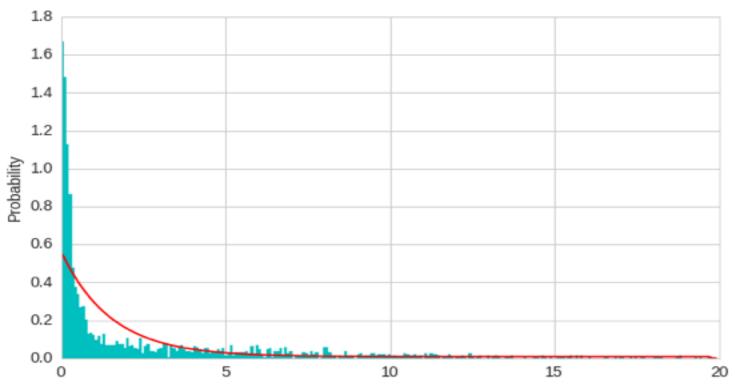
### A mixture of exponentials is better



model = GeneralMixtureModel.from\_samples(ExponentialDistribution, 2, X)



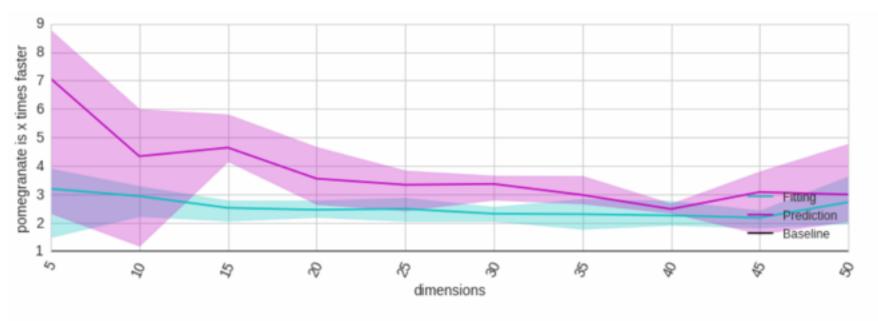
### Heterogeneous mixtures natively supported



model = GeneralMixtureModel.from\_samples([ExponentialDistribution, UniformDistribution], 2, X)



#### GMMs faster than sklearn





#### Overview: this talk

#### Overview

#### Major Models/Model Stacks

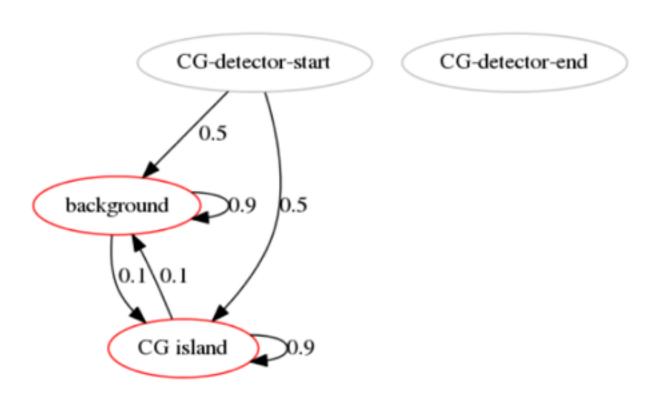
- 1. General Mixture Models
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#### CG enrichment detection HMM

#### GACTACGACTCGCGCTCGCACGTCGCTCGACATCATCGACA





#### CG enrichment detection HMM

#### GACTACGACTCGCGCTCGCACGTCGCTCGACATCATCGACA

```
d1 = DiscreteDistribution(\{'A': 0.25, 'C': 0.25, 'G': 0.25, 'T': 0.25\})
d2 = DiscreteDistribution(\{'A': 0.10, 'C': 0.40, 'G': 0.40, 'T': 0.10\})
s1 = State(d1, name="background")
s2 = State(d2, name="CG island")
hmm = HiddenMarkovModel("CG-detector")
hmm.add states(s1, s2)
hmm.add transition(hmm.start, s1, 0.5)
hmm.add transition(hmm.start, s2, 0.5)
hmm.add transition(s1, s1, 0.9)
hmm.add transition(s1, s2, 0.1)
hmm.add transition(s2, s1, 0.1)
hmm.add transition(s2, s2, 0.9)
hmm.bake()
                                                                         47
```



# pomegranate HMMs are feature rich

Feature	pomegranate	hmmlearn
Graph Structure		
Silent States	✓	
Optional Explicit End State	✓	
Sparse Implementation	✓	
Arbitrary Emissions Allowed on States	✓	
Discrete/Gaussian/GMM Emissions	✓	✓
Large Library of Other Emissions	✓	
Build Model from Matrices	✓	✓
Build Model Node-by-Node	✓	
Serialize to JSON	✓	
Serialize using Pickle/Joblib	✓	✓

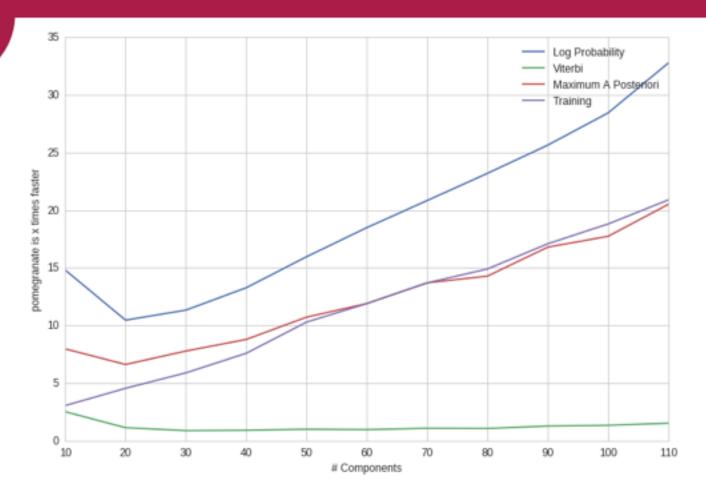
Algorithms		
Priors		✓
Sampling	✓	✓
Log Probability Scoring	<b>√</b>	✓
Forward-Backward Emissions	✓	✓
Forward-Backward Transitions	✓	
Viterbi Decoding	✓	✓
MAP Decoding	✓	✓
Baum-Welch Training	✓	✓
Viterbi Training	✓	
Labeled Training	✓	
Tied Emissions	✓	
Tied Transitions	✓	
Emission Inertia	✓	
Transition Inertia	✓	
Emission Freezing	✓	✓
Transition Freezing	✓	✓
Multi-threaded Training	<b>√</b>	



#### GMM-HMM easy to define

```
d1 = GeneralMixtureModel([NormalDistribution(5, 2), NormalDistribution(5, 4)])
d2 = GeneralMixtureModel([NormalDistribution(15, 1), NormalDistribution(15, 5)])
s1 = State(d1, name="GMM1")
s2 = State(d2, name="GMM2")
model = HiddenMarkovModel()
model.add_states(s1, s2)
model.add_transition(model.start, s1, 0.75)
model.add_transition(model.start, s2, 0.25)
model.add_transition(s1, s1, 0.85)
model.add_transition(s1, s2, 0.15)
model.add_transition(s2, s2, 0.90)
model.add_transition(s2, s1, 0.10)
model.bake()
```

#### HMMs are faster than hmmlearn





#### Overview: this talk

#### Overview

#### Major Models/Model Stacks

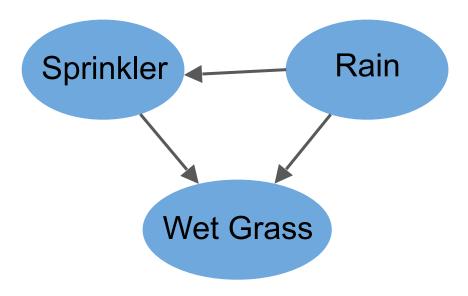
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### Bayesian networks

Bayesian networks are powerful inference tools which define a dependency structure between variables.

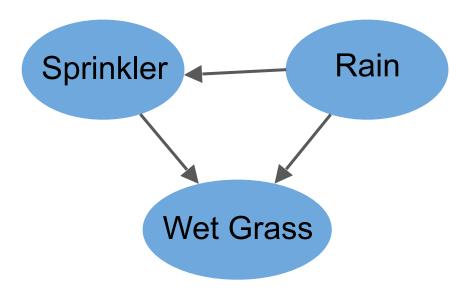




### Bayesian networks

Two main difficult tasks:

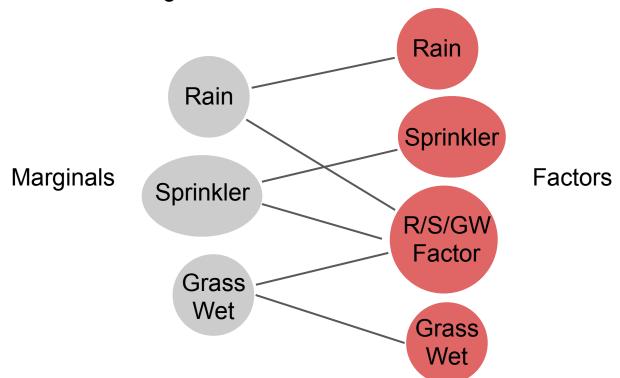
- (1) Inference given incomplete information
- (2) Learning the dependency structure from data





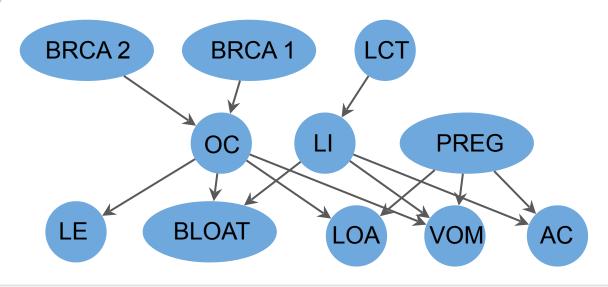
### Bayesian network inference

Inference is done using Belief Bropagation on a factor graph. Messages are sent from one side to the other until convergence.





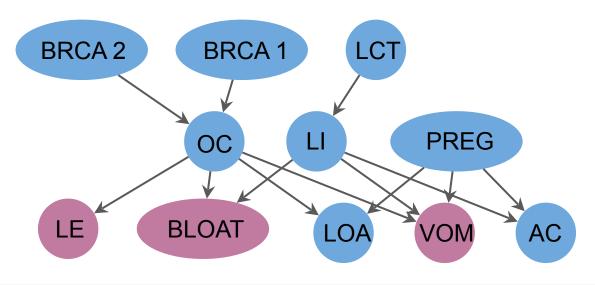
### Inference in a medical diagnostic network



```
d = model.predict_proba()
print "\t".join( "{:7}".format(state.name) for state in model.states )
print "\t".join( "{:4.2}".format(model.parameters[0][1]) for model in d )
BRCA1
        BRCA2
                LCT
                                        PREG
                                                        BLOAT
                                                                         VOM
                                                                                 AC
                        oc
                                LI
                                                LE
                                                                 LOA
                                         0.1
0.001
        0.015
                0.05
                        0.005
                                0.05
                                                0.014
                                                        0.16
                                                                 0.017
                                                                         0.091
                                                                                 0.15
```



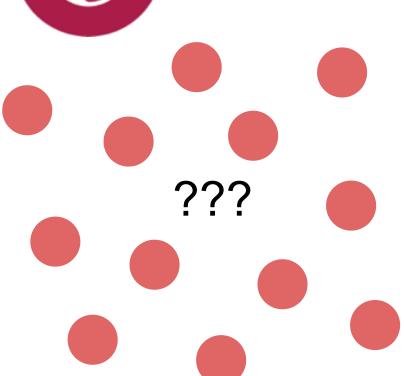
### Inference in a medical diagnostic network



```
d = model.predict_proba({'VOM' : 1, 'BLOAT' : 1, 'LE' : 1})
print "\t".join( "{:7}".format(state.name) for state in model.states )
print "\t".join( "{:4.2}".format(model.parameters[0][1]) for model in d )
BRCA1
        BRCA2
                LCT
                        OC
                                 LI
                                         PREG
                                                 LE
                                                         BLOAT
                                                                  LOA
                                                                          VOM
                                                                                  AC
0.056
        0.68
                0.087
                        0.91
                                0.096
                                          0.2
                                                  1.0
                                                          1.0
                                                                  0.52
                                                                           1.0
                                                                                  0.24
```



### Bayesian network structure learning

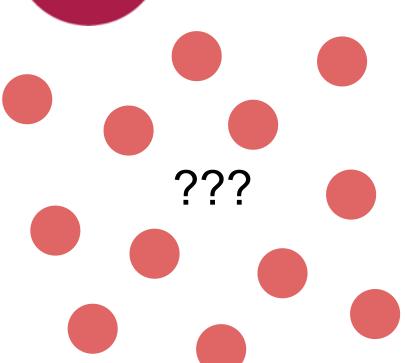


#### Three primary ways:

- "Search and score" / Exact
- "Constraint Learning" / PC
- Heuristics



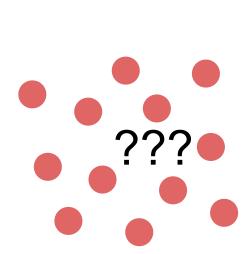
### Bayesian network structure learning

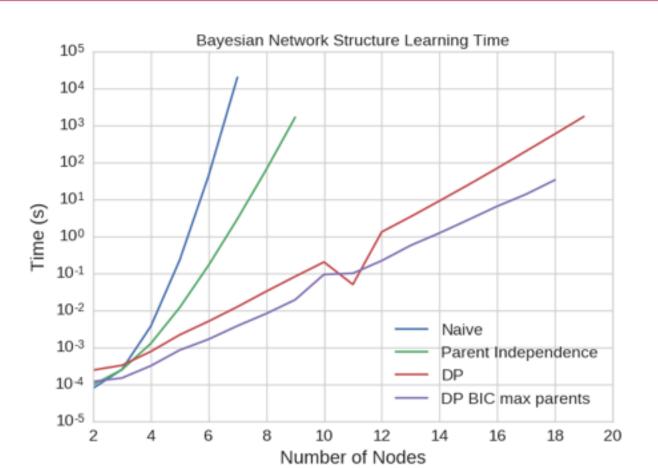


#### pomegranate supports:

- "Search and score" / Exact
- "Constraint Learning" / PC
- Heuristics

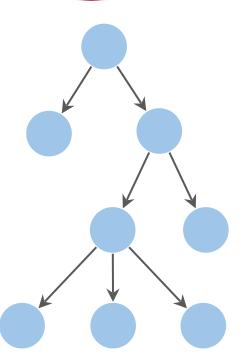
#### Exact structure learning is intractable

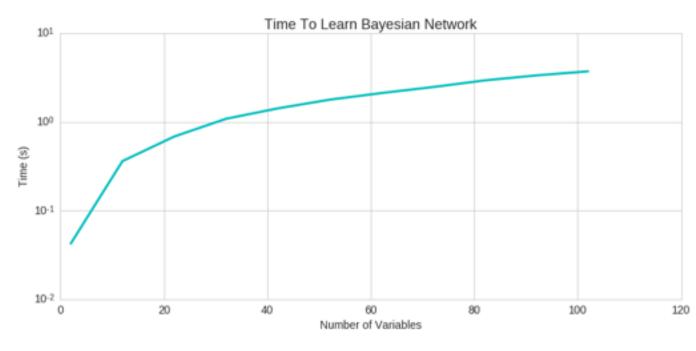




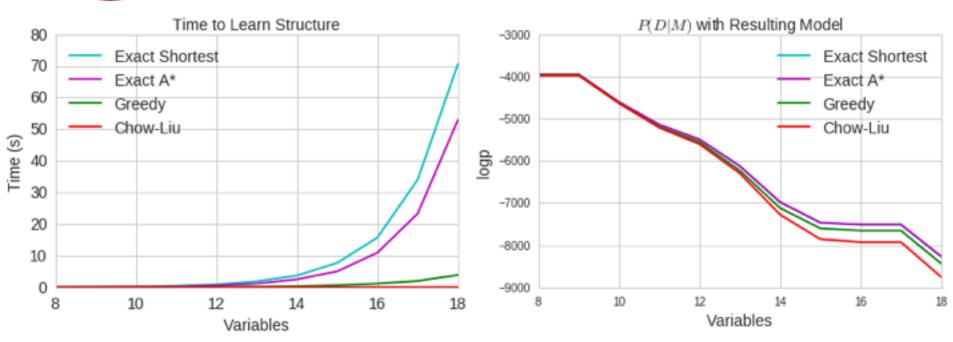


# Chow-Liu trees are fast approximations



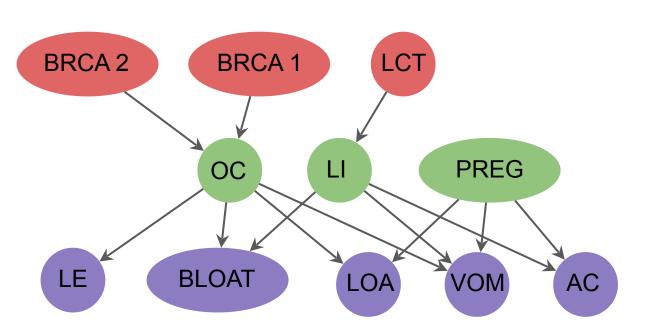


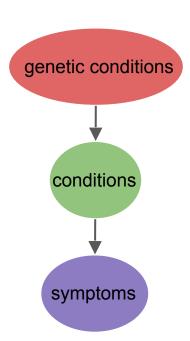
### pomegranate supports four algorithms



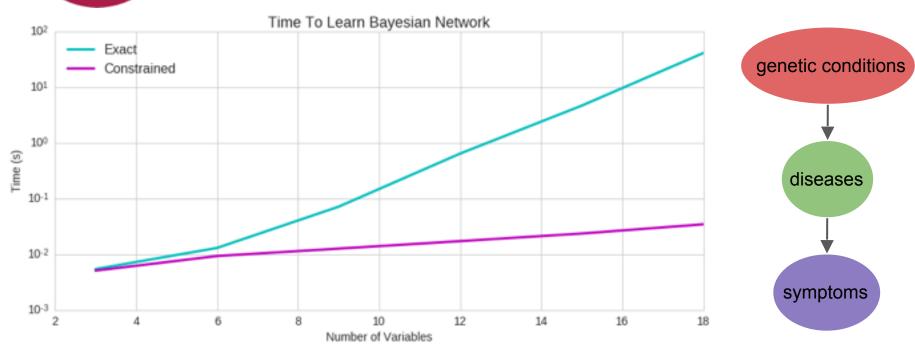


# Constraint graphs merge data + knowledge



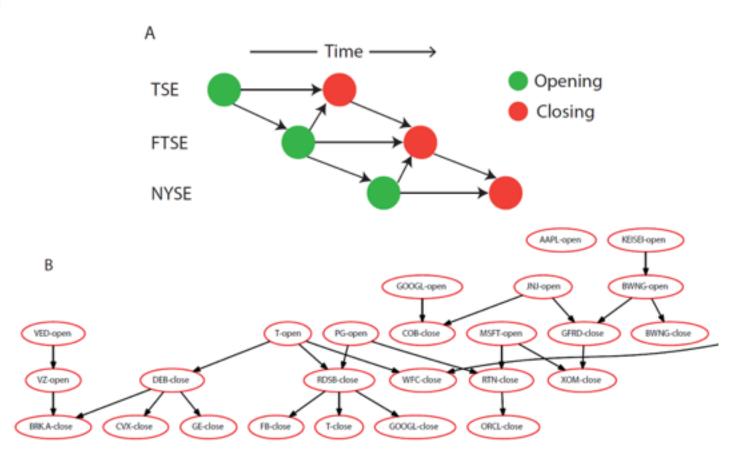


# Constraint graphs merge data + knowledge





### Modeling the global stock market





### Constraint graph published in PeerJ CS

# Finding the optimal Bayesian network given a constraint graph

Jacob M. Schreiber<sup>1</sup> and William S. Noble<sup>2</sup>

#### **ABSTRACT**

Despite recent algorithmic improvements, learning the optimal structure of a Bayesian network from data is typically infeasible past a few dozen variables. Fortunately, domain knowledge can frequently be exploited to achieve dramatic computational savings, and in many cases domain knowledge can even make structure learning tractable. Several methods have previously been described for representing this type of structural prior

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Department of Genome Science, University of Washington, Seattle, WA, United States of America



#### Overview: this talk

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Finale: Train a mixture of HMMs in parallel

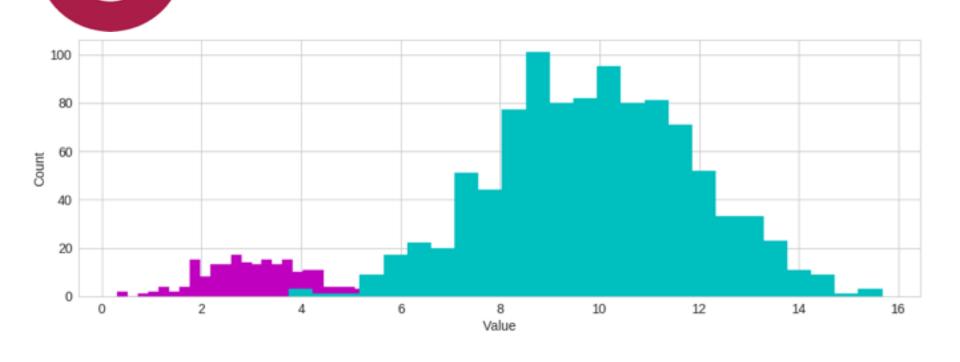


### Bayes classifiers rely on Bayes' rule

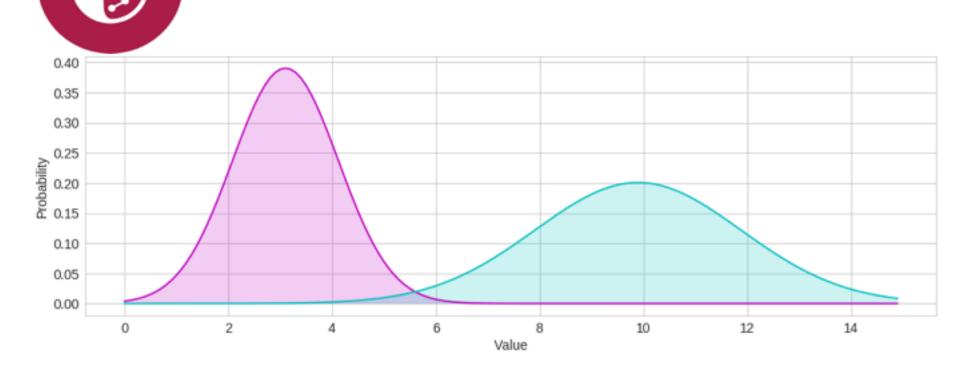
$$P(M|D) = \frac{P(D|M)P(M)}{\sum\limits_{M} P(D|M)P(M)}$$

$$Posterior = \frac{Likelihood * Prior}{Normalization}$$

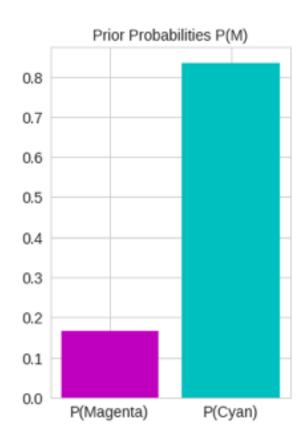
# Let's build a classifier on this data



# Likelihood function alone is not good

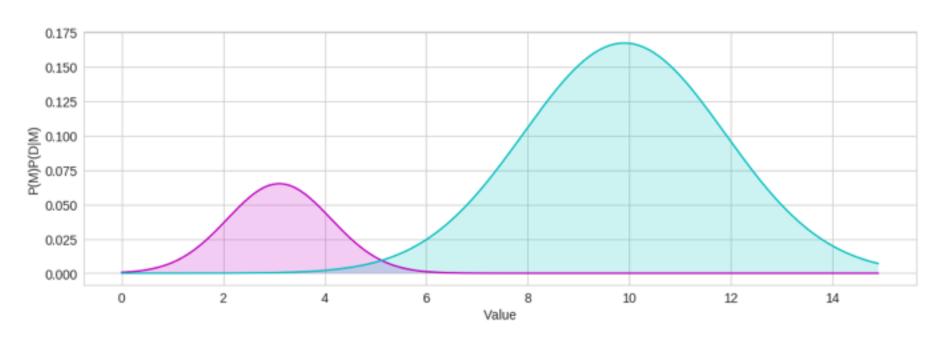


#### Priors can model class imbalance





# The posterior is a good model of the data





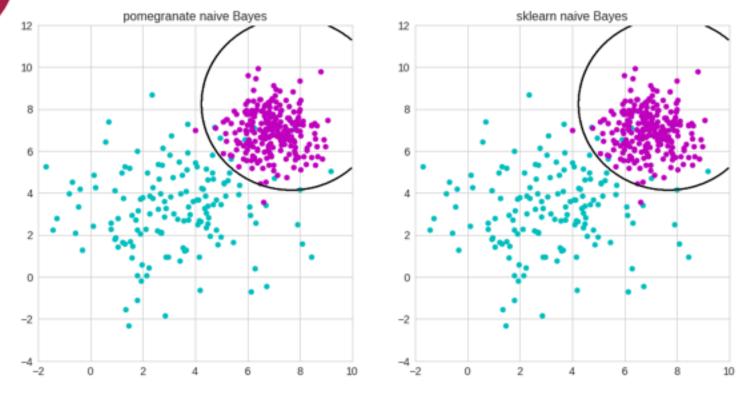
### Naive Bayes assumes independent features

$$P(M|D) = \frac{\prod_{i=1}^{d} P(D_i|M)P(M)}{\sum_{M} \prod_{i=1}^{d} P(D_i|M)P(M)}$$

$$Posterior = \frac{Likelihood * Prior}{Normalization}$$



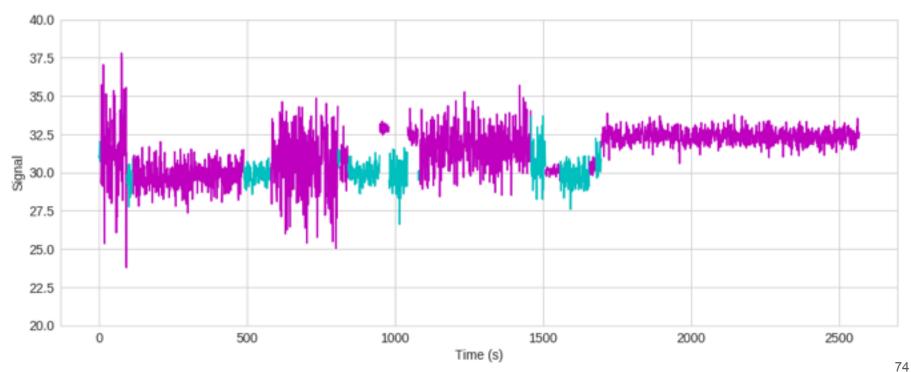
## Naive Bayes produces ellipsoid boundaries



model = NaiveBayes.from\_samples(NormalDistribution, X, y)

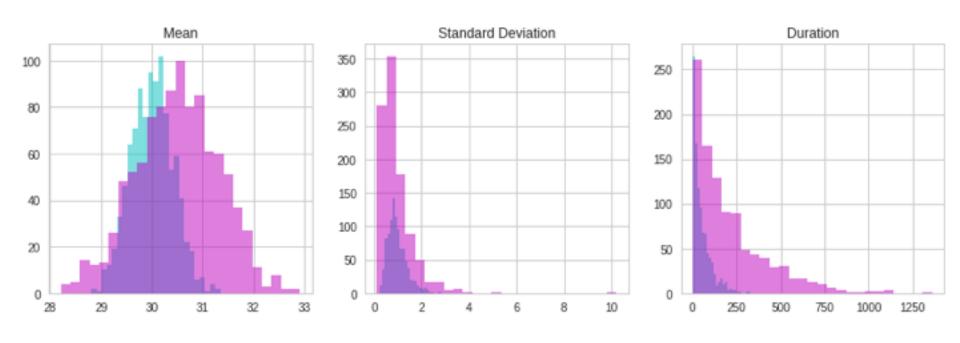


## Naive Bayes can be heterogeneous





## Data can fall under different distributions





## Using appropriate distributions is better

```
model = NaiveBayes.from_samples(NormalDistribution, X_train, y_train)

print "Gaussian Naive Bayes: ", (model.predict(X_test) == y_test).mean()

clf = GaussianNB().fit(X_train, y_train)

print "sklearn Gaussian Naive Bayes: ", (clf.predict(X_test) == y_test).mean()

model = NaiveBayes.from_samples([NormalDistribution, LogNormalDistribution,

ExponentialDistribution], X_train, y_train

print "Heterogeneous Naive Bayes: ", (model.predict(X_test) == y_test).mean()
```

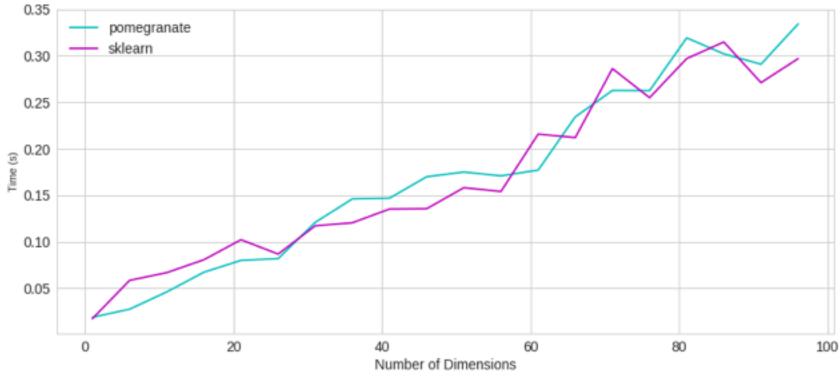
Gaussian Naive Bayes: 0.798

sklearn Gaussian Naive Bayes: 0.798 Heterogeneous Naive Bayes: 0.844

76

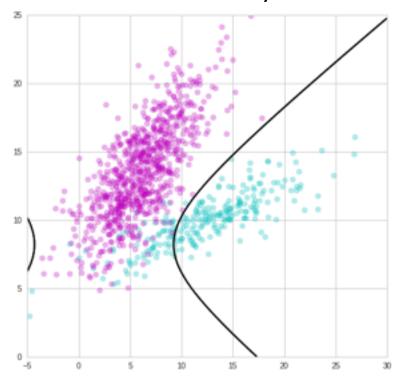
# This additional flexibility is just as fast



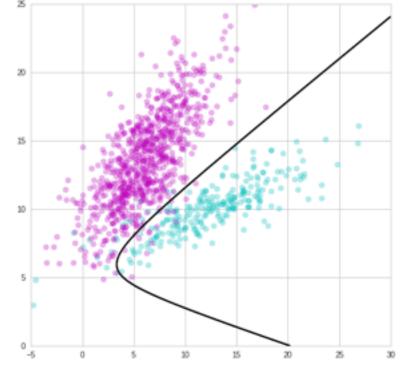


## Bayes classifiers don't require independence



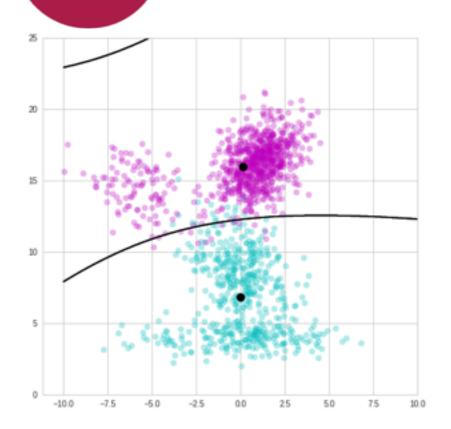


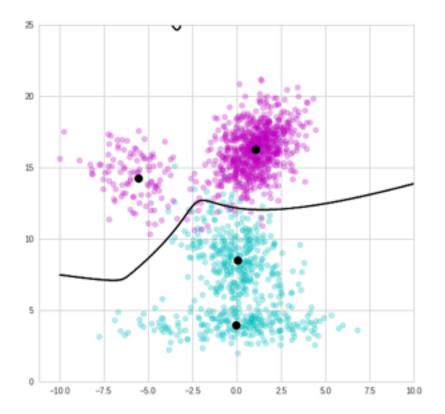
### bayes classifier accuracy: 0.966





# Gaussian mixture model Bayes classifier







## Creating complex Bayes classifiers is easy

```
gmm_a = GeneralMixtureModel.from_samples(MultivariateGaussianDistribution, 2, X[y == 0]) gmm_b = GeneralMixtureModel.from_samples(MultivariateGaussianDistribution, 2, X[y == 1]) model_b = BayesClassifier([gmm_a, gmm_b], weights=numpy.array([1-y.mean(), y.mean()]))
```



## Creating complex Bayes classifiers is easy

```
mc a = MarkovChain.from samples(X[y == 0])
mc b = MarkovChain.from samples(X[y == 1])
model b = BayesClassifier([mc_a, mc_b], weights=numpy.array([1-y.mean(), y.mean()]))
hmm a = HiddenMarkovModel.from samples(X[y == 0])
hmm b = HiddenMarkovModel.from samples(X[y == 1])
model b = BayesClassifier([hmm_a, hmm_b], weights=numpy.array([1-y.mean(), y.mean()]))
bn a = BayesianNetwork.from samples(X[y == 0])
bn b = BayesianNetwork.from samples(X[y == 1])
model b = BayesClassifier([bn_a, bn_b], weights=numpy.array([1-y.mean(), y.mean()]))
```



## Overview: this talk

#### Overview

Major Models/Model Stacks

- 1. General Mixture Models
- 2. Hidden Markov Models
- 3. Bayesian Networks
- 4. Bayes Classifiers

Finale: Train a mixture of HMMs in parallel



## Training a mixture of HMMs in parallel

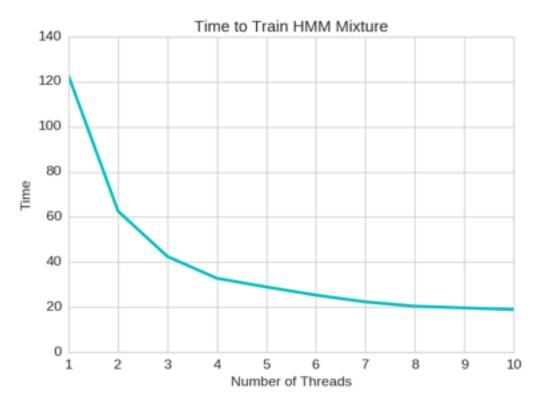
Creating a mixture of HMMs is just as simple as passing the HMMs into a GMM as if it were any other distribution

```
model_C = create_profile_hmm(dC, I)
model_mC = create_profile_hmm(dmC, I)
model_hmC = create_profile_hmm(dhmC, I)

model = GeneralMixtureModel([model_C, model_mC, model_hmC])
return model
```



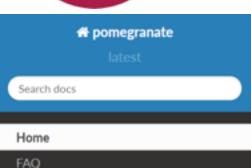
## Training a mixture of HMMs in parallel



fit(model, X, n\_jobs=n)



## Documentation available at Readthedocs



Out of Core Probability Distributions

General Mixture Models Hidden Markov Models

Bayes Classifiers and Naive Bayes

Markov Chains

Bayesian Networks

Factor Graphs





build passing obuild passing docs latest

#### Home

pomegranate is a python package which implements fast, efficient, and extremely flexible probabilistic models ranging from probability distributions to Bayesian networks to mixtures of hidden Markov models. The most basic level of probabilistic modeling is the a simple probability distribution. If we're modeling language, this may be a simple distribution over the frequency of all possible words a person can say.



## Tutorials available on github

Branch: master ▼ pomegranate / tutorials /		Create new file	Upload files	Find file	History
jmschrei ADD bayes backend		Latest commit 724518d 10 hours ago			
-					
⊚ GGBlasts.xlsx	PyData Chicago 2016			8 mor	nths ago
PyData_2016_Chicago_TutoriaLipynb	FIX markov chain notebooks			3 mor	nths ago
README.md	Update README.md			2 y	ears ago
Tutorial_0_pomegranate_overview.ipynb	Minor typos			3 mor	nths ago
☐ Tutorial_1_Distributions.ipynb	ENH tutorials			2 y	ears ago
Tutorial_2_General_Mixture_Models.ipynb	FIX hmm dimensionality			11 mor	nths ago
☐ Tutorial_3_Hidden_Markov_Models.ipynb	edit tutorial 3 to remove deprecated bake			7 mor	nths ago
Tutorial_4_Bayesian_Networks.ipynb	ENH pomegranate vs libpgm tutorial			7 mor	nths ago
☐ Tutorial_4b_Bayesian_Network_Structure_Learning.i	ENH a* search			28 c	days ago
☐ Tutorial_5_Bayes_Classifiers.ipynb	ADD bayes backend			10 h	ours ago
☐ Tutorial_6_Markov_Chain.ipynb	FIX markov chain notebooks			3 mor	nths ago
Tutorial_7_Parallelization.ipynb	ADD tutorial 7 parallelization			8 mor	nths ago

https://github.com/jmschrei/pomegranate/tree/master/tutorials



## Acknowledgements











# pomegranate

fast and flexible probabilistic modeling in python

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