

Getting Started with DPP

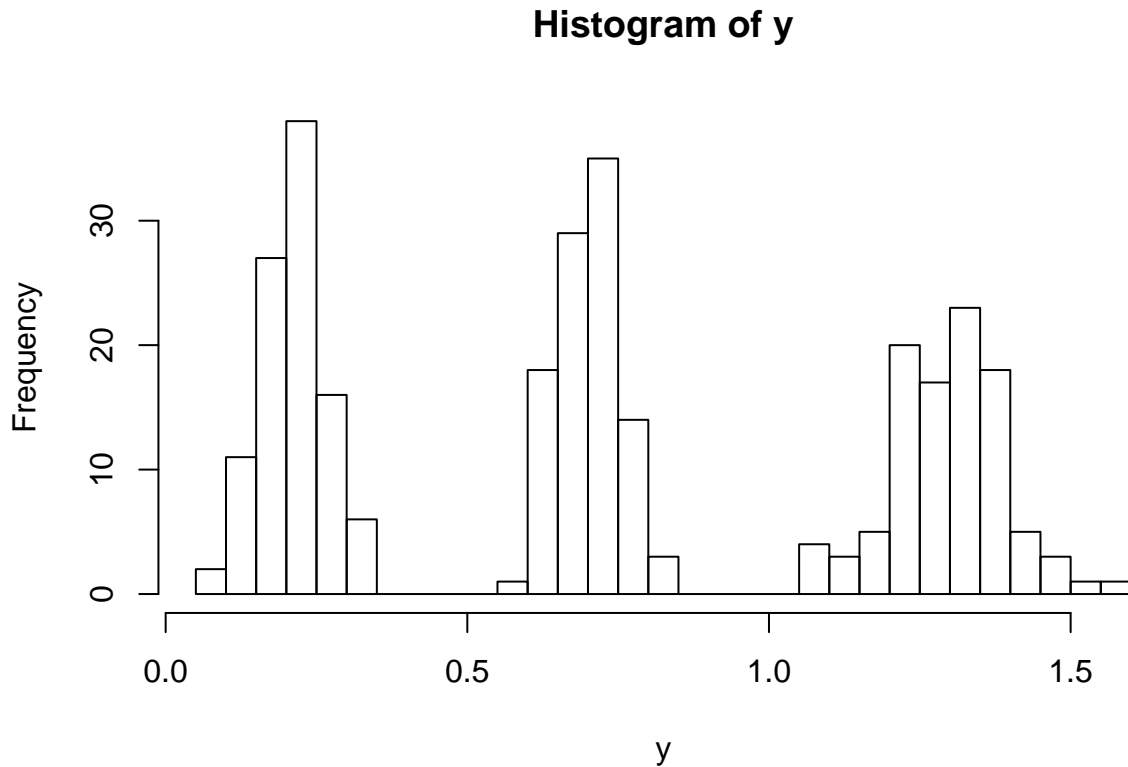
Introduction

DPP can be used to infer the number of categories or clusters in a one dimensional numeric vector. From a potentially infinite number of normal distributions the MCMC algorithm will try to find the most likely number of normal distributions (k) that describes the data.

Simulating data

For a very simple example, we generate data from three normal distributions

```
set.seed(12345)
y <- c(rnorm(100,mean=0.2,sd=0.05), rnorm(100,0.7,0.05), rnorm(100,1.3,0.1))
hist(y,breaks=30)
```



Setup

We load the DPP library and create a NormalModel object with the initial (prior) parameters for the potentially infinite number of normal distributions we will infer from the data.

```
library(DPP)
normal.model<-new(NormalModel,
                  mean_prior_mean=0.5,
```

```
mean_prior_sd=0.1,  
sd_prior_shape=3,  
sd_prior_rate=20,  
estimate_concentration_parameter=TRUE,  
concentration_parameter_alpha=10,  
proposal_disturbance_sd=0.1)
```

Creating a dppMCMC_C object and running the MCMC

We setup some additional mcmc parameters and instantiate an object of the class dppMCMC_C. Note that we are passing the previously created NormalModel object as a paramter.

```
my_dpp_analysis <- dppMCMC_C(data=y,  
                             output = "output_prefix_",  
                             model=normal.model,  
                             num_auxiliary_tables=4,  
                             expected_k=1.5,  
                             power=1)  
  
#this might take a few minutes  
my_dpp_analysis$run(generations=1000,auto_stop=TRUE,max_gen = 10000,min_ess = 500)
```

Results

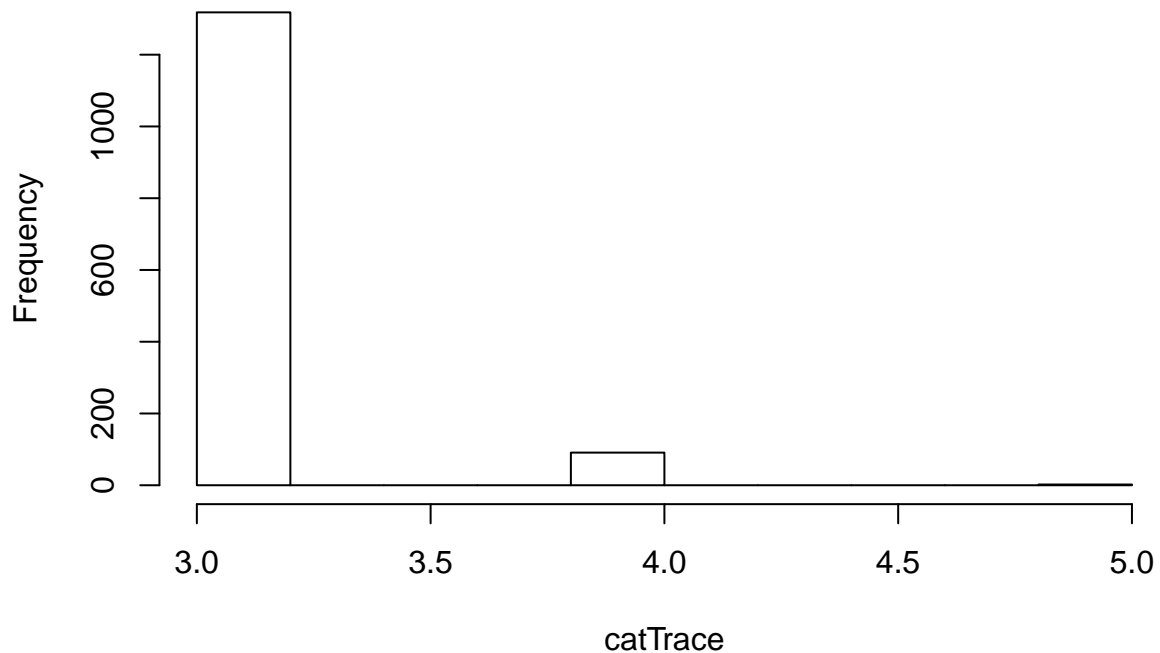
The inferred number of categories/clusters/distributions

To infer of the number of categories we look at the actual posterior distribution of the parameter k or its MCMC trace .

A histogram of the trace

```
catTrace<-my_dpp_analysis$getNumCategoryTrace(0.25) # we discard the first 25% results  
length(catTrace)  
  
## [1] 1411  
hist(catTrace)
```

Histogram of catTrace



The probabilities for k categories

```
category_probabilities<-my_dpp_analysis$getNumCategoryProbabilities(0.25)
category_probabilities
```

```
##           1           2           3           4           5
## 0.000000000 0.000000000 0.934089298 0.064493267 0.001417434
```

The most likely number of categories

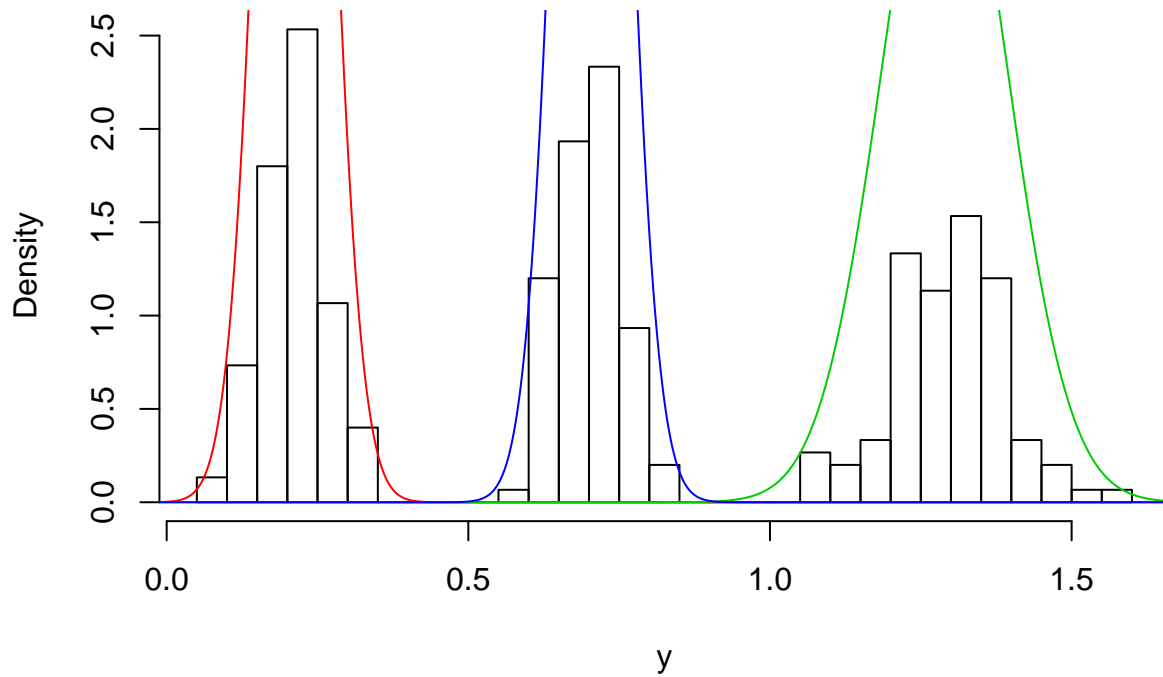
```
topNumCat<-as.numeric(names(which.max(category_probabilities)))
topNumCat
```

```
## [1] 3
```

Plotting the inferred normal distributions

```
hist(y,breaks=30,prob=TRUE)
params<-my_dpp_analysis$dpp_mcmc_object$getParamVector()
for(j in 1:topNumCat) {
  curve(dnorm(x,
             mean=params[[1]][j],
             sd=params[[2]][j]),
        from=-10,
        to=10,
        col=1+j,
        add=TRUE,
        n=20001)
}
```

Histogram of y



```
params
```

```
## $means  
## [1] 0.2122830 1.2894813 0.7043112  
##  
## $sds  
## [1] 0.05298712 0.10338958 0.05251156
```

And the allocation of the individual elements of the numeric vector as classified in one of the inferred normal distributions

```
allocations<- my_dpp_analysis$dpp_mcmc_object$getAllocationVector()  
head(allocations)
```

```
## [1] 1 1 1 1 1 1
```

```
table(allocations)
```

```
## allocations  
## 1 2 3  
## 100 100 100
```