

The Dirichlet Process and Clustering

The Dirichlet Process is a model for a *random discrete distribution* represented by pmf $\tilde{f}$.

Suppose we want to sample

- $\tilde{f} \sim DP(\alpha, G_X)$, then
- $Y_1, \dots, Y_n \sim \tilde{f}$ independently

and study the *marginal distribution* for $Y_1, \dots, Y_n$

$$f_{Y_1, \dots, Y_n}(y_1, \dots, y_n) = \int \prod_{i=1}^n \tilde{f}(y_i) \pi_0(d\tilde{f})$$

where $\pi_0(d\tilde{f}) \equiv DP(\alpha, G_X)$.

The marginal distribution is merely the *prior predictive distribution* under the nonparametric model.

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To sample from the marginal distribution *directly* using the *Polya Urn*:

- Sample $Y_1 \sim G_X$
- For $i = 2, \dots, n$, sample $Y_i | Y_1, \dots, Y_{i-1}$ from the conditional distribution, which is a mixture of the uniform *discrete* distribution on $\{y_1, \dots, y_{i-1}\}$ and G_X , with weights

$$\frac{i-1}{\alpha + i - 1} \quad \text{and} \quad \frac{\alpha}{\alpha + i - 1}$$

respectively. That is, for $j = 1, \dots, i-1$,

$$\Pr[Y_i = y_j | Y_1 = y_1, \dots, Y_{i-1} = y_{i-1}] = \frac{1}{\alpha + i - 1}$$

and with the remaining probability $\alpha/(\alpha + i - 1)$, $Y_i \sim G_X$.

The Dirichlet Process and Clustering

```
polya.urn<-function(nv,alv,muv,sigv){  
  
  y<-rep(0,nv)  
  y[1]<-rnorm(1,muv,sigv)  
  u<-runif(nv)  
  for(i in 2:nv){  
    if(u[i] < alv/(alv+i-1)){  
      y[i]<-rnorm(1,muv,sigv)  
    }else{  
      y[i]<-sample(y[1:(i-1)],size=1)  
    }  
  }  
  return(y)  
  
}  
set.seed(3)  
polya.urn(5,alv=2,0,1)  
  
+ [1] -0.96193342 -0.53999302 -0.53999302 -0.53999302 0.08541773
```

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```
n<-20
a1<-2
nreps<-10000
Y.samp<-replicate(nreps,polya.urn(n,2,0,1))
library(dplyr,warn.conflicts = FALSE)
K.samp<-apply(Y.samp,2,n_distinct)
table(K.samp)           #Counts of numbers of distinct Y values

+ K.samp
+   1     2     3     4     5     6     7     8     9    10    11    12    14
+  41   283   980 1867 2320 2106 1376  684  241   84   15    2    1

prob.K.samp<-tabulate(K.samp,n)/nreps  #Proportions
```

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Exact calculation:

$$\Pr[K = k] = \frac{\alpha^k B(n, k)}{\sum_{j=1}^n \alpha^j B(n, j)}$$

where $B(n, k)$ is an (unsigned) Stirling Number of the First Kind.

```
library(gmp)    #For the Stirling numbers
Stirling1.all(n)

+ Big Integer ('bigz') object of length 20:
+  [1] -121645100408832000  431565146817638400  -668609730341153280
+  [4] 610116075740491776   -371384787345228000  161429736530118960
+  [7] -52260903362512720   12953636989943896   -2503858755467550
+ [10] 381922055502195       -46280647751910     4465226757381
+ [13] -342252511900          20692933630         -973941900
+ [16] 34916946               -920550              16815
+ [19] -190                   1
```

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```
S.nk<-abs(as.numeric(Stirling1.all(n)))
lprob.vec<-c(1:n)*log(al)+log(S.nk)
prob.vec<-exp(lprob.vec-max(lprob.vec))
prob.vec<-prob.vec/sum(prob.vec)
round(prob.vec,6)

+ [1] 0.004762 0.033788 0.104693 0.191068 0.232611 0.202218 0.130931
+ [9] 0.025092 0.007655 0.001855 0.000358 0.000055 0.000007 0.000001
+ [17] 0.000000 0.000000 0.000000 0.000000

prob.compare<-cbind(prob.vec,prob.K.samp)
row.names(prob.compare)<-paste('K =',1:n)
colnames(prob.compare)<-c('True','Sample')
```

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```
prob.compare[1:10,]
```

		True	Sample
+			
+ K = 1	0.004761905	0.0041	
+ K = 2	0.033787997	0.0283	
+ K = 3	0.104693271	0.0980	
+ K = 4	0.191068256	0.1867	
+ K = 5	0.232610962	0.2320	
+ K = 6	0.202217902	0.2106	
+ K = 7	0.130931146	0.1376	
+ K = 8	0.064906438	0.0684	
+ K = 9	0.025092034	0.0241	
+ K = 10	0.007654746	0.0084	

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We can sample the cluster membership *directly* in the Polya Urn

```
polya.urn.labels<-function(nv, alv, muv, sigv) {  
  z<-rep(0, nv)  
  z[1]<-1  
  u<-runif(nv)  
  Kco<-1  
  for(i in 2:nv) {  
    if(u[i] < alv/(alv+i-1)) {  
      Kco<-Kco+1  
    }  
    z[i]<-Kco  
  }  
  return(z)  
}  
  
set.seed(3)  
polya.urn.labels(5, alv=2, 0, 1)  
  
+ [1] 1 1 2 3 3
```

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```
K.samp.labels<-replicate(nreps,polya.urn.labels(n,2,0,1))[,n]
prob.K.samp.labels<-tabulate(K.samp,n)/nreps #Proportions
prob.compare<-cbind(prob.vec,prob.K.samp,prob.K.samp.labels)
row.names(prob.compare)<-paste('K =',1:n)
colnames(prob.compare)<-c('True','Sample','Labels')
prob.compare[1:10,]
```

	True	Sample	Labels
+ K = 1	0.004761905	0.0041	0.0041
+ K = 2	0.033787997	0.0283	0.0283
+ K = 3	0.104693271	0.0980	0.0980
+ K = 4	0.191068256	0.1867	0.1867
+ K = 5	0.232610962	0.2320	0.2320
+ K = 6	0.202217902	0.2106	0.2106
+ K = 7	0.130931146	0.1376	0.1376
+ K = 8	0.064906438	0.0684	0.0684
+ K = 9	0.025092034	0.0241	0.0241
+ K = 10	0.007654746	0.0084	0.0084

In both approaches we can sample the *observables* Y *without* having to sample the components of $\tilde{f}$.

The Dirichlet Process and Clustering

In the *posterior distribution* we have $\alpha^* = \alpha + n$, for any set B

$$G_X^*(B) = \frac{\alpha}{\alpha + n} G_X(B) + \frac{1}{\alpha + n} \sum_{i=1}^n \delta_{y_i}(B).$$

and then

$$\pi_n(\tilde{df}) \equiv DP(\alpha^*, G_X^*).$$

Posterior predictive: To obtain the posterior predictive, we compute in the usual way

$$f_{Y_{n+1}, \dots, Y_{n+m} | Y_1, \dots, Y_n}(y_{n+1}, \dots, y_{n+m} | y_1, \dots, y_n) = \int \prod_{i=n+1}^{n+m} \tilde{f}(y_i) \pi_n(d\tilde{f})$$

To obtain the sample $Y_{n+1}, \dots, Y_{n+m}$ from the posterior predictive we may use *direct* simulation

- sample $\tilde{f} \sim \pi_n(d\tilde{f})$
- sample $Y_{n+1}, \dots, Y_{n+m}$ independently from $\tilde{f}$

We may also use the *Polya Urn*

- Sample $Y_{n+1} \sim G_X^*$, that is

$$Y_{n+1} \sim \begin{cases} G_X & \text{w.p. } \alpha/(\alpha + n) \\ \delta_{y_i}(y) & \text{w.p. } 1/(\alpha + n), i = 1, \dots, n. \end{cases}$$

- For $i = 2, \dots, m$, sample

$$Y_{n+i} \sim \begin{cases} G_X^* & \text{w.p. } \alpha^*/(\alpha^* + i - 1) \\ \delta_{y_{n+j}}(y) & \text{w.p. } 1/(\alpha^* + i - 1), j = 1, \dots, i - 1. \end{cases}$$

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That is,

$$Y_{n+i} \sim \begin{cases} G_X & \text{w.p. } \alpha/(\alpha + n + i - 1) \\ \delta_{y_j}(y) & \text{w.p. } 1/(\alpha + n + i - 1), j = 1, \dots, n + i - 1. \end{cases}$$

This sequential generation treats the *all* samples obtained *before* $n + i$,

$$y_1, \dots, y_{n-1}, y_n, y_{n+1}, \dots, y_{n+i-1}$$

on an equal basis.

In the limiting case of $\alpha \rightarrow 0$, we have that $\alpha^* = n$ and

$$G_X^*(B) = \frac{1}{n} \sum_{i=1}^n \delta_{y_i}(B).$$

The limiting posterior distribution places random probabilities

$$\pi \sim \text{Dirichlet}(n-1; 1, \dots, 1)$$

on the observed data $\{y_1, \dots, y_n\}$.

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Sample the limiting posterior using stick-breaking:

```
limit.DP<-function(nv,Yv,Mv=10000){
  V<-rbeta(Mv,1,nv)
  pivec<-c(V[1],cumprod(1-V[-Mv])*V[-1])
  Xvec<-sample(Yv,size=Mv,rep=T)
  ptot<-rep(0,nv)
  for(i in 1:nv){
    ptot[i]<-sum(pivec[Xvec==Yv[i]])
  }
  return(ptot)
}

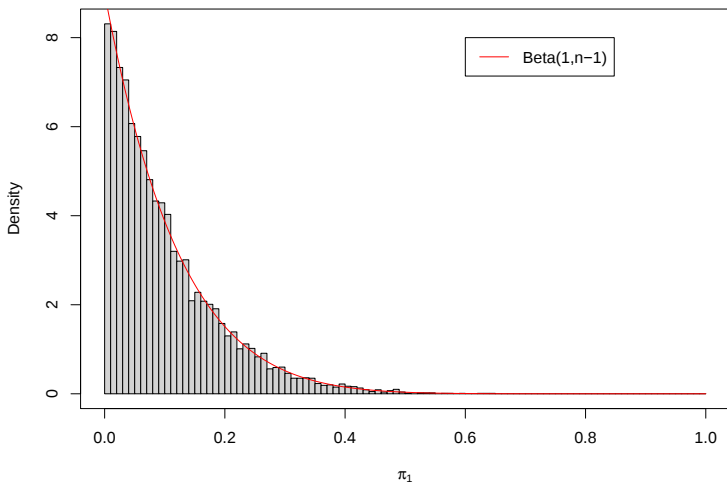
nreps<-10000
n<-10
Y0<-runif(n)
pimat<-replicate(nreps,limit.DP(n,Y0))
```

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Sampled probabilities on y_1 are distributed as $Beta(1, n - 1)$.

```
hist(pimat[1,], freq=FALSE, br=seq(0, 1, by=0.01),  
     main='', xlab=expression(pi[1])); box()  
xv<-seq(0, 1, by=0.001); yv<-dbeta(xv, 1, n-1)  
lines(xv, yv, col='red')  
legend(0.6, 8, c('Beta(1, n-1)'), lty=1, col='red')
```

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Posterior predictive: Direct sampling

```
library(extraDistr)
n<-10
m<-1000
Zsamp<-matrix(0,nrow=nreps,ncol=n)
for(i in 1:nreps){
  pi.vec<-rdirichlet(1,rep(1,n))
  Z<-sample(1:n,size=m,prob=pi.vec,rep=T)
  Zsamp[i,]<-tabulate(Z,nbins=n)
}
```

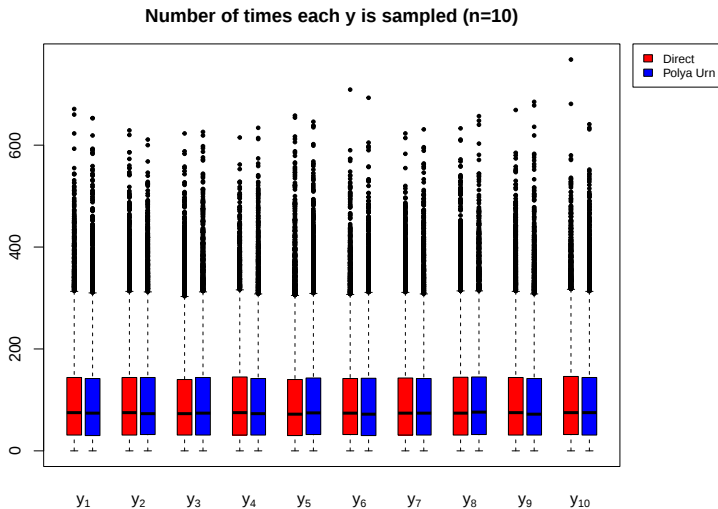
Posterior predictive: Polya Urn

```
set.seed(2413)
Zsamp0<-matrix(0,nrow=nreps,ncol=n)
for(i in 1:nreps){
  Z<-1:n
  for(j in 1:m){Z<-c(Z,sample(Z,size=1))}
  Zsamp0[i,]<-tabulate(Z,nbins=n)-1
}
```

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```
all.Z<-cbind(Zsamp[,1],Zsamp0[,1])
for(j in 2:n){all.Z<-cbind(all.Z,Zsamp[,j],Zsamp0[,j])}
par(mar=c(5,4,3,6),xpd=TRUE,xaxt='n')
avec<-1:(3*n);avec<-avec[-3*(1:n)]
boxplot(all.Z,pch=19,cex=0.5,col=c('red','blue'),at=avec)
legend("topright", c("Direct", "Polya Urn"),cex=0.75,
      fill = c("red", "blue"),inset=c(-0.175,0))
nvec<-c(expression(y[1]),expression(y[2]),
        expression(y[3]),expression(y[4]),
        expression(y[5]),expression(y[6]),
        expression(y[7]),expression(y[8]),
        expression(y[9]),expression(y[10]))
text(1.5+c(0:(n-1))*3,rep(-100,10),nvec)
title('Number of times each y is sampled (n=10)')
```

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Contrast this with ordinary *bootstrap* resampling, which resamples y values with *deterministic* probabilities

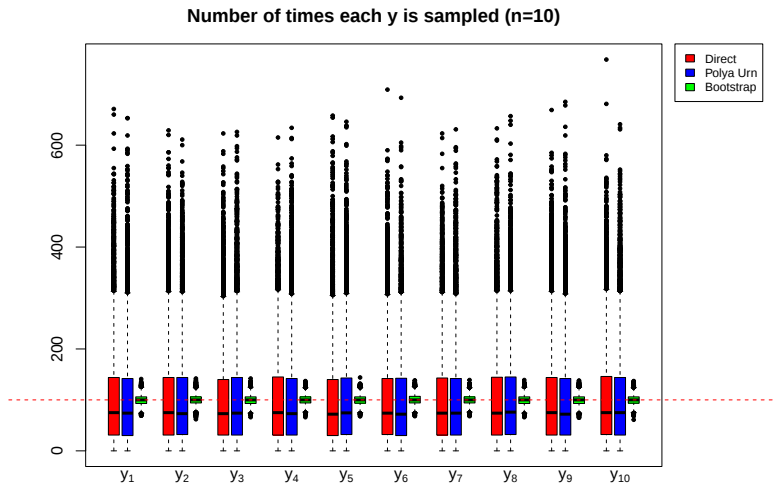
$$\left\{ \frac{1}{n}, \dots, \frac{1}{n} \right\}$$

```
set.seed(2413)
ZsampB<-matrix(0,nrow=nreps,ncol=n)
for(i in 1:nreps){
  Z<-sample(1:n,size=m,rep=T)
  ZsampB[i,]<-tabulate(Z,nbins=n)
}
```

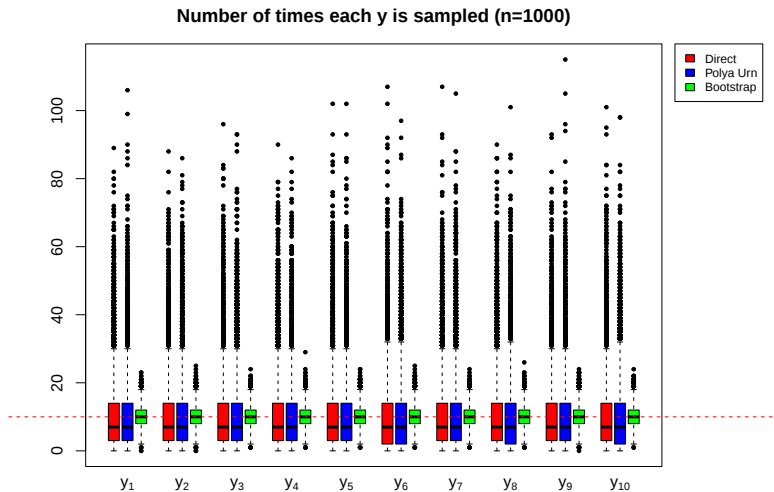
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```
all.Z<-cbind(Zsamp[,1],Zsamp0[,1],ZsampB[,1])
for(j in 2:n){all.Z<-cbind(all.Z,Zsamp[,j],Zsamp0[,j],ZsampB[,j])}
par(mar=c(5,4,3,6),xpd=TRUE,xaxt='n')
avec<-1:(4*n);avec<-avec[-4*(1:n)]
boxplot(all.Z,pch=19,cex=0.5,col=c('red','blue','green'),at=avec)
legend("topright", c("Direct", "Polya Urn", 'Bootstrap'),cex=0.75,
      fill = c("red", "blue", "green"),inset=c(-0.175,0))
nvec<-c(expression(y[1]),expression(y[2]),
        expression(y[3]),expression(y[4]),
        expression(y[5]),expression(y[6]),
        expression(y[7]),expression(y[8]),
        expression(y[9]),expression(y[10]))
text(2+c(0:(n-1))*4,rep(-50,10),nvec)
title('Number of times each y is sampled (n=10)')
abline(m/n,0,col='red',lty=2)
```

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The Bayesian nonparametric formulations always yield *more variable* samples, although the difference gets less marked as n increases.