A Bayesian nonparametric method for the LR assessment in case of rare type match

Giulia Cereda

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Forensic Statistics

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$$\frac{\Pr(H_p \mid D)}{\Pr(H_d \mid D)} = \underbrace{\frac{\Pr(D \mid H_p)}{\Pr(D \mid H_d)}}_{LR} \frac{\Pr(H_p)}{\Pr(H_d)}$$

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- Background (B): database of DNA profiles from the population of possible perpetrators

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For H_d the match is a random event with probability p_h = frequency of the profile h of the suspect in the population of possible perpetrators.

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Person 1 $(4-10-6-7)$
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The database is used to find out the rarity of the matching profile.

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How rare?

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"DNA types" or "colors" is now the same.

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Assumption 2 $\rightarrow$ data can be replaces by the equivalence classes on the indices of the relation "to have the same DNA type".
This is a partition of the set $[n]$: $\{\{1\},\{2,9\},\{3,5,6,8,10\},\{4\},\{7\}\}$

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We can see the data as a random variable. In that case,

$$\mathcal{D} = \Pi_{[n+2]}.$$

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We can consider directly the ordered vector
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For instance, p_3= the frequency of the third most frequent DNA type in Nature.

Prior distribution on $\mathbf{p} \in \nabla_\infty$

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Parameters:
$0 < \alpha < 1$, $\theta > -\alpha$

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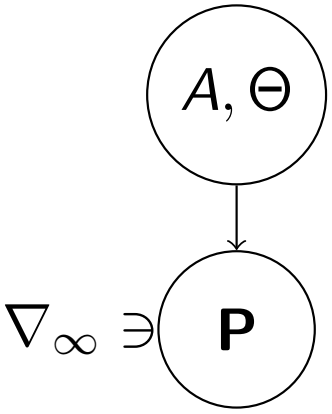

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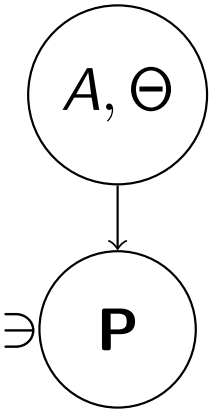
$$\mathbf{P}|\alpha,\theta \sim \mathrm{PD}(\alpha,\theta) \qquad \nabla_\infty \ni$$



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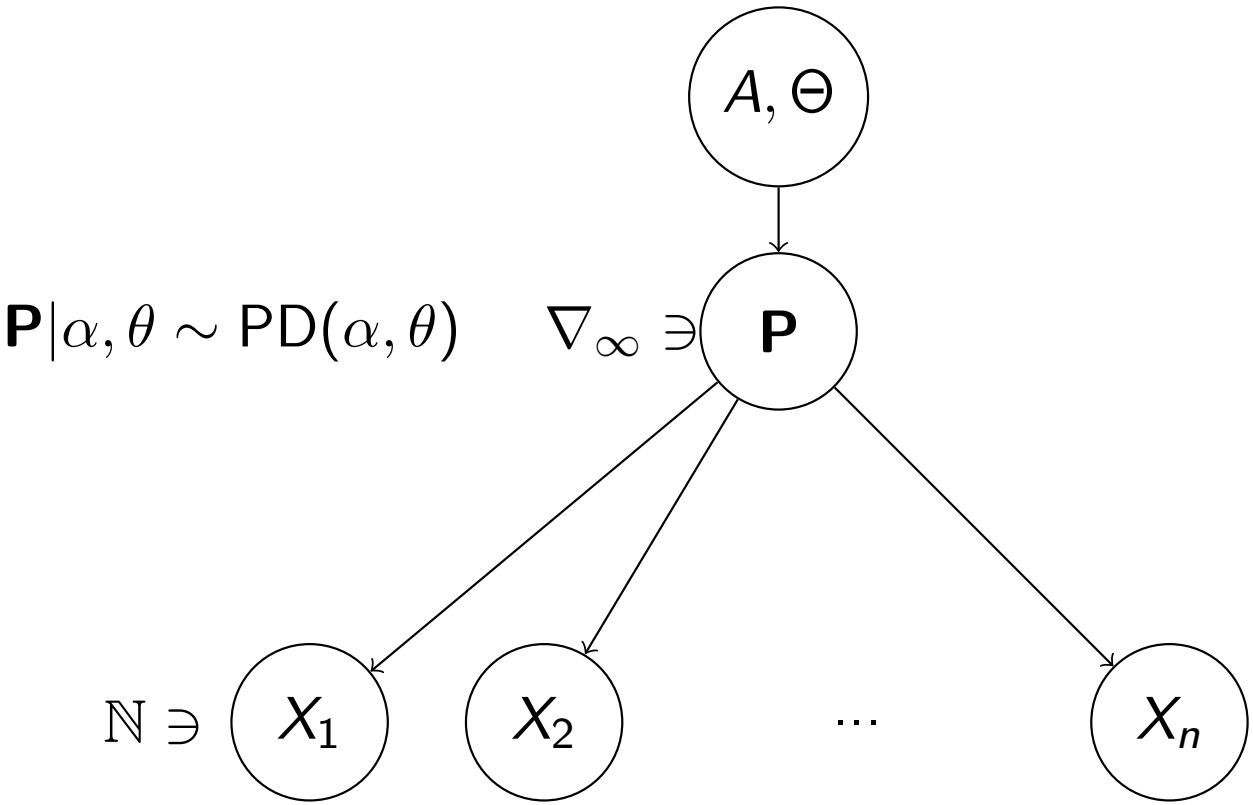

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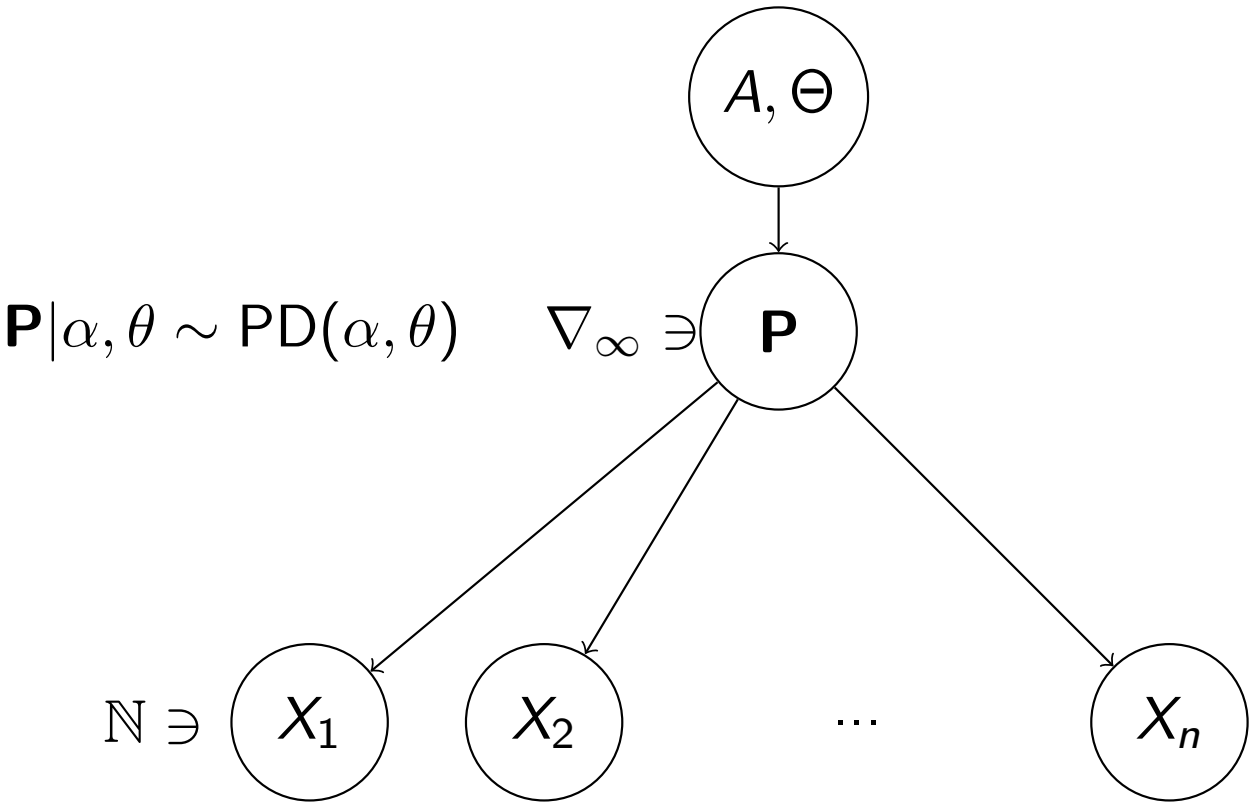

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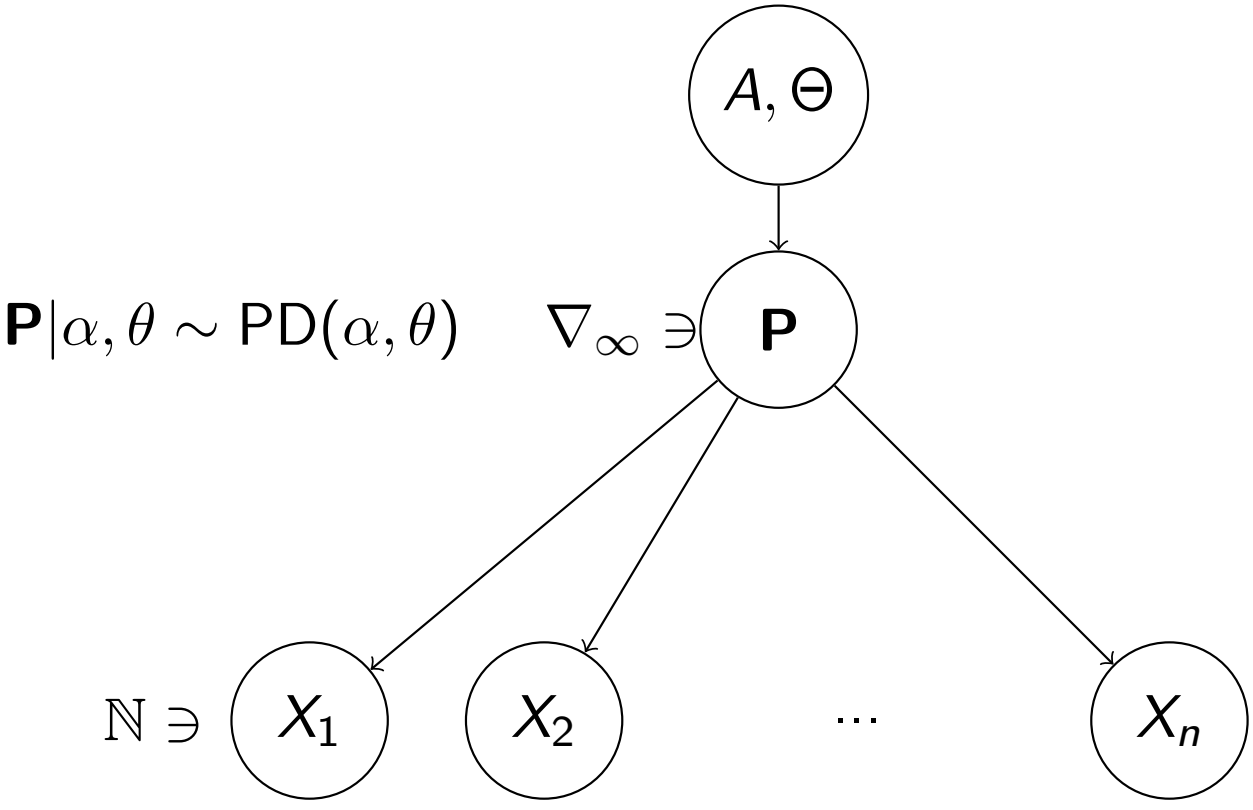

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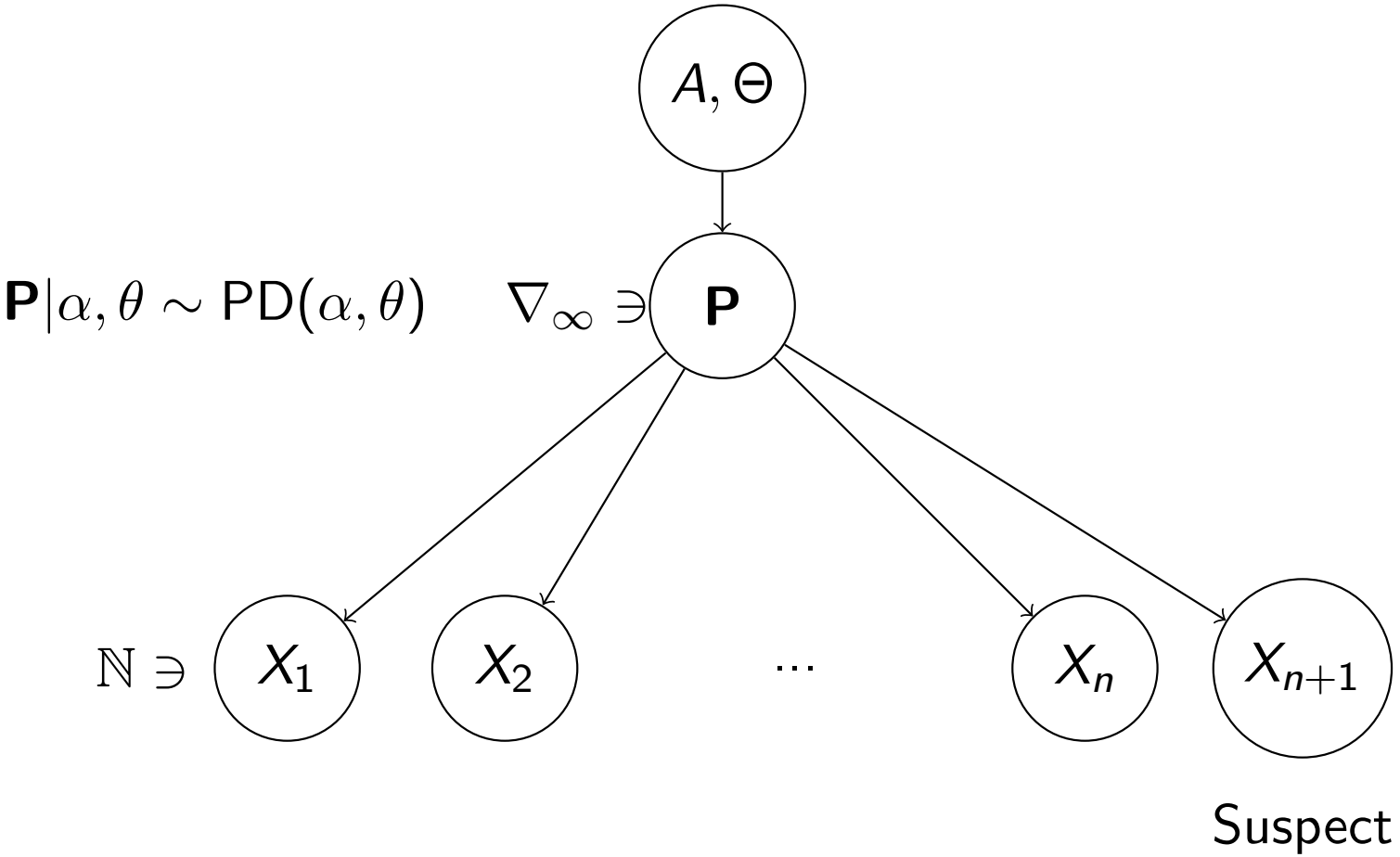

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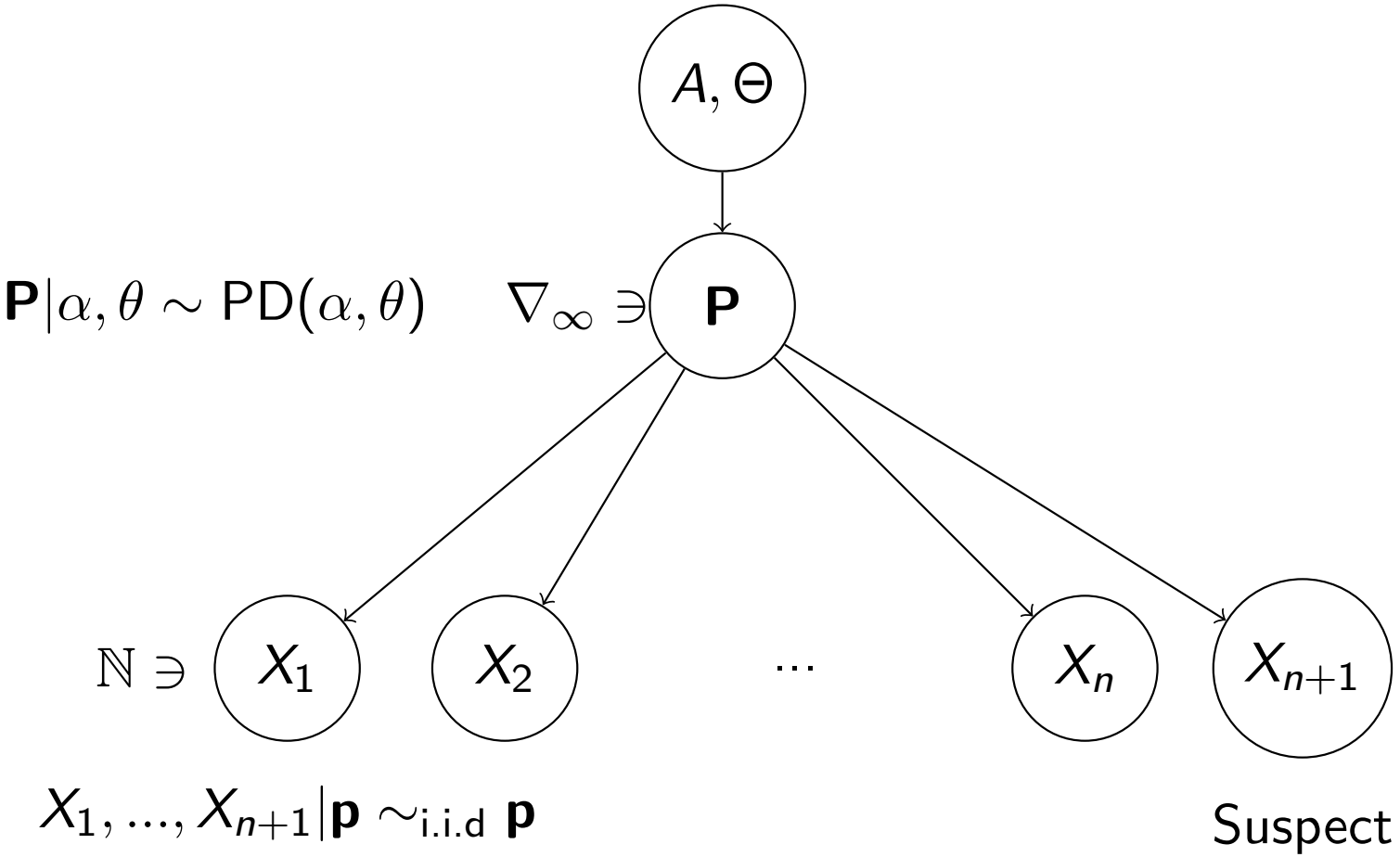

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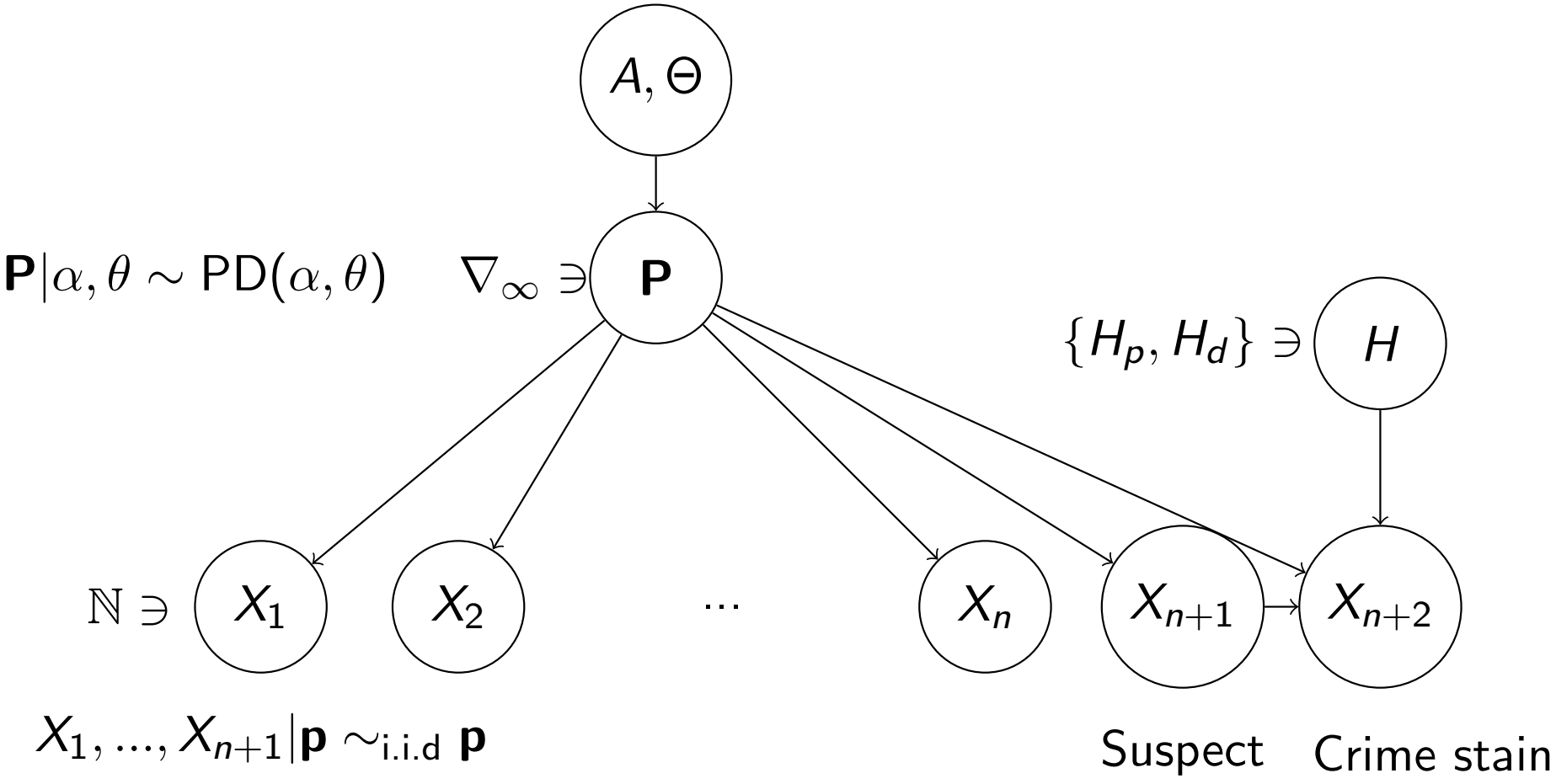

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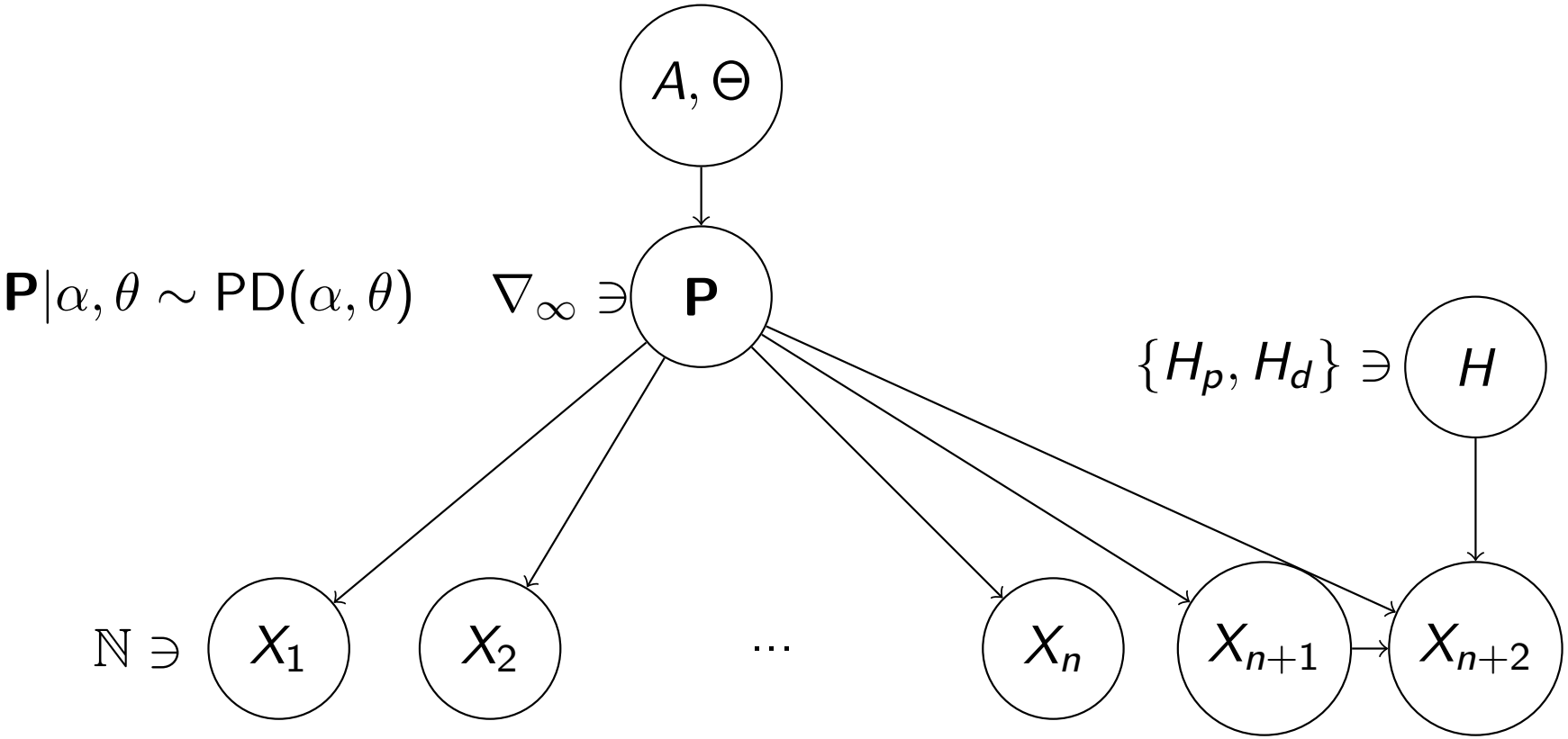

$X_1, ..., X_{n+1}|\mathbf{p} \sim_{\text{i.i.d}} \mathbf{p}$

Suspect Crime stain

$$X_{n+2}|\mathbf{p}, H, x_{n+1} \sim \begin{cases} \delta_{x_{n+1}} & \text{if } H = H_p \\ \mathbf{p} & \text{if } H = H_d \end{cases}$$

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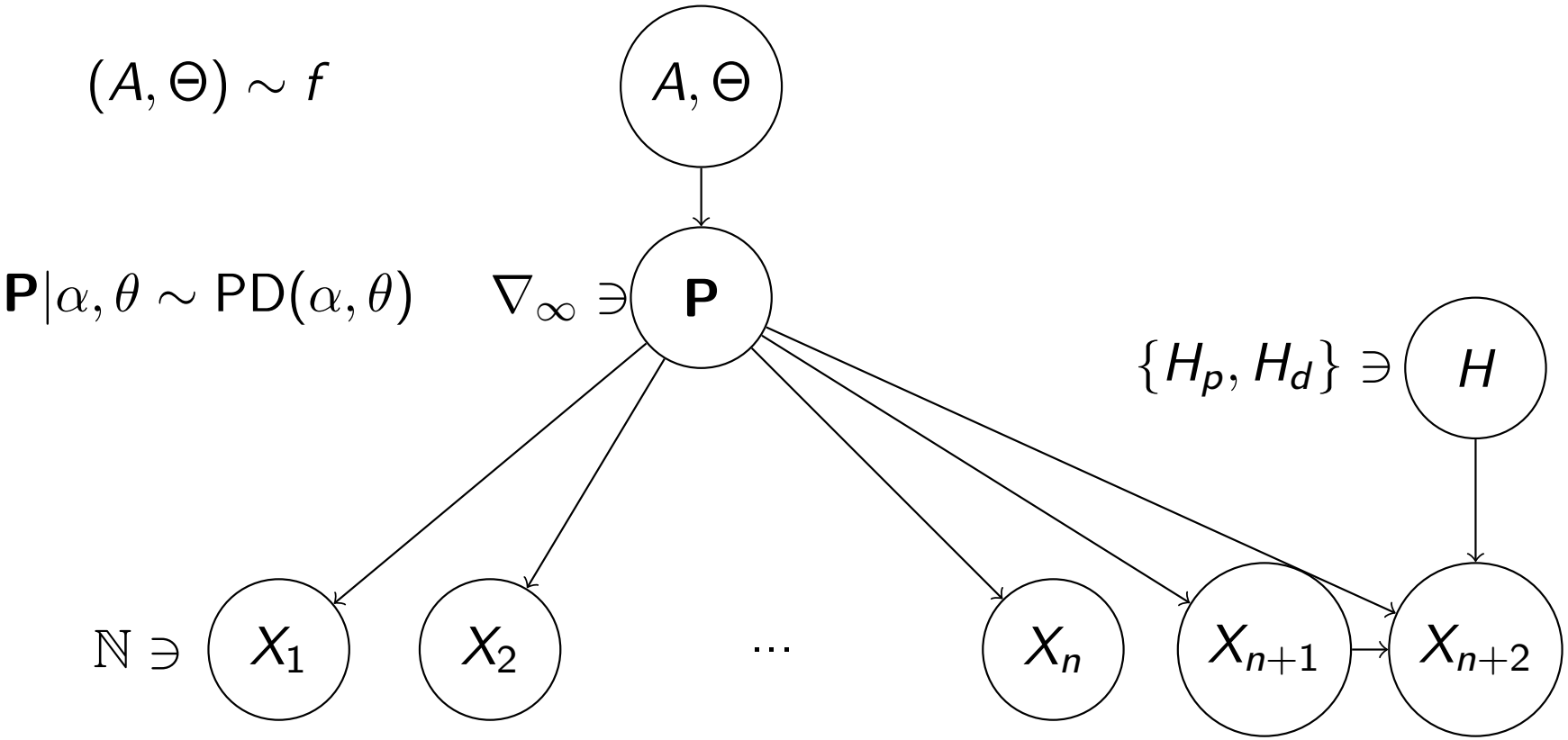

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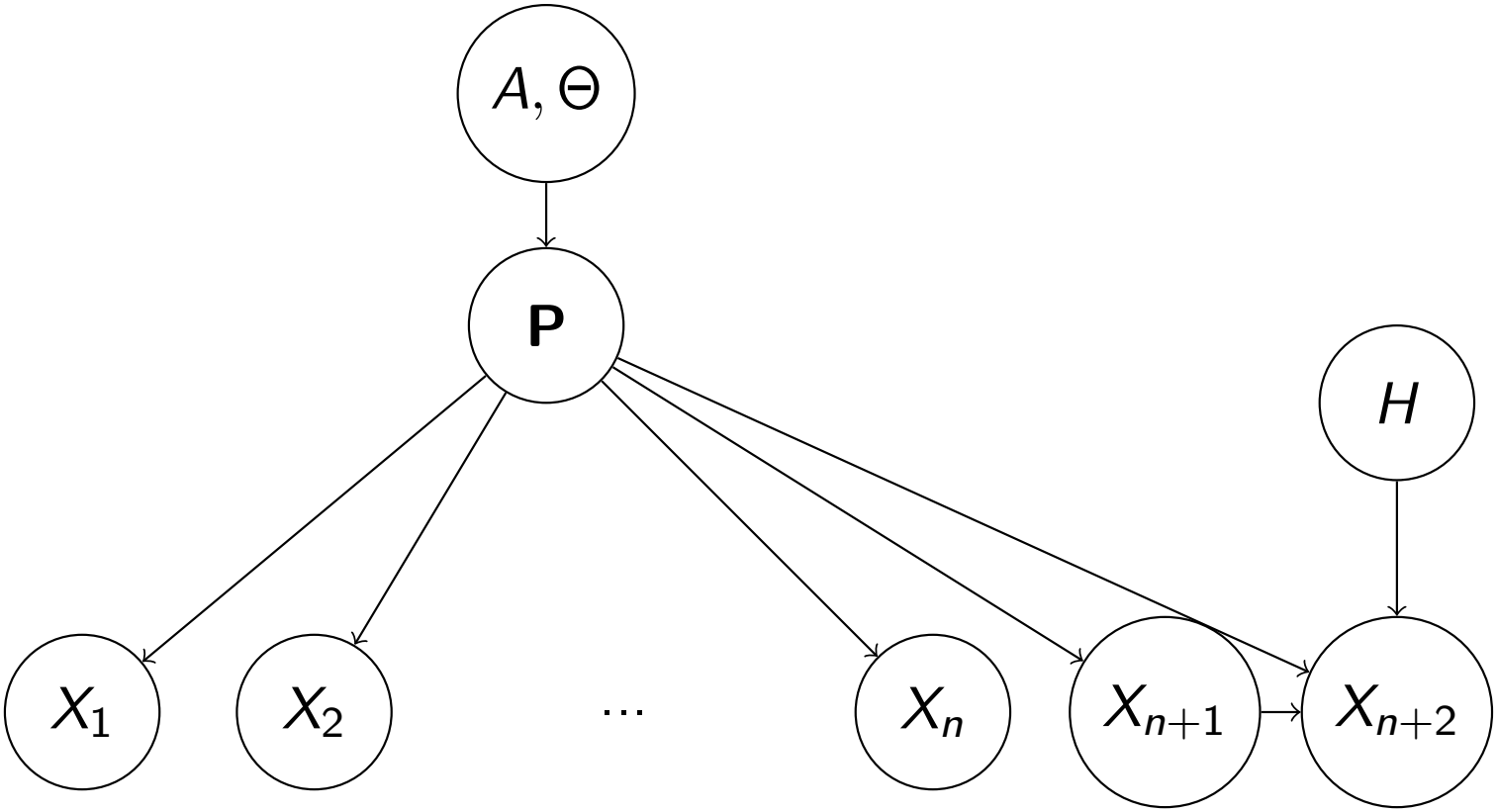

Random partitions

Some notation:
Given $X_1, ..., X_n \in \mathbb{N}$, random variables, $\Pi_{[n]}(X_1, X_2, ..., X_n)$ is the random partition defined by the equivalence classes of $i \sim j$ iff $X_i = X_j$.

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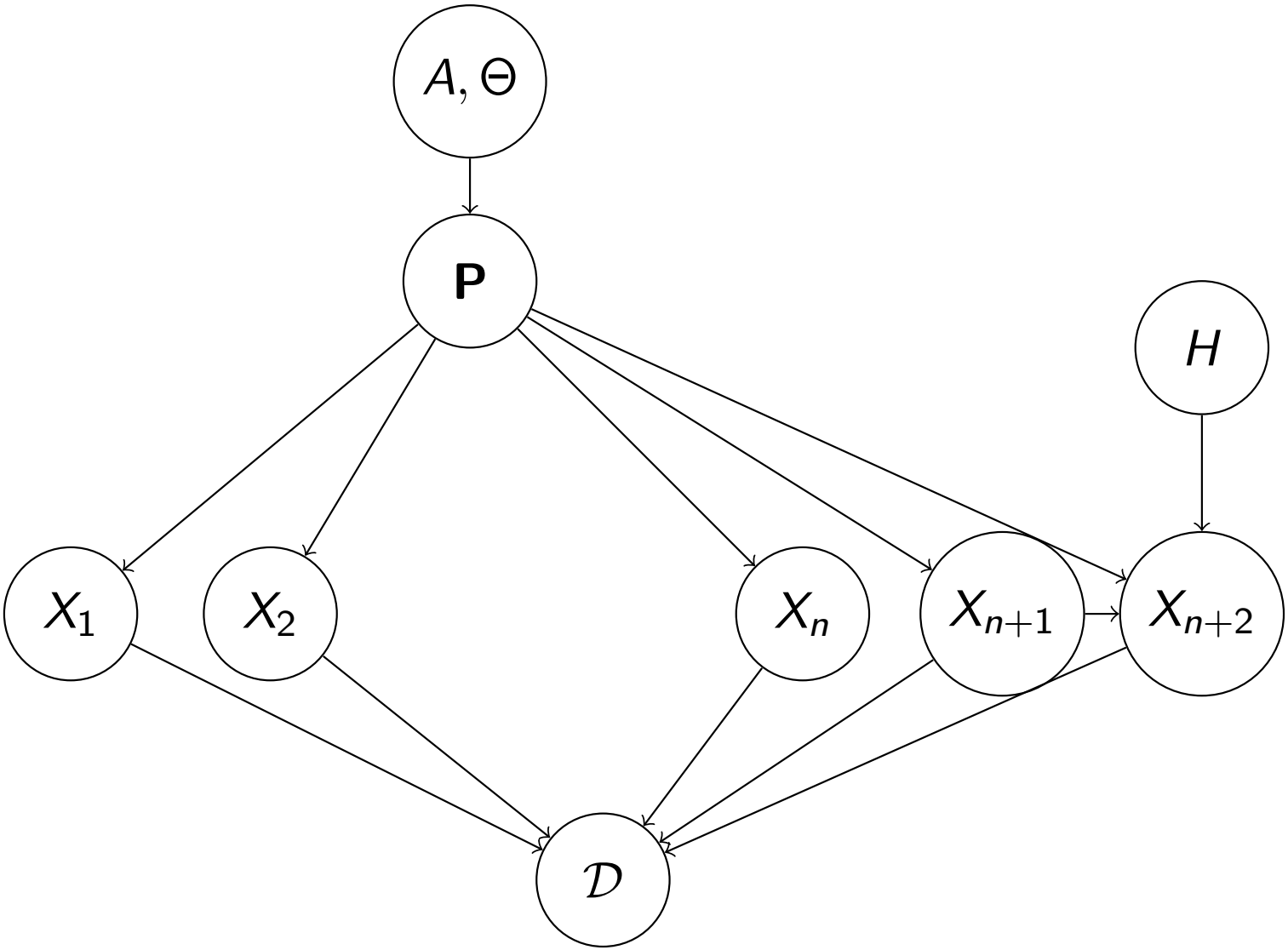
$X_1, ..., X_n$ are not observed, but generates the same partition as the original database.
Data can be defined as $\mathcal{D} = \Pi_{[n+2]}$.

The complete model



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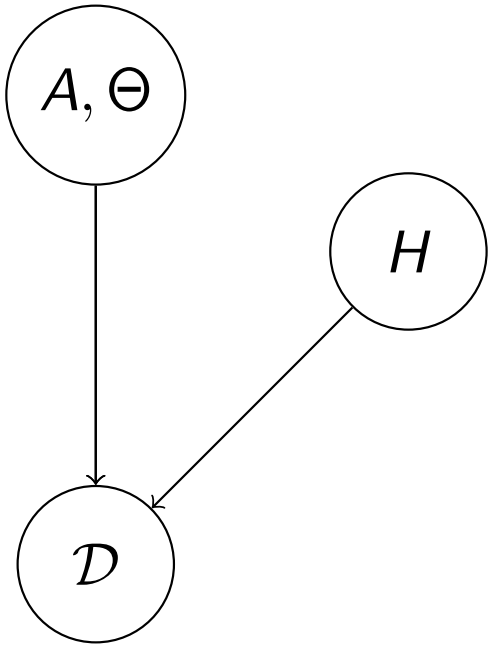
In our model

$$\Pr(D|\alpha, \theta, h) = \Pr(\Pi_{[n+2]} = \pi^{Db++}_{[n+2]} | \alpha, \theta, h) = \begin{cases} \mathbb{P}^{n+2}_{\alpha,\theta}(\pi^{\text{Db++}}_{[n+2]}) & \text{if } h = H_d \\ \mathbb{P}^{n+1}_{\alpha,\theta}(\pi^{\text{Db+}}_{[n+1]}) & \text{if } h = H_p \end{cases}$$

The model, simplified



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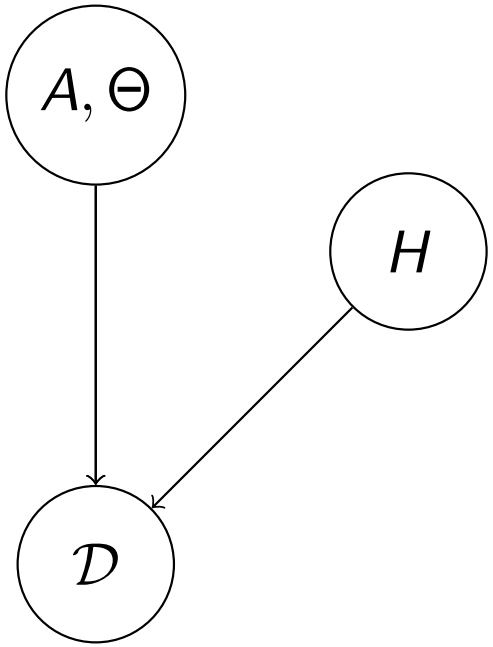

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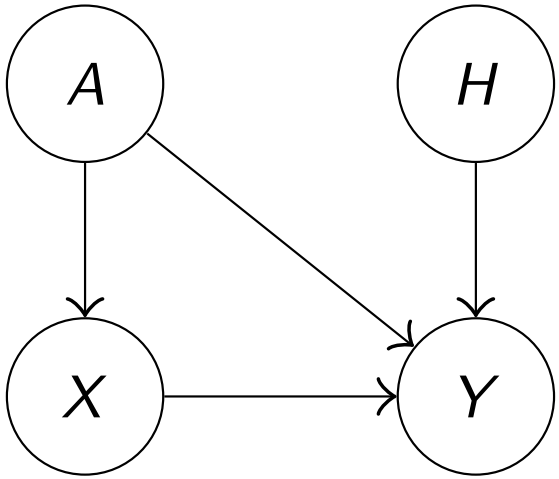
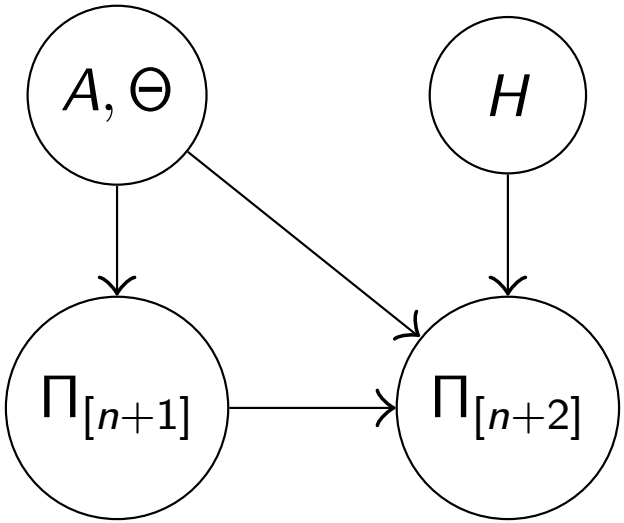


Lemma

Given four random variables A, H, X and Y, as above, the likelihood function for h, given $X = x$ and $Y = y$, satisfies

$$\mathrm{lik}(h \mid x, y) \propto \mathbb{E}(p(y \mid x, A, h) \mid X = x).$$

Lemma



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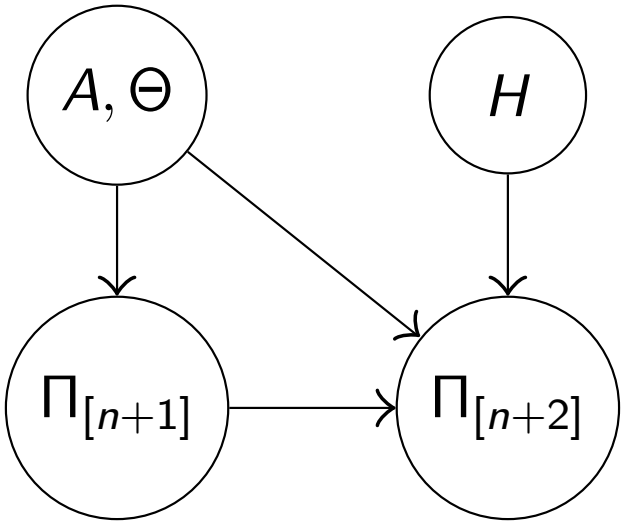

$$\text{lik}(h \mid \pi_{[n+1]}, \pi_{[n+2]}) \propto \mathbb{E}(p(\pi_{[n+2]} \mid \pi_{[n+1]}, A, \Theta, h) \mid \Pi_{[n+1]} = \pi_{[n+1]}).$$

Likelihood ratio

$$\text{LR} = \frac{p(\pi_{[n+2]}|H_p)}{p(\pi_{[n+2]}|H_d)} = \frac{p(\pi_{[n+1]}, \pi_{[n+2]}|H_p)}{p(\pi_{[n+1]}, \pi_{[n+2]}|H_d)} = \frac{\text{lik}(H_p|\pi_{[n+1]}, \pi_{[n+2]})}{\text{lik}(H_d|\pi_{[n+1]}, \pi_{[n+2]})}$$

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Lemma allows to write

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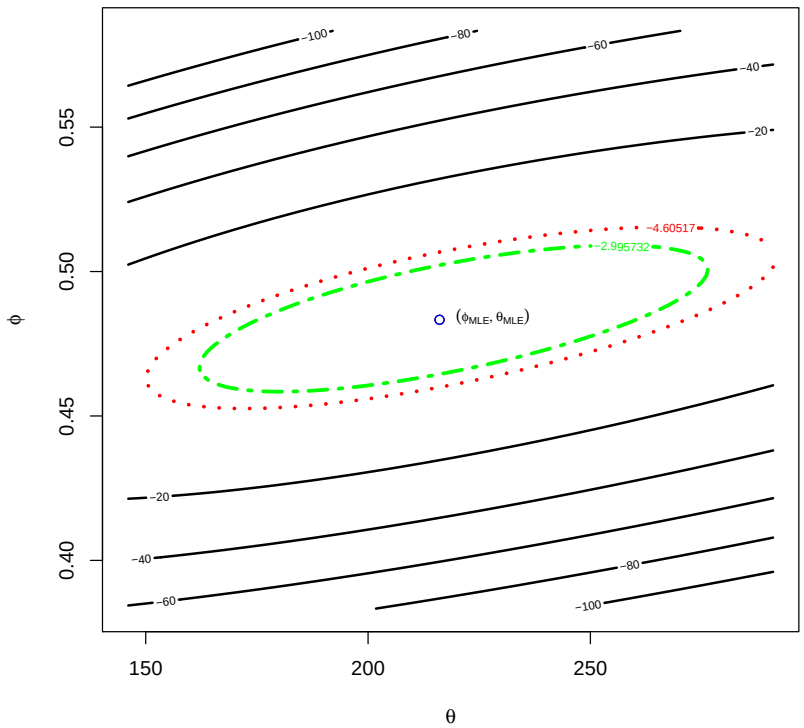
Log likelihood with ϕ and θ

$\log_{10} p(\pi_{[n+1]} \mid \phi, \theta)$



Dutch Y-STR database, 7 loci, N=18,925

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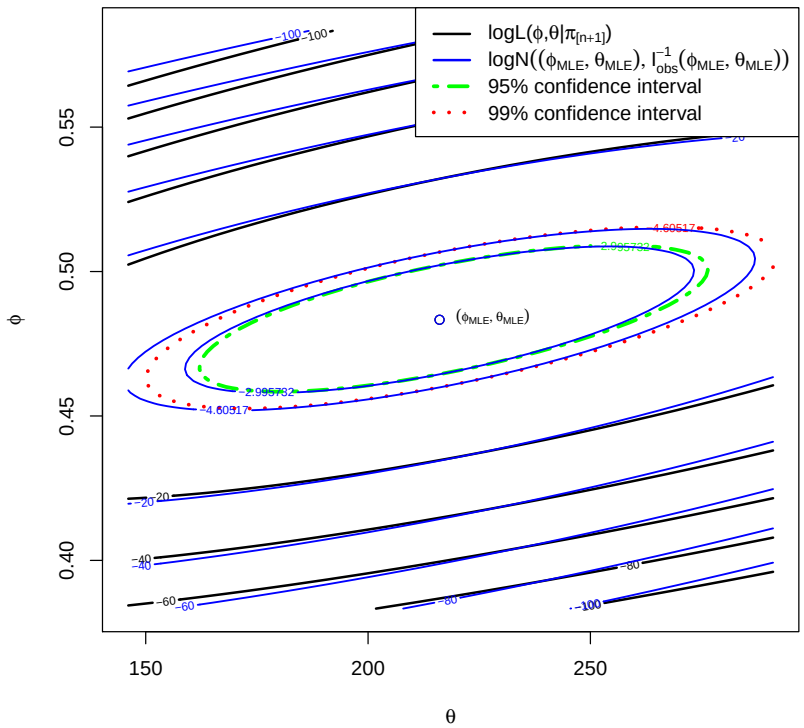

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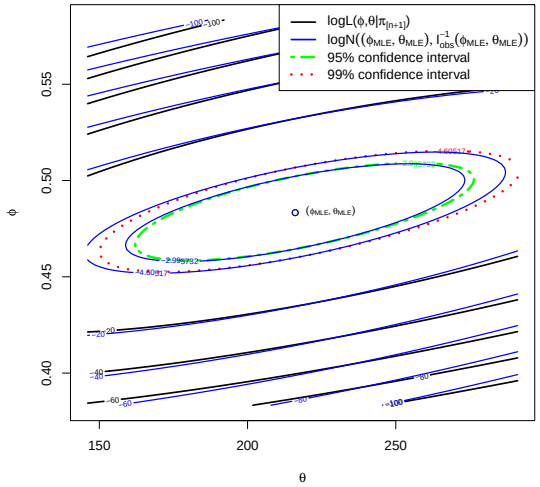
Log likelihood as a function of ϕ and θ



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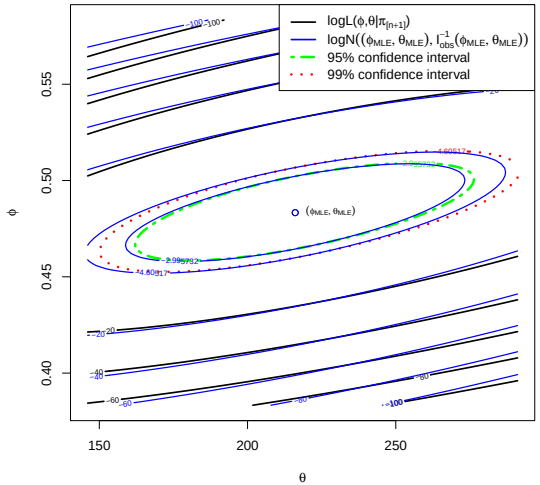

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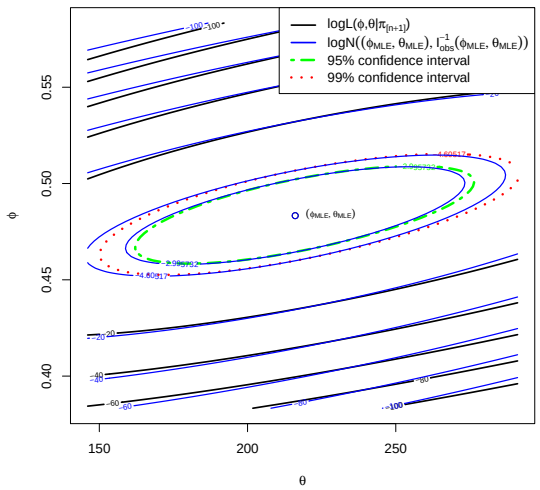

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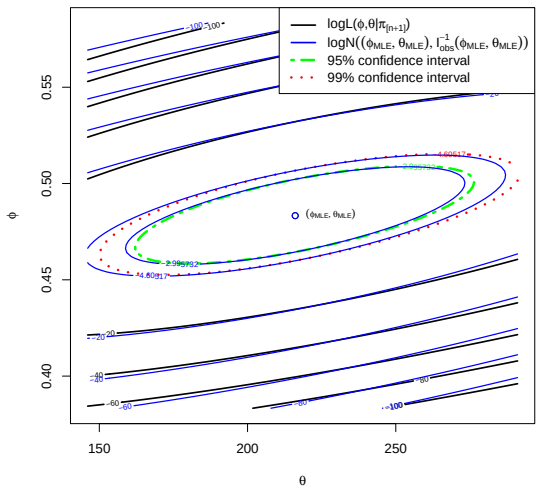

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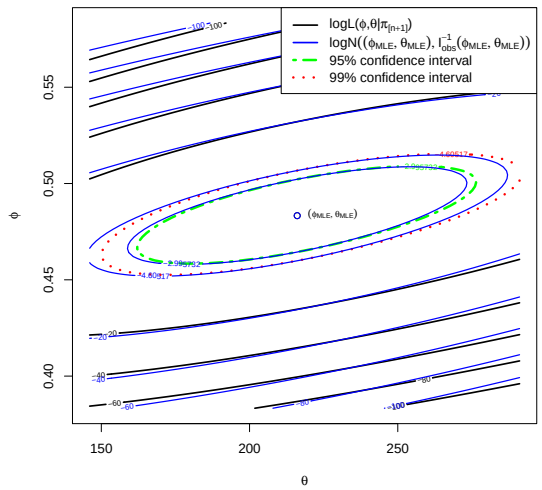

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$$\text{LR} = \frac{n}{\mathbb{E}(\Phi \mid \Pi_{[n+1]} = \pi_{[n+1]})} \approx \frac{n + 1 + \theta_{MLE}}{1 - \alpha_{MLE}}$$

Sorted relative frequencies: how good is our prior?

Comparison between the spectrum from a big database, and simulations from PD(α, θ) using MLE estimators of the parameters.

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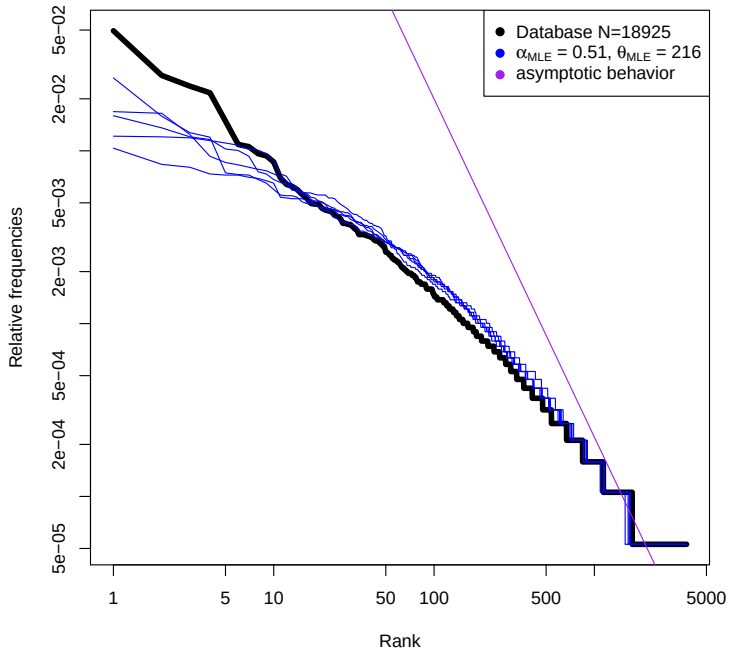

Thick black line: ranked relative frequencies in the database.
Thin black lines: simulations from the PD($\alpha_{MLE}, \theta_{MLE}$).
Dotted line: asymptotics.

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Imagine we know $\mathbf{p}$.

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How is this compared to the one we get with our method when $\mathbf{p}$ is unknown?

Test Dutch database (N=2085, 7 loci)

Database of 2085 Y-STR profiles form Dutch men.

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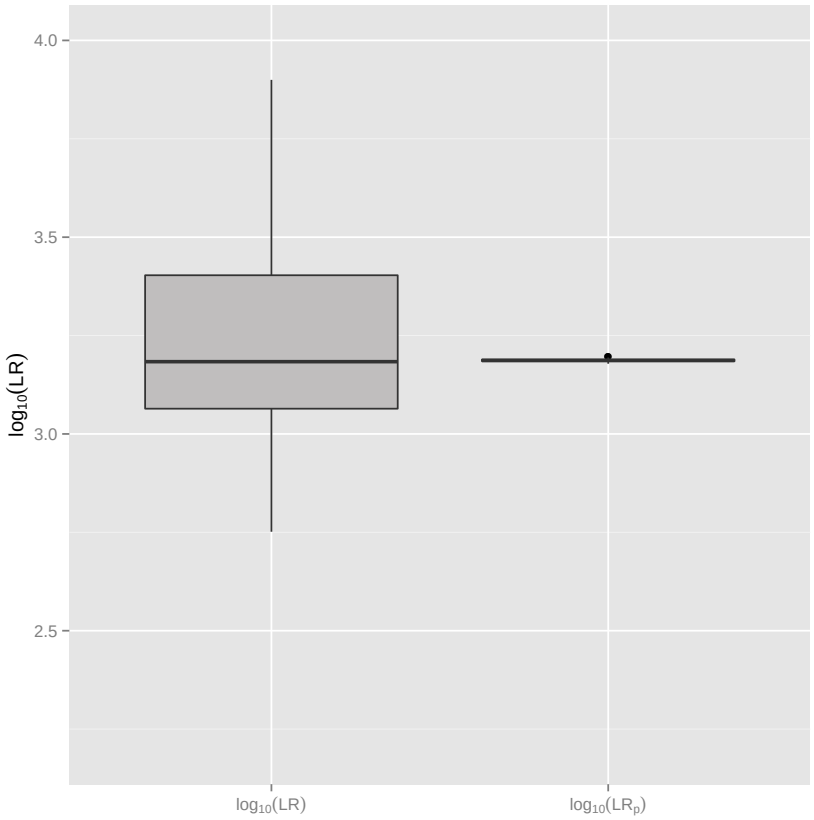
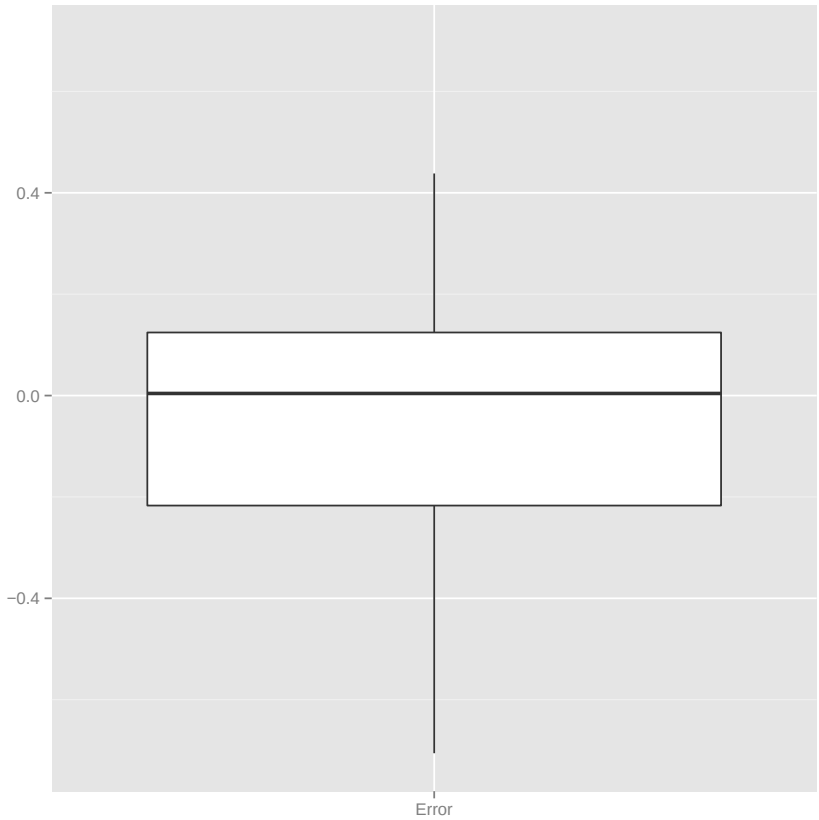
Test: Compare the distribution of $\log_{10}(\mathrm{LR}_{|\mathbf{p}})$ and $\log_{10}\mathrm{LR}$ obtained by 100 samples of size 100 from this population.

Results

Compare the distribution of $\log_{10}(\mathrm{LR}_{|\mathbf{p}})$ and $\log_{10}\mathrm{LR}$ obtained by 100 samples of size 100 from this population



(a) Comparison



(b) Error