A BNP Approach to the Multi-Armed Bandit Problem for Traits Allocation Models

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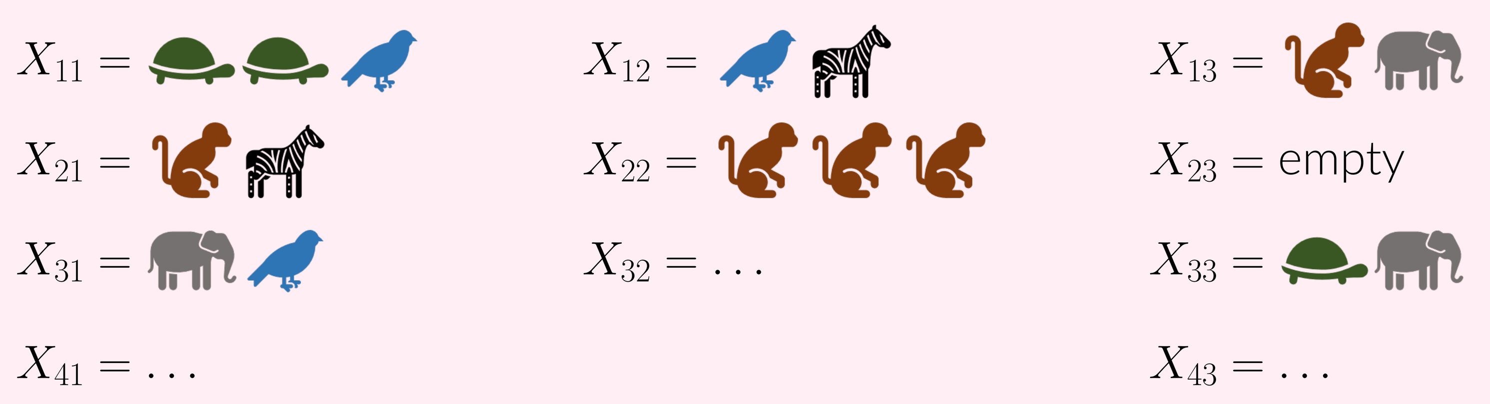
Traits allocation models

Consider a **countable set** of **traits** or **features** (e.g. species, topics, genes):

- each observation displays a **finite subset** of traits, with a **level of belonging** (here, a count) for each trait;
- observations are collected from **multiple populations**, e.g. forests, books;
- the same trait may appear in different observations both **within** the same population and **across** populations → the set of traits is **shared** among populations!



Consider d **populations**, with n_j **observations** collected from population $j = 1, \dots, d$. The observation X_{ij} from population j is represented as

$$X_{ij} = \sum_{k \geq 1} A_{ijk}\, \delta_{\psi_k}, \qquad i = 1, \dots, n_j,$$

where $A_{ijk} \geq 0$ is the **count** for trait ψ_k in population j.

Nonparametric model: each observation X_{ij} is an i.i.d. realization of a **Poisson process**, driven by the finite discrete measure μ_j:

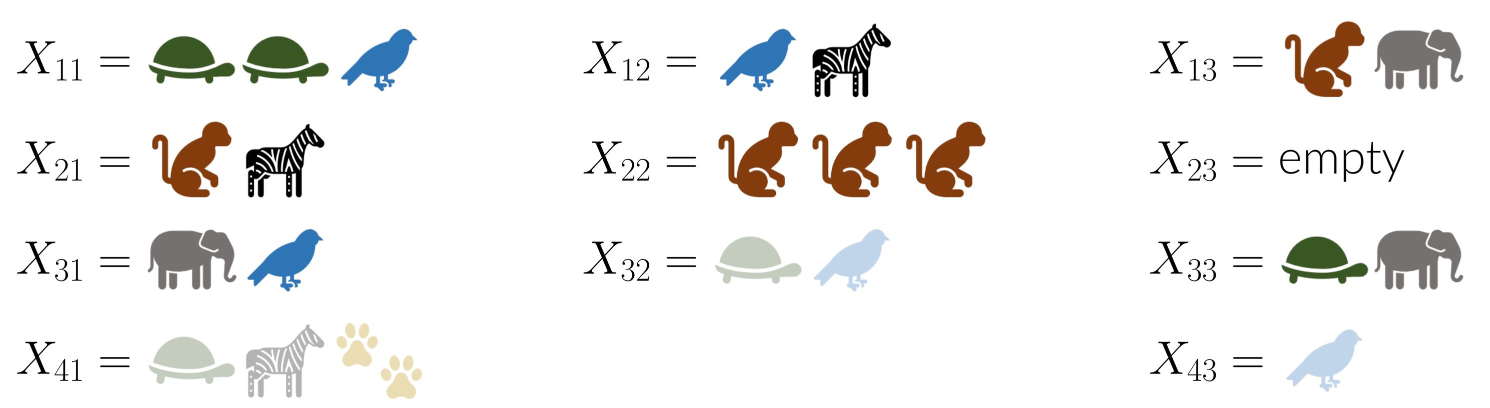
$$A_{ijk} \overset{ind}{\sim} \text{Poisson}(\lambda_{jk}), \qquad \mu_j = \sum_{k \geq 1} \lambda_{jk}\, \delta_{\psi_k}.$$

Some useful notation:

- the **total count** for trait X_k in population j is $M_{jk} = \sum_{i=1}^{n_j} A_{ijk}$;
- the set of traits appearing **at least once** in population j is $\mathcal{K}_j = \{k \geq 1 \colon M_{jk} > 0\}$.

Multi-armed bandit for traits discovery

Problem: choose from which population to sample the next observation, with the goal of **discovering new traits**.



Multi-armed bandit formulation: sequentially select one among the possible **actions** (sampling from a certain population) to maximize the cumulative **reward** (the number of discovered traits).

The **random reward** of population j is the number of **new traits** discovered in a new observation:

$$R_j = \sum_{k \geq 1} \mathbb{1}\left(A_{(n_j+1)jk} > 0,\, \textstyle\sum_{j=1}^{d} M_{jk} = 0\right) = \sum_{k \notin \mathcal{K}} \mathbb{1}\left(A_{(n_j+1)jk} > 0\right),$$

where $\mathcal{K} = \cup_{j=1}^{d} \mathcal{K}_j$ is the set of traits appearing in **at least one** population.

Optimal strategy: choose the population **maximizing** the conditional **expected reward**, given the past observations,

$$\mathbb{E}\left[R_j \mid \boldsymbol{X}\right] = \sum_{k \notin \mathcal{K}} \left(1 - e^{-\lambda_{jk}}\right), \qquad j = 1, \dots, d.$$

Statistical problem: how to **estimate** the population **parameters** $\mu_1, \dots, \mu_d$?

Bayesian nonparametric approach

Hierarchical prior: the distribution of measures $\mu_1, \dots, \mu_d$ is a hierarchical **process**:

$$\mu_j = \sum_{k \geq 1} \lambda_{jk}\, \delta_{\psi_k}, \qquad \lambda_{jk} \mid \lambda_{0k} \overset{ind}{\sim} \text{Gamma}(\theta_j \lambda_{0k}, 1), \qquad j = 1, \dots, d,$$

$$\mu_0 = \sum_{k \geq 1} \lambda_{0k}\, \delta_{\psi_k} \sim \text{CRM}(\theta_0 \rho),$$

- where $\theta_0, \theta_1, \dots, \theta_d > 0$ are **concentration parameters**,
- and ρ is the Lévy measure characterizing the **distribution of jumps** $(\lambda_{0k})_{k \geq 1}$ in μ_0.

Posterior distribution: the posterior of the parameters for the **unseen traits** is **tractable**:

$$\mu_j^* = \sum_{k \notin \mathcal{K}} \lambda_{jk}\, \delta_{\psi_k}, \qquad \lambda_{jk} \mid \lambda_{0k}, \boldsymbol{X}_j \overset{ind}{\sim} \text{Gamma}(\theta_j \lambda_{0k}, 1 + n_j), \qquad j = 1, \dots, d,$$

$$\mu_0^* = \sum_{k \notin \mathcal{K}} \lambda_{0k}\, \delta_{\psi_k} \mid \boldsymbol{X} \sim \text{CRM}(\theta_0 \rho^*), \qquad \rho^*(\mathrm{d}s) = \prod_{j=1}^{d} (1 + n_j)^{-\theta_j s} \rho(\mathrm{d}s).$$

Important remarks:

- the posterior parameters of unseen traits depend exclusively on the **number of observations** in each population!
- to model **biodiversity** across populations, consider exponential **hyperpriors** on concentration parameters $\theta_0, \theta_1, \dots, \theta_d$.

Thompson sampling for traits discovery

Since population parameters are **unknown**, common **heuristic** strategies balance:

- **exploration**, selecting less sampled populations to learn their parameters;
- **exploitation**, selecting populations with highest chances of seeing new traits.

Thompson sampling: choose the population **randomly**, according to the **posterior probability** of maximizing the conditional expected reward:

$$p_j = \int \mathbb{1}\left(j = \arg\max_{\ell} \mathbb{E}\left[R_\ell \mid \boldsymbol{X}, \boldsymbol{\mu}\right]\right) p(\boldsymbol{\mu} \mid \boldsymbol{X}).$$

In practice, consider two possible **implementations**:

- standard Thompson sampling:
  1. sample posterior measures $\mu_1, \dots, \mu_d$;
  2. select the population $j^* = \arg\max_j \mathbb{E}\left[R_j \mid \boldsymbol{X}, \boldsymbol{\mu}, \boldsymbol{\theta}\right] = \arg\max_j \sum_{k \notin \mathcal{K}} \left(1 - e^{-\lambda_{jk}}\right)$
- partially marginalized Thompson sampling:
  1. sample posterior parameters $\theta_1, \dots, \theta_d$;
  2. select the population $j^* = \arg\max_j \mathbb{E}\left[R_j \mid \boldsymbol{X}, \boldsymbol{\theta}\right] \approx \arg\max_j \theta_j \log\left(1 + \frac{1}{1+n_j}\right)$.

Idea: the more you **marginalize**, the more you **exploit**!

Trees species in Japanese forests

Dataset containing trees species counts from ecological **survey plots** collected in various forest sites in Japan:

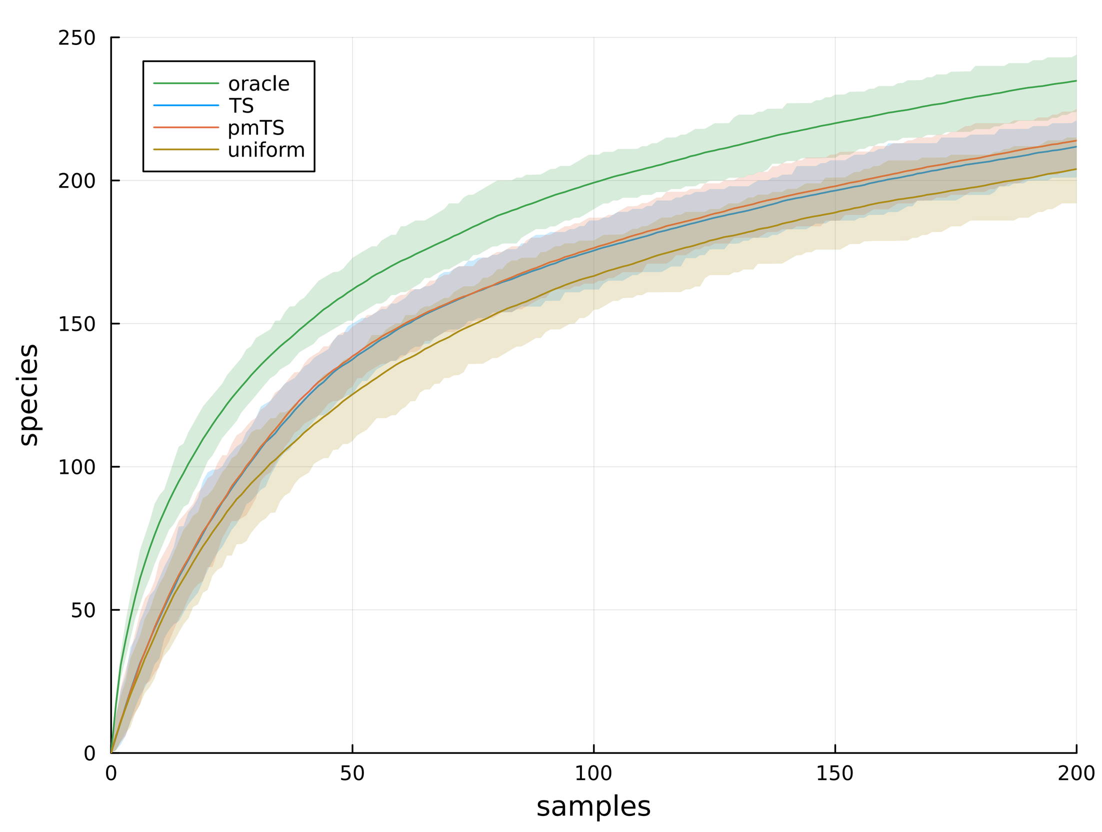
- consider $d = 41$ **populations** (forest plots) classified in 4 macro-types;
- around 100 **observations** per forest → trees counts in 10×10 m areas;
- records for 365 **species** across forest sites.

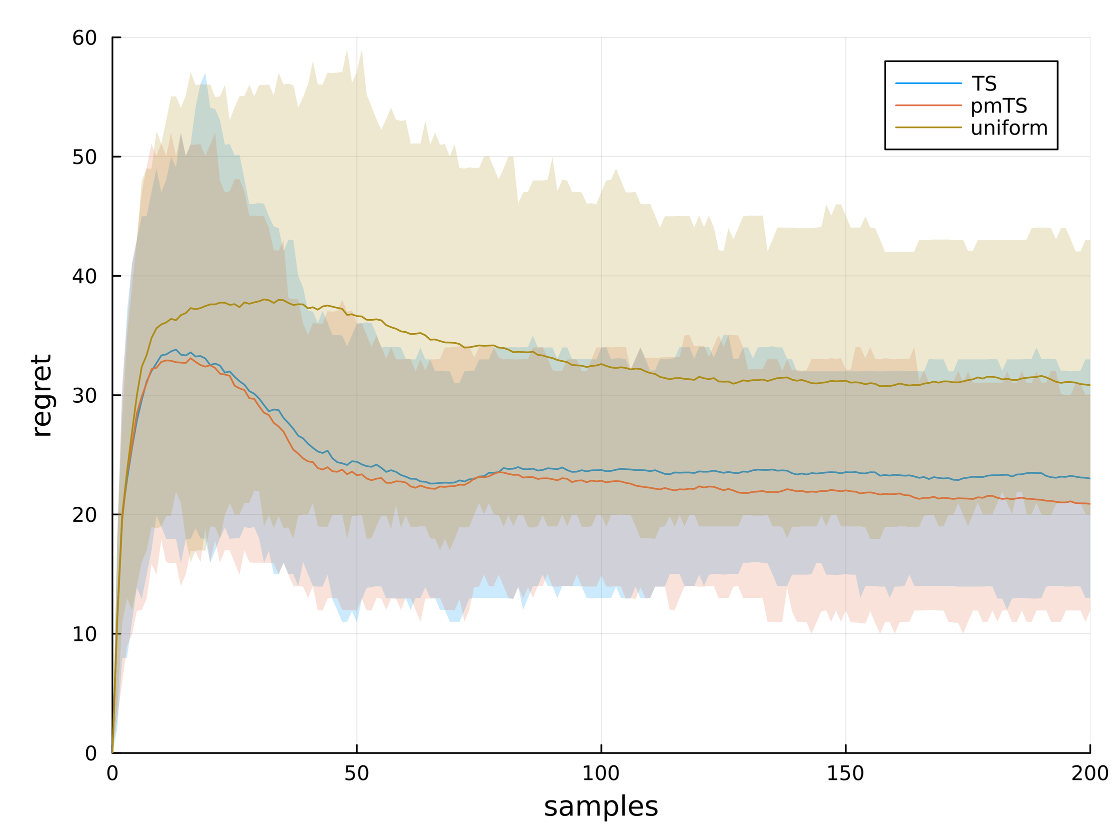
Preliminary analysis:

→ number of **discovered** species;

→ **regret** from optimal strategy.

Results are averaged over 100 experiments.





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