

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 \rightarrow the set of traits is shared among populations!

$$X_{11} =$$

$$X_{21} =$$

$$X_{21} = X_{31} = X_{31}$$

$$X_{41}=\dots$$

$$X_{12} =$$

$$X_{21} = 16$$

$$X_{32}=\ldots$$

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$$X_{43} =$$

 $X_{43} = \dots$

 $X_{33} =$

 $X_{13} = 1$

 $X_{23} = \text{empty}$

 $X_{13} = 1$

 $X_{23} = \text{empty}$

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

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

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_i :

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

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 $\mathcal{K}_i = \{k \geq 1 : M_{jk} > 0\}$.

Multi-armed bandit for traits discovery

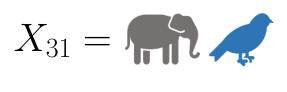
Problem: choose from which population to sample the next observation, with the goal of discovering new traits.

$$X_{11} =$$

$$X_{21} =$$













$$X_{32} =$$

$$X_{32} =$$

$$X_{32} =$$

$$X_{33} =$$

$$X_{43} =$$

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:

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

where $\mathcal{K} = \bigcup_{j=1}^{d} \mathcal{K}_j$ 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,

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

Statistical problem: how to **estimate** the population **parameters** μ_1, \ldots, μ_d ?

Bayesian nonparametric approach

Hierarchical prior: the distribution of measures μ_1, \ldots, μ_d is a hierarchical **process**:

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

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

- 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:

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

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

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 μ_1, \ldots, μ_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 $\theta_1, \ldots, \theta_d$;
- 2. select the population $j^* = \arg \max_j \mathbb{E}[R_j \mid \boldsymbol{X}, \boldsymbol{\theta}] \approx \arg \max_j \theta_j \log \left(1 + \frac{1}{1+n_i}\right)$.

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

Trees species in Japanese forests

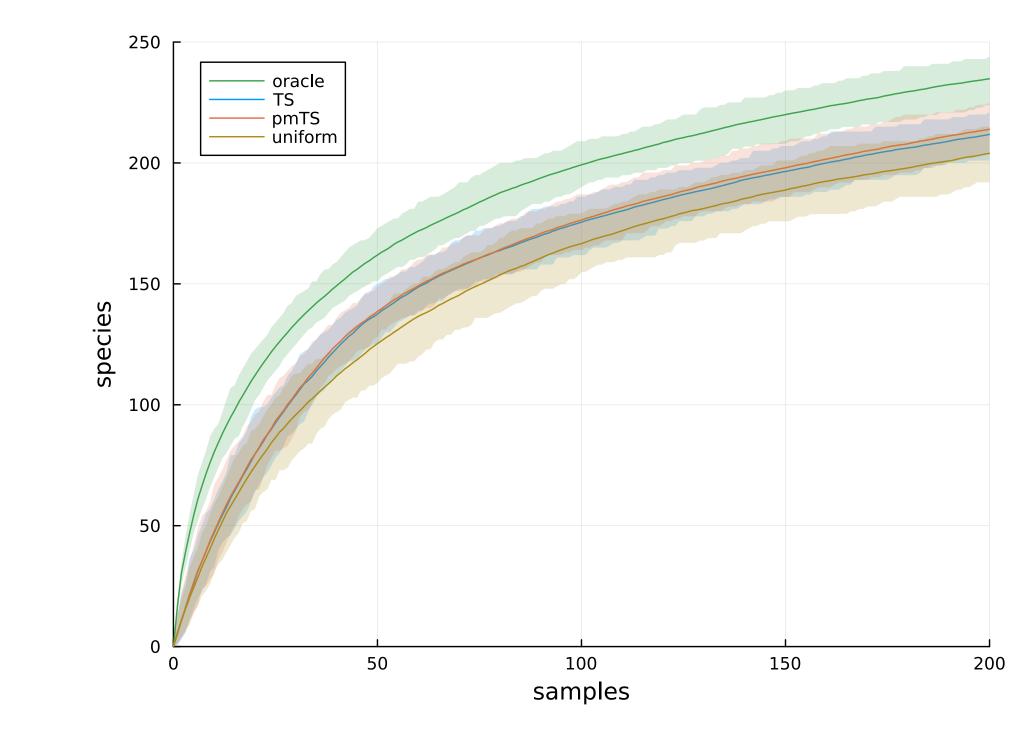
Dataset containing trees species counts from ecological survey plots collected in various forest sites in Japan:

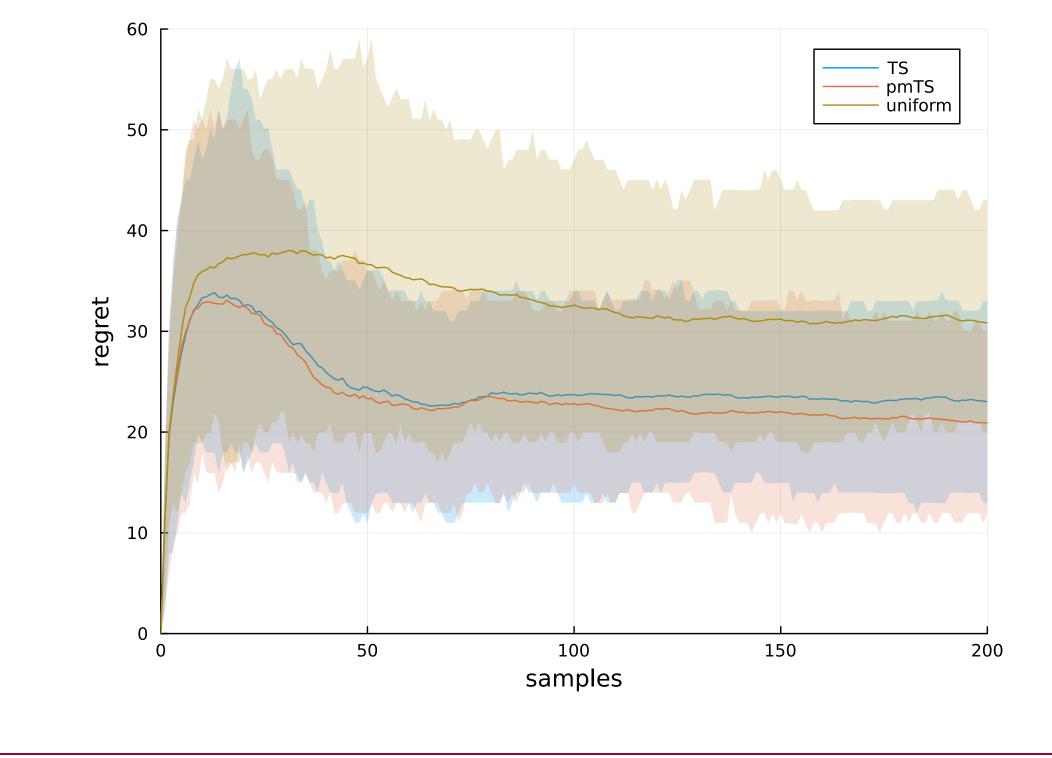
- consider d=41 populations (forest plots) classified in 4 macro-types;
- around 100 **observations** per forest \rightarrow trees counts in 10×10 m areas;
- records for 365 **species** across forest sites.

Preliminary analysis:

- → number of **discovered** species;
- → regret from optimal strategy.

Results are averaged over 100 experiments.





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