Bayesian Nonparametric Mixtures Why and How?
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Bayesian Nonparametric Mixtures
Why and How?

www.julyanarbel.com, Inria, Mistis

Introduction
Bayesian nonparametric framework
○ Massively many parameters
  ○ Inference on curves: pdf, cdf, hazard, link…
  ○ Mixtures, exchangeable data $X^\prime = (X_1, \ldots, X_n)$
  \[ X_1, \ldots, X_n \mid P \sim \left\{ \frac{P}{\Phi} \right\} \]
  → ① ② ③
○ Natural uncertainty quantification
○ Flexibility, avoids over-fitting by regularization (prior)
○ Adapt to data complexity
○ Underlying clustering
○ Justify prior, expert
○ Efficient posterior sampling
○ Quantify truncation error

What prior for $P$?
○ Learn about data through posterior dist.
○ Discrete random probability measure prior
○ Random weights $(p_i)$, and locations $(\theta_j)$
\[ P = \sum_{i=1}^{\infty} p_i \delta_{\theta_i} \]
→ Dirichlet process $DP(\alpha, G_0)$ (Ferguson, 1973)
Predictive: Chinese Restaurant Process
\[ P(X_{n+1} \in \cdot | X^\prime) = \frac{\alpha}{\alpha + n} G_0 + \frac{1}{\alpha + n} \sum_{j=1}^{n} p_j \delta_{\theta_j} \]
→ Or for varying $P(X_{n+1} \text{ new})$ … ∼

Survival Analysis
Bayesian hazard mixture (Arbel et al., 2016c)
○ Data are (remission) times possibly censored
○ Prior on hazard rate $h(t)$ for every time $t$
○ Induces prior on survival function $S(t)$
→ Availability of post. mean, median, mode
→ Smooth estimator VS Kaplan–Meier
→ Proper uncertainty quantification

Open Questions
○ How to best use underlying clustering? (Wade and Ghahramani, 2015)
○ Find consistent estimator of number of clusters: posterior inconsistent (Miller and Harrison, 2014), what about posterior mode?
○ Devise efficient posterior sampling, truncation error (Arbel and Prünster, 2016)

Species Modeling
Data can be species, microbes, words, genes…
Discovery probabilities (Arbel et al., 2016a)
○ Estimation of $\ell$-discovery
  $D_\ell = P(X_{n+1} \text{ is a species seen } \ell \text{ times})$
○ Comparison with Good-Turing estimator
→ Closed form posterior and estimators
→ Uncertainty quantified, unavailable for GT
→ 2nd order (fast) approximations

Diversity in ecology (Arbel et al., 2015, 2016d)
○ Assess impact of pollution on microbial community via study of diversity
  $\text{Div} = -\sum_i p_i \log p_i$
→ Model detects an hormetic effect
→ Uncertainty quantification
→ Prediction across full range of covariates

Density Estimation
Ecological risk assessment (Arbel et al., 2016b)
○ Data are species critical effect concentrations (CEC), possibly censored
○ Estimation of species sensitivity distribution (SSD), the density of CEC
○ Safe concentration which protects most of the species: 5th percentile of the SSD (HC5)
○ Very moderate sample sizes, ~ 10 – 50
→ BNP describes well variability of the data, without being prone to over-fitting
→ Species clustering as an outcome

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References & Collaborators