Discussion on

“Nested nonparametric processes”

by Federico Camerlenghi

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Brief summary (1)

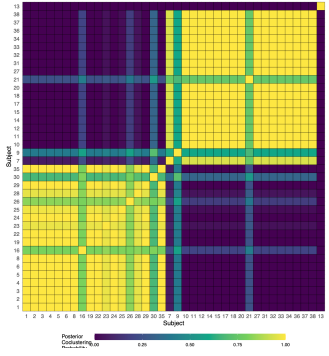
- Federico reviewed the degeneracy property of the nDP presented in Camerlenghi et al (2019, BA), i.e. two random probability measures are either identical or share no common atoms
- To solve the above issue the large class of latent nested processes (LNP) is introduced
- In Denti et al (2022, JASA), instead, the common atom model (CAM) is introduced:

$$y_{i,j} \mid G_j \qquad G_j \mid Q \sim Q, \qquad Q = \sum_{h \geq 1} \pi_h \delta_{G_h^*}, \qquad G_h^* = \sum_{l \geq 1} w_{hl} \delta_{\theta_l^*}.$$

Brief summary (2)

- CAM does not suffer from the degeneracy property and allows a two-layer clustering
  - Distributional clustering: G_j are clustered to the G_h^*
  - Observational clustering $y_{i,j}$ are clustered in the atoms θ_l^*.

- CAM is applied to analyze complex microbiome data
- Data consist of a $n \times J$ abundance table, a matrix formed by n operational taxonomic unit (OTU) measurements (obervations) for each of the J individuals (groups)
- In this case the distributional clustering are grouping the individuals



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1) Possible CAM generalizations

- In the CAM all the sequences of weights have a DP-like construction, i.e.

$$\pi_h = \nu_h \prod_{\ell<h}(1-\nu_\ell), \qquad \nu_h \sim Beta(1, a)$$

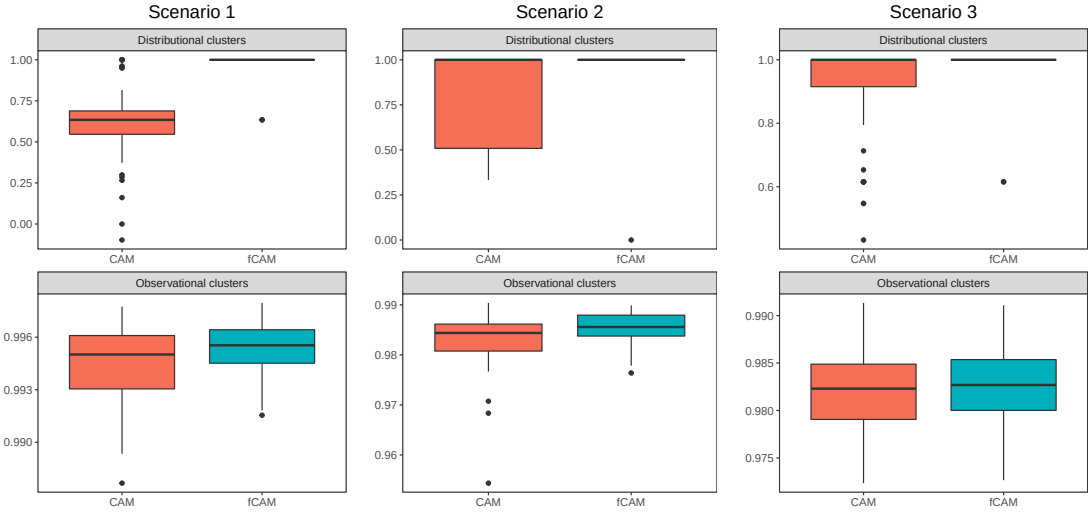
- Natural extensions include general stick-breaking priors, e.g. the Pitman-Yor process

$$\pi_h = \nu_h \prod_{\ell<h}(1-\nu_\ell), \qquad \nu_h \sim Beta(1-\sigma, a+h\sigma)$$

  this would allow more flexible distributional clustering behaviour.

- In D'Angelo et al. (2022, Biometrics) we defined a mixture of finite mixture (MFM) version of the CAM also employing the computational strategies of Frühwirth-Schnatter, et al. (2021, BA)

finite-CAM: clustering performance on simulation



2) Testing group differences

- The CAM is reminiscent of the shared kernel (SK) screening approach by Lock and Dunson (2015, Biometrika) and Canale and Dunson (2017, Stat. Sinica).
- Consider data belonging to two groups (e.g. cases and controls) and assume to measure some outcome $y_{i,1} \sim f_1$ for group 1 and $y_{j,0} \sim f_0$ for group 0 with interest on

$$H_0 : f_0 = f_1 \qquad H_1 : f_0 \neq f_1$$

- Assume a SK mixture model for both cases and controls, e.g.

$$f_h(\cdot) = \sum_{\ell} \pi_{\ell,h} K(\cdot; \theta_\ell)$$

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- Can we consider this a special case of CAM mixture? Can we use CAM mixtures for testing group differences?

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- In both cases, for a finite sample ($i = 1, dots, n$) data cluster into $k_n \leq n$ clusters
- In finite mixtures y_{n+1} can be assigned in a new cluster but up to a prespecified upper bound.
- In CAM, however,

$$Q = \sum_{h \geq 1} \pi_h \delta_{G_h^*}, \qquad G_h^* = \sum_{l \geq 1} w_{hl} \delta_{\theta_l^*}$$

is an infinite sum. Does it really make sense to assume an infinite mixture for the groups?

Questions/comments

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2. Similarities with the SK approach. Is the SK approach a special case of CAM mixture? Can we use CAM mixtures for testing group differences?
3. Do we really need to assume an infinite mixture for $Q = \sum_{h \geq 1} \pi_h \delta_{G_h^*}$?

References

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