Borrowing Strength with Non-exchangeable Priors over Subpopulations

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Outline

1. Intro: hierarchical models; random partitions
2. Random partition models: PPM, SSM, MBC ...
3. Random partition: non-exchangeable units
4. Simulation study

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Example: Irinotecan in advanced sarcomas (similar to Thall et al., 2003 StatMed).

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- Borrow strength across j by hierarchical model, regression, and/or clustering of sub-populations

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Hierarchical model with clusters: Group subtypes into clusters, $\{1, \ldots, J\} = S_1 \cup \ldots \cup S_K$, assume equal θ_j for all subtypes in cluster, $\theta_j = \theta_k^\star \; \forall j \in S_k$ and

$$\theta_k^\star \mid \mu \sim N(\mu, \tau)$$

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Allow for increased prob of co-clustering subtypes with same prognosis.

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Random partition: $p(\rho)$

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x by cluster: $x_k^* = \{x_j;\ j \in S_k\}$

Random Partition Models w/o Covariates

Sampling model: conditional on partition ρ, assume

$$p(y_{ji} \mid \rho, \theta^{\star}) = p(y_{ji} \mid \theta^{\star}_{s_j}) \qquad (*)$$

with cluster-specific parameters $\theta^{\star}_k$

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Prior $p(\rho)$: PPM, SSM, model-based clustering etc. $\longrightarrow$ next slide

Random Partition Models

General models for $p(\rho)$, unrelated to the application.

Product partition model (PPM): Hartigan (1990 Comm Stat), Barry and Hartigan (1993 JASA), Crowley (1997 JASA), Quintana (2006 JSPI)

cohesion functions $c(S_j)$ define similarity of a cluster,

$$p(\rho) \propto \prod_{k=1}^{K} c(S_k).$$

together with the sampling model (*)

Species sampling model (SSM): Pitman (1996), Ishwaran and James (2003 Stat Sinica)

$p(\rho)$ depends on S indirectly through $|S_k|$:

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Random Partition Models (ctd.)

Model based clustering: Fraley and Raftery (2002 JASA), Richardson and Green (1997 JRSSB) implicitely define $p(\rho)$ by

$$p(y_j \mid K, \theta, \pi) = \sum_{k=1}^{K} \pi_k f_k(y_j \mid \theta_K),$$

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and equivalent hierarchical model with latent s_j:

$$p(y_j \mid s_j = k, \theta, K) = f_k(y_j \mid \theta_k^\star)$$
$$Pr(s_j = k) = \pi_k$$

Polya urn: predictive rule; let K_j = no. clusters among $\{1, \ldots, j\}$.

$$p(s_{j+1} \mid s_1, \ldots, j) = \begin{cases} s_h & \text{with prob } 1/(M+j) \\ & h = 1, \ldots, j \\ K_j + 1 & \text{with prob } M/(M+j) \end{cases}$$

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$$\theta_j \sim G \text{ and } G \sim DP(G^\star, M)$$

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- This is $p(\rho)$ used in Mallick & Walker (1997).

Random Partition for Non-exchangeable Units

PPM-hier: Let m_{k1}, m_{k2}, m_{k3} denote the number of poor, medium and good prognosis subtypes in the k-th cluster. Let $m_k = |S_k|$

$$p(\rho) \propto \prod_{k=1}^{K} \underbrace{\left(\frac{m_{k1}!m_{k2}!m_{k3}!}{m_k!}\right)^{\gamma}}_{g(x_k^\star)} \cdot c(S_k)$$

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with norm. const. $\sum_\rho \prod_{k=1}^K g(x_k^\star) c(S_k)$

Note: accomodate missing x_j for some sub-populations by including in the counts $m_\star$ only sub-populations with known x_j.

Non-exchangeable PPM: Desiderata

Symmetry: $p(\rho)$ is invariant w.r.t. permutations of the indices $j = 1, \ldots, J$, i.e., $p(\rho)$ does not depend on the order of subtypes.

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Exchangeable model as special case:

If $m_{k1} = m_k$ and $m_{k2} = m_{k3} = 0$

$\rightarrow$ model reduces to original model $p(\rho) \propto \prod c(S_j)$.

Random Partition with Covariates

PPMx: In Müller, Quintana & Rosner (2008) we consider random partitions with covariates, using

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PPM-hier: with

$$g(\cdot) = (m_{k1}! m_{k2}! m_{k3}!)/m_k!)^\gamma$$

is a special case for clustering the sub-populations in a hierarchical model.

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  - $p(s_j, \theta_j \mid \mathbf{s}_{-j}, \boldsymbol{\theta}_{-j}, y)$: Let $m_k^- = |S_k \setminus \{j\}|$, $K^- =$ no. clusters w/o $\{j\}$ and $x = x_j$. Then the conditional *prior* for s_j is

$$(s_j \mid \mathbf{s}_{-j}) = \begin{cases} s_h,\ h \neq j & \text{w. pr} \propto m_k^- \left(\frac{m_{kx}+1}{m_k^-+1}\right)^\gamma \\ & \qquad \text{with } k = s_h \\ K^- + 1 & \text{w. pr} \propto M \end{cases}$$

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  Polya urn with additional factor.
  Conditional posterior is now easy to derive.
- Inference on θ_j: average over all imputed ρ

Example

Monte Carlo study: under assumed truth, $p_j =$ (by prognosis):

$$\underbrace{.59, .55, .47,}_{good} \; \underbrace{.45, .4, .36, .34, .3, .26}_{intermediate} \; \underbrace{.23, .19, .17}_{poor}$$

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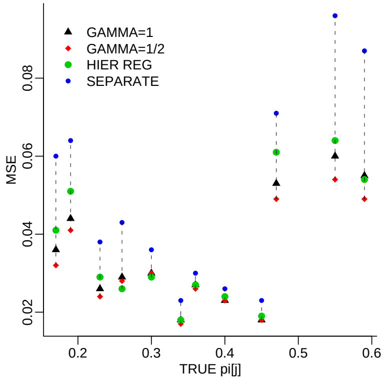
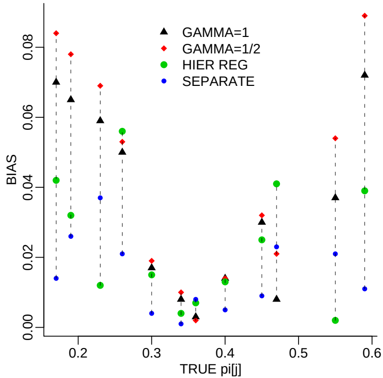
Hierarchical model w. regression: $\theta_j \sim N(\mu + \beta_1 x_j, \tau)$ and

$(\mu, \tau) \sim N(0, I)$.


GAMMA=1
GAMMA=1/2
HIER REG
SEPARATE
MSE
0.02
0.04
0.06
0.08
0.2
0.3
0.4
0.5
0.6
TRUE pi[j]

MSE


GAMMA=1
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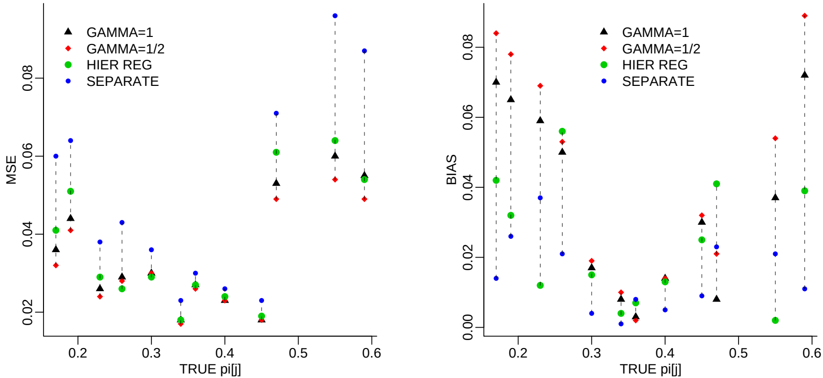

MSE bias

Simulation of $M = 100$ possible study realizations.

Summary

- Borrowing strength across non-exchangeable sub-populations
- Compromise between separate analyses (no borrowing strength) and regression (too much borrowing strength)
- Easy computation.
- The specific factor $g(x_k^\star) = (m_{k1}! \ldots)^\gamma$ was an example. Many other formats are possible.
- Limitation: Impact only for small sample sizes (like an early phase clinical trial).