Contamination models: Estimation, test & clustering

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1. Motivation and framework
2. Estimation and Test (with $k \geq 2$ samples)
3. Clustering (with $K \geq 2$ samples)

THE CONTAMINATION MODEL FRAMEWORK

An admixture (aka contamination) model is a specific 2-component mixture model where **one of the two components is known**.

Consider an iid random sample $X = (X_1, ..., X_n)$ drawn from the admixture model with cdf L.

We have :

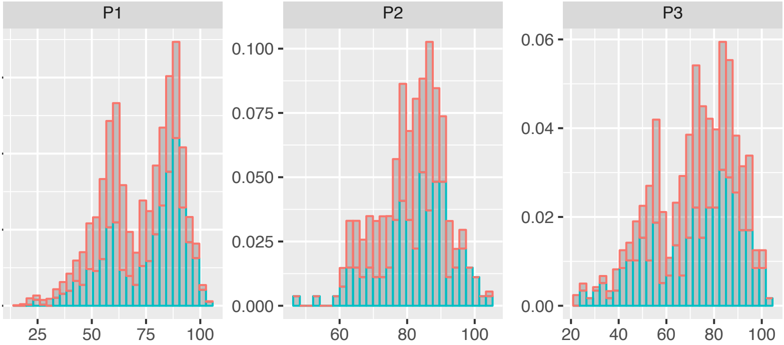
$$L(x) = p\,F(x) + (1 - p)\,G(x), \qquad x \in \mathbb{R} \tag{1}$$

with **G a known cdf** (gold standard), and $p \in]0, 1[$.

Goal : estimate from $(X_1, ..., X_n)$ the unknown component weight p and the unknown cdf F, under minimal assumptions.

AN EXAMPLE : MORTALITY EXPERIENCE

Women (blue), men (red)



In actuarial science/finance, plenty of situations where the distribution looks like this (claim distributions, customer behaviours, ...).

HYPOTHESIS TEST ON THE UNKNOWN COMPONENT

To perform the test, we use the **decontaminated** version of the unknown component density F.

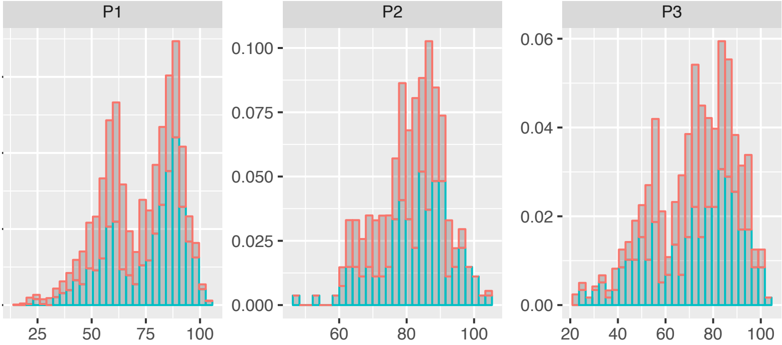
Suppose that p has been consistently estimated, then from the sample providing $\hat{L}$ the decontaminated unknown cdf follows

$$\hat{F}(x) = \frac{\hat{L}(x) - (1-\hat{p})G(x)}{\hat{p}}, \qquad x \in \mathbb{R}. \tag{2}$$

With 1 sample : test $H_0: \; F \in \mathcal{F}$ against $H_1: F \notin \mathcal{F}$.

With 2 samples, one could test $[H_0: \; F_1 = F_2$ against $H_1: F_1 \neq F_2]$

PRICING WITH 'UNCAPTURED' HETEROGENEITY



Assume P1, P2 and P3 are portfolios with low exposure...and

- heterogeneous age-at-death distributions (mixture profile),
- well-known age-at-death distrib. in general pop. (gold standard).

$\Rightarrow$ Could we pool them to increase exposure for pricing ?

THE IBM APPROACH (2 samples)

→ Cramer-Von Mises type test : CLT for estimators of unknown p_i's and F_i's and known stochastic behavior of empirical contrast $n\hat{d}_n(\hat{\theta}_n)$.

→ Inversion / Best Matching (IBM) : with the discrepancy measure

$$d(\theta) = \int_{\mathbb{R}} (F_1(x, p_1) - F_2(x, p_2))^2 dU(x), \tag{3}$$

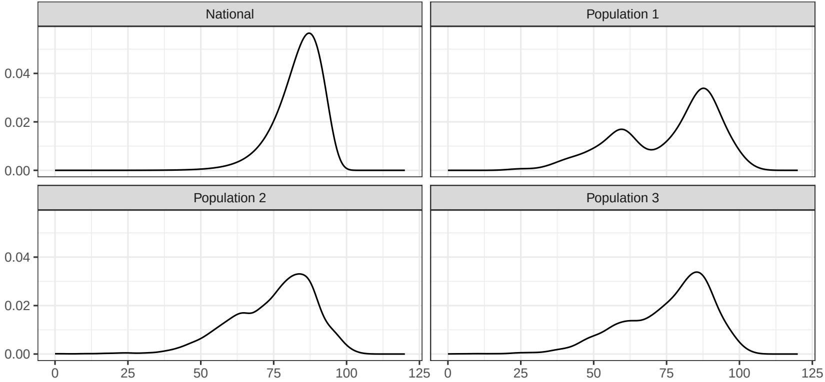
with $\theta = (p_1, p_2) \in \Theta = [\delta_1, \delta_2]^2$.

→ X.M., D.P., Y.S., P.V. **Two-sample contamination model test**. Bernoulli (2023), `https://hal.science/hal-03985733`.

→ R package admix :
`https://cran.r-project.org/web/packages/admix/index.html`

APPLICATION : SPECIFIC MORTALITY POOLING

→ Back to our 3 portfolios (age-at-death densities for female here). From top left to bottom right : french national pop., P1, P2, and P3.



No obvious similar behaviour... Maybe populations 2 and 3 ?

RESULTS

	Size	Life expectancy	Weight $\hat{p}$	P1	P2	P3
P1	1 251	75.42	0.4603	—	23.28	0.717
P2	7 356	74.91	0.7003	1.4e-06	—	18.48
P3	3 456	75.56	0.6281	0.397	1.7e-05	—

→ According to the test, populations 1 and 3 share a common behaviour (F_1 and F_3) characterizing their specific mortality profile...
... whereas other portfolios combinations lead to reject H_0.

⇒ P1 and P3 could be pooled together for pricing !

Limit : pairwise comparisons instead of global test...

EXTENSION OF THE TEST TO THE k-SAMPLE CASE

Consider $k > 2$ samples, each sample $X^{(i)} = (X_1^{(i)}, ..., X_{n_i}^{(i)})$ follows

$$L_i(x) = p_i F_i(x) + (1 - p_i) G_i, \qquad x \in \mathbb{R}.$$

The test to perform is given by

$$H_0 : \; F_1 = ... = F_k \quad \text{against} \quad H_1 : \; F_i \neq F_j \text{ for some } i \neq j.$$

To do so, compare pop. i and j by defining sub-(i, j)-testing problem :

$$H_0(i, j) : \; F_i = F_j \qquad \text{against} \qquad H_1(i, j) : \; F_i \neq F_j \; , \tag{4}$$

Then,
→ Apply **IBM** for each pair (i, j) & build a series of **embedded statistics**.
→ Add a penalization term to select the right number of terms in the final test statistic.

CLUSTER POPULATIONS INSTEAD OF INDIVIDUALS

Adapt the previous test procedure to obtain a data-driven method to cluster K unknown populations into N subgroups (characterized by a common unknown mixture component).

- N of clusters is automatically chosen by the procedure,
- Each subgroup is validated by the previous testing method.

Novelty : allows to cluster unobserved subpopulations (via unknown components).

→ Not trivial because of unknown p_i's...

→ Preprint : X.M., D.P., Y.S., P.V.. **Contamination source based K-sample clustering**, submitted, 2023. `https://hal.science/hal-04129130`.

ALGORITHM : A BASIC IDEA

K-sample 2-component mixture clustering (K2MC)

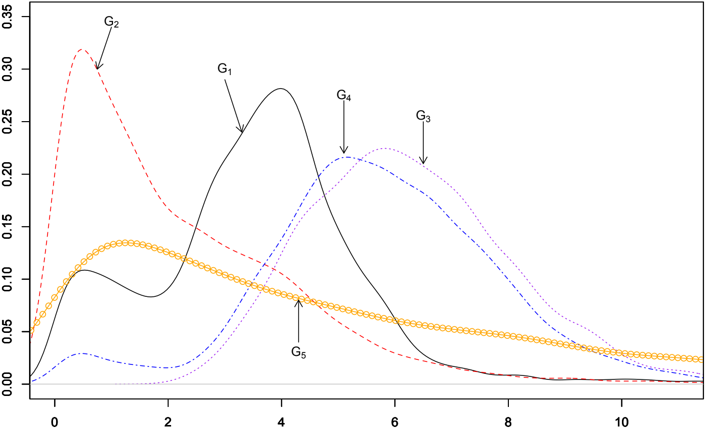
1] Initialization : create the first cluster to be filled, *i.e.* $c = 1$.
By convention, $S_0 = \emptyset$.

2] Select $\{x, y\} = \text{argmin}\{d_n(i,j); i \neq j \in S \setminus \bigcup_{k=1}^{c} S_{k-1}\}$.

3] Test H_0 between x and y.
If H_0 is not rejected then $S_1 = \{x, y\}$,
Else $S_1 = \{x\}$, $S_{c+1} = \{y\}$ and then $c = c + 1$.

4] While $S \setminus \bigcup_{k=1}^{c} S_k = \emptyset$ **do**
Select $u = \text{argmin}\{d(i,j); i \in S_c, j \in S \setminus \bigcup_{k=1}^{c} S_k\}$;
Test H_0 the simultaneous equality of all the f_j (k-sample test), $j \in S_c$:
If H_0 not rejected, then put $S_c = S_c \bigcup \{u\}$;
Else $S_{c+1} = \{u\}$ and $c = c + 1$.
End While

PLEASE CLUSTER THESE 5 POPULATIONS



Possible choices : [(3,4), (2,5), 1] or [(3,4), 1, 2, 5)] or [(1,2), (4,5), 3] ?

Connect to `www.menti.com` (code : 2732 4825)

SOLUTION

	Pop.1	Pop.2	Pop.3	Pop.4	Pop.5
Size n_i	2000	2500	2000	4500	4000
Unknown weight p_i	0.6	0.12	0.15	0.08	0.1
Known distribution G_i	$\mathcal{E}(1/3)$	$\mathcal{E}(1/2)$	$\mathcal{G}(13,2)$	$\mathcal{G}(12,2)$	$\mathcal{E}(1/6)$
"Unknown" distribution F_i	$\mathcal{G}(16,4)$	$\mathcal{G}(16,4)$	$\mathcal{G}(15,3)$	$\mathcal{E}(1/2.5)$	$\mathcal{E}(1/2.5)$

1. Population 1 : $0.6\,\mathcal{G}(16;4) + 0.4\,\mathcal{E}(1/3)$
2. Population 2 : $0.12\,\mathcal{G}(16;4) + 0.88\,\mathcal{E}(1/2)$
3. Population 3 : $0.15\,\mathcal{G}(15;3) + 0.85\,\mathcal{G}(13;2)$
4. Population 4 : $0.08\,\mathcal{E}(1/2.5) + 0.92\,\mathcal{G}(12;2)$
5. Population 5 : $0.1\,\mathcal{E}(1/2.5) + 0.9\,\mathcal{E}(1/6)$

$\Rightarrow$ **Clusters to be found :**

<u>3 clusters</u> (pop. (1,2) ; (4,5) and 3) !

CONCLUSION

Fully implemented in R package admix !

→ Fully tractable solution **without shape constraints** ;

→ Allows for hypothesis testing and clustering ;

→ Clustering is made on unknown/unobserved phenomenons ;

→ An application to the covid-19 pandemics in our last paper (clustering countries).

→ Actuarial applications whenever pooling can benefit !

Thanks for your attention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APPENDIX 1 : 2-sample TESTING STRATEGY

- Inner model convergence regime caracterized by $Z(\theta^*, L_1, L_2)$ and $Z(\theta^c, L_1, L_2)$ under both H_0 and H_1 (closed form stochastic integrals) $\Rightarrow$ Hypothesis-free test quality !
- Possibility to sample them using $Z(\hat{\theta}_n, \hat{L}_1, \hat{L}_2)$.
- $(1-\alpha)$-quantile Monte Carlo estimation of the stochastic integral $Z(\hat{\theta}_n, \hat{L}_1, \hat{L}_2)$ denoted $\hat{q}_{1-\alpha}$.

Finally, H_0-rejection rule :

$$n\hat{d}_n(\hat{\theta}_n) \quad \geq \quad \hat{q}_{1-\alpha}. \tag{5}$$

Interpretation : *if the test statistic is too far from the inner model convergence regime we suspect that something goes wrong.*

APPENDIX 2 : k-sample test, steps of the approach

Apply the theoretical results of IBM for each pair of populations (i, j), and then **build a series of embedded statistics**.

Then, $\forall i \neq j \in \{1, ..., k\}$,

1. Estimate $\widehat{\theta}_n(i,j) = \arg\min_{\theta \in \Theta_{i,j}} d_n[i,j](\theta)$,
2. Compute the statistic $T_{i,j} = n\, d_n[i,j](\widehat{\theta}_n(i,j))$.

We then obtain $d(k) = k(k-1)/2$ comparisons that we embed :

$$
\begin{aligned}
U_1 &= T_{1,2} \\
U_2 &= T_{1,2} + T_{1,3} \\
&\vdots \\
U_{d(k)} &= T_{1,2} + \cdots + T_{k-1,k},
\end{aligned}
$$

Consider the penalization rule (mimicking Schwarz criteria) :

$$S(n) = \min \left\{ \arg \max_{1 \leq r \leq d(k)} \left(U_r - r \sum_{(i,j) \in S(k)} l_n(i,j) \mathbb{I}_{\{r_k(i,j)=r\}} \right) \right\}.$$

N.B. : l_n if of the form n^ϵ, where ϵ should be tuned depending on our guess (H_0, H_1) to improve the test quality (further details in the paper).

$\Rightarrow$ Our data-driven test statistic is given by

$$\tilde{U}_n = U_{S(n)}.$$

Simulation results :
$\rightarrow$ The test shows good empirical levels in many different situations,
$\rightarrow$ It also has satisfactory empirical power, provided that $n_i p_i$ is high enough.