FlowVB: Automatic determination of the number of mixture components in Flow Cytometry with Variational Bayes

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- Aware of covariance-structure
- Mathematically convenient
- Can be fit (relatively) easily with the Expectation-Maximization (EM) Algorithm

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But:

Closed form solutions don't exist for all parameters of the distribution

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- Therefore optimizing over *M* is an degenerate (ill-posed) problem

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Task

Develop an algorithm to fit SMMs using Variational Bayes

Demo - Robustness to noise

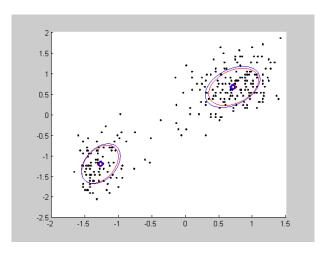


Figure: GMM (blue) vs. SMM(red) fit with VB without added noise

Demo - Robustness to noise

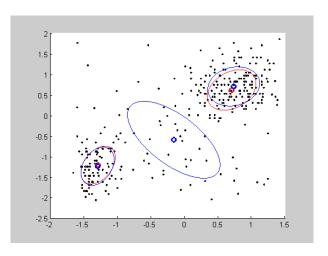
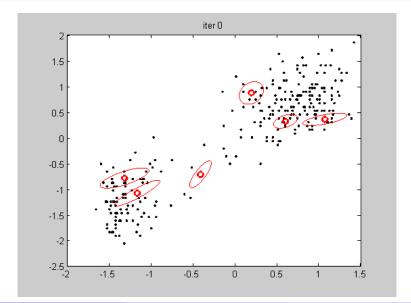
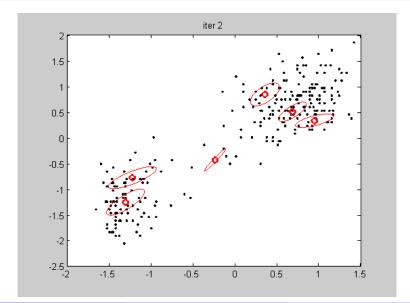
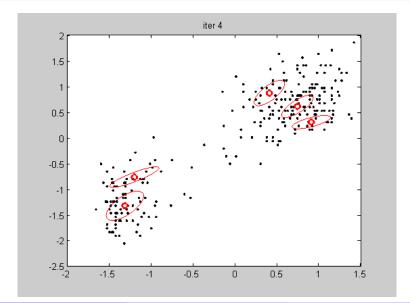
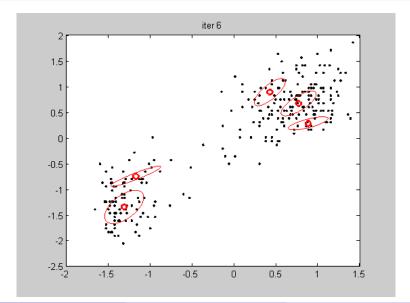


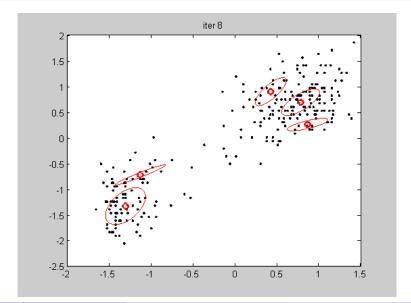
Figure: GMM (blue) vs. SMM(red) fit with VB with 20% added noise

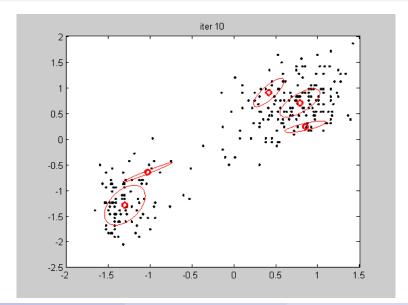


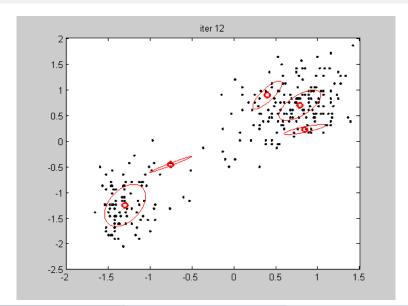


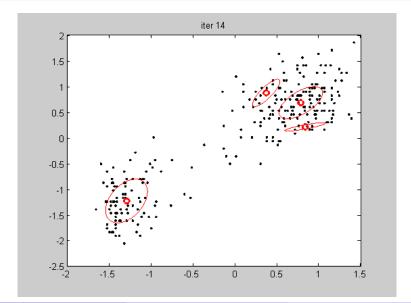


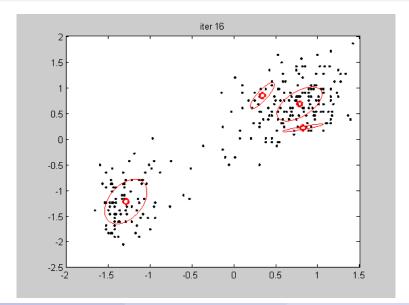


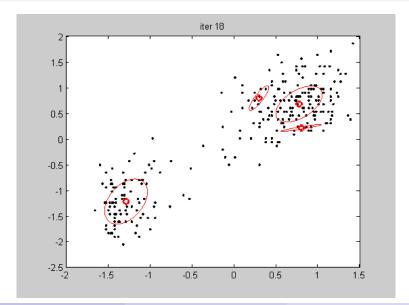


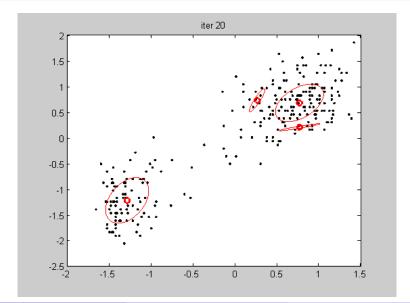


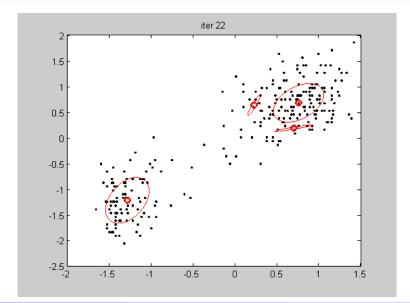


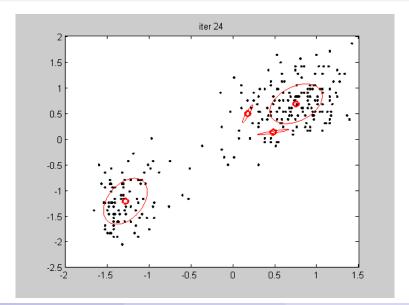


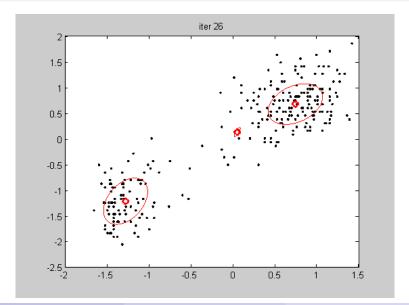


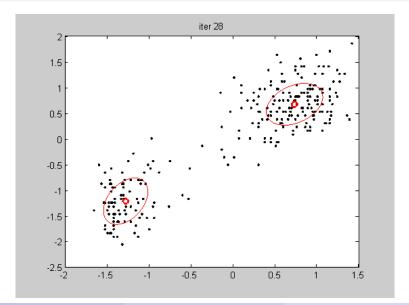


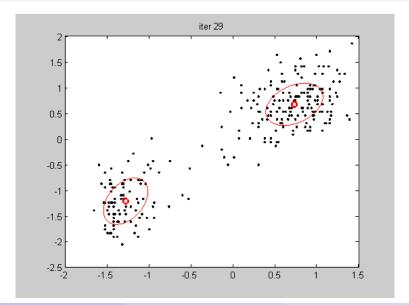












FlowVB is largely based on the algorithm presented in

C Archambeau and M Verleysen. Robust Bayesian Clustering. *Neural Networks*, 20(1):129–138, 2007.







Robust Bayesian clustering

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Received 25 October 2005; accepted 12 June 2006

Abstract

A new variational Bayesian learning algorithm for Students' mixture models is introduced. This algorithm leads to (i) robust density estimation, (ii) robust clustering and (iii) robust density automatic model selection. Gaussian mixture models are learning machines which are based on divide-and-conquer approach. They are commonly used for density estimation and clustering tasks, but are sensitive to outliers. The Students' distribution and is therefore less sensitive to any denarrative of the memirical distribution and is unsersainty. As

The latent variable model

A finite Student-t mixture model (SMM) is of the form

$$p(\mathbf{x}|\boldsymbol{\theta}_s) = \sum_{m=1}^{M} \pi_m \mathcal{S}(\mathbf{x}|\boldsymbol{\mu}_m, \boldsymbol{\Lambda}_m, \nu_m),$$

where

 π_m Mixing proportions, with $\sum_{m=1}^{M} \pi_m = 1$

 μ_m Expected value of component m

 Λ_m Precision matrix of component m

 ν_m Degrees of freedom of component m

 θ_s Ensemble of parameters

The latent variable model

Let us introduce a set of indicator variables $Z = \{z\}_{n=1}^{N}$, where $z_{nm} = 1$ iff datapoint n belongs to component m (and $z_{nm} = 0$ otherwise).

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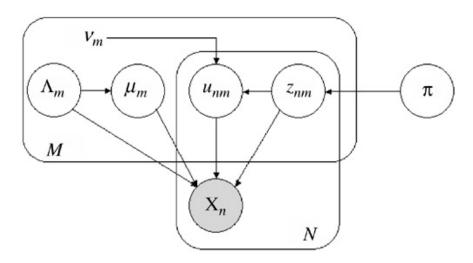
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In contrast to GMM we need a further latent variable. Note that the Student-t density can be written as an *infinite scale mixture*:

$$\mathcal{S}(\mathbf{x}|\boldsymbol{\mu},\boldsymbol{\Lambda},
u) = \int_0^{+\infty} \mathcal{N}(\mathbf{x}|\boldsymbol{\mu},u\boldsymbol{\Lambda}) \,\mathcal{G}\left(u\left|\frac{\nu}{2},\frac{\nu}{2}\right) \,du$$

We therefore have unobserved variables z_{nm} and u_{nm} for every observation and component.

Representation as Bayesian Graphical Model



from Archambeau & Verleysen (2007)

Variational Bayesian Inference

The evidence of the data

$$p(X|\mathcal{H}_M),$$

given the model structure \mathcal{H}_M , is untractable when using the real posterior

$$p(U, Z, \theta_s | X, \mathcal{H}_M)$$
.

Instead use an approximation and assume that it factorizes as

$$q(U, Z, \theta_s) = q(U, Z) q(\theta_s).$$

It can be shown that this leads to a lower bound for the real evidence.

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During the iteration we remove clusters where π_m is close to zero.

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 - Initialize k-means with 3 × M clusters
 - For every restart randomly select *M* points from this solution

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- Found that some Pre- and Post-processing improved results with GvHD

Pre-processing: Principal components analysis (PCA)

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- some performance gains

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- Finak et al. Merging Mixture Components for Cell Population Identification in Flow Cytometry. Advances in Bioinformatics, 2009.
- wrote our own implementation of FlowMerge

Keypoints of our FlowVB-algorithm

■ Robust inference by using Student-t distribution

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- Optional random restarts to improve results

- Robust inference by using Student-t distribution
- One-pass determination of number of mixture components
- Optional random restarts to improve results
- Improve performance by using PCA and flowMerge

Further developement

We are porting the algorithm to Python for further developement.

We are looking for additional developers and feedback from users.

Get involved:

Project page: http://github.com/FlowVB/FlowVB

Mailing list: http://groups.google.com/group/flowvb

Appendix

Variational Bayesian Inference

For a given model structure \mathcal{H}_M , the evidence is given by:

$$p(X|\mathcal{H}_M) = \int_{\theta_s} \int_U \sum_{Z} p(X, U, Z, \theta_s | \mathcal{H}_M) dU d\theta_s$$

This quantity is untractable, but it can be lower-bounded by

$$\log p(X|\mathcal{H}_M) \ge \log p(X|\mathcal{H}_M) - KL[q(U, Z, \theta_s)||p(U, Z, \theta_s|X, \mathcal{H}_M)],$$

where $\mathit{KL}(\cdot)$ is the Kullback-Leibler divergence, and $q(U, Z, \theta_s)$ is an approximation to $p(U, Z, \theta_s | X, \mathcal{H}_M)$.

By assuming that q factorizes as $q(U, Z, \theta_s) = q(U, Z) q(\theta_s)$, this quantity becomes tractable.

The latent variable model (cont.)

Putting the above together we get the following latent variable model:

$$p(\boldsymbol{z}_{n}|\boldsymbol{\theta}_{s},\mathcal{H}_{M}) = \prod_{m=1}^{M} \pi_{m}^{z_{nm}}$$

$$p(\boldsymbol{u}_{n}|\boldsymbol{\theta}_{s},\mathcal{H}_{M}) = \prod_{m=1}^{M} \mathcal{G}\left(u_{nm}\left|\frac{\nu_{m}}{2},\frac{\nu_{m}}{2}\right.\right)^{z_{nm}}$$

$$p(\boldsymbol{x}_{n}|\boldsymbol{\theta}_{s},\mathcal{H}_{M}) = \prod_{m=1}^{M} \mathcal{N}(\boldsymbol{x}_{n}|\boldsymbol{\mu}_{m},u_{nm}\boldsymbol{\Lambda}_{m})^{z_{nm}}$$

Priors

We introduce the following conjugate priors for our parameters:

Parameter	Prior
$\boldsymbol{\pi} = \{\pi_m\}_{m=1}^M$	$\mathcal{D}(\pi arkappa_0)$ (Dirichlet)
μ_m, Λ_m	$\mathcal{NW}(\mu_m, \mathbf{\Lambda}_m \boldsymbol{\theta}_{\mathcal{NW}_0}) = \mathcal{N}(\mu_m \boldsymbol{m}_0, \eta_0 \mathbf{\Lambda}_m) \mathcal{W}(\mathbf{\Lambda}_m \gamma_0, \mathbf{S}_0)$ (Joint Gaussian-Wishart)
$ u_{m}$	no prior, since no conjugate prior exists