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Data: y^* , prior $p(\theta)$, model $p(y|\theta)$. Likelihood $p(y|\theta)$ cannot be computed, but we can sample from it.

Repeat:

- 1 Sample $\theta \sim p(\theta)$
- 2 Sample $y \sim p(y|\theta)$
- 3 Accept $\boldsymbol{\theta}$ iff $\|\boldsymbol{s}(\boldsymbol{y}) \boldsymbol{s}(\boldsymbol{y}^{\star})\| \leq \epsilon$

ABC target



The previous algorithm targets:

$$p_{\epsilon}(\boldsymbol{ heta}|\boldsymbol{y}^{\star}) \propto p(\boldsymbol{ heta}) \int p(\boldsymbol{y}|\boldsymbol{ heta}) \mathbbm{1}_{\{\|\boldsymbol{s}(\boldsymbol{y})-\boldsymbol{s}(\boldsymbol{y}^{\star})\| \leq \epsilon\}} d\boldsymbol{y}$$

which approximates the true posterior $p(\theta|y)$. Two levels of approximation:

- Non-parametric error, governed by "bandwidth" ϵ ; $p_{\epsilon}(\theta|\mathbf{y}^{*}) \rightarrow p(\theta|s(\mathbf{y}^{*}))$ as $\epsilon \rightarrow 0$. (Curse of dimensionality with respect to $d = \dim(s)$.
- 2 Bias introduced by summary stat. s, since $p(\theta|s(y^*)) \neq p(\theta|y^*)$.

Note that $p(\theta|s(y^*)) \approx p(\theta|y^*)$ may be a reasonable approximation, but $p(y^*)$ and $p(s(y^*))$ have no clear relation: hence standard ABC cannot reliably approximate the evidence.



- Mostly trial and error.
- 2 Difficult trade-off: increasing the dimension of s reduces the bias (point 2 above), but increases the NP-error (point 1 above). This may be compensated by decreasing e, but then the CPU costs increases.
- **3** No clear theory on how to choose *s* so that $p(\theta|s(y^*)) \approx p(\theta|y^*)$.

Divide and conquer

Main idea behind EP-ABC: cut our 'big' ABC problems into *n* 'small' ABC problems.

Say, data \boldsymbol{y} decomposes into (y_1, \ldots, y_n) , leading to some factorisation of the likelihood

$$p(oldsymbol{y}|oldsymbol{ heta}) = \prod_{i=1}^n l_i(oldsymbol{ heta})$$

where:

- $l_i(\boldsymbol{\theta}) = p(y_i|\boldsymbol{\theta})$ (IID model)
- $l_i(\boldsymbol{\theta}) = p(y_i|y_{i-1}, \boldsymbol{\theta})$ (Markov model)

• or more generally, something like $l_i(\theta) = p(y_i|y_{1:i-1}, \theta)$ Clearly, doing ABC on one single factor should be much easier (provided we can sample from the likelihood factor); that is (a) easier to design a summary statistics for y_i only (perhaps even $s_i(y_i) = y_i$); and (b) easier to implement ABC (rejection).



$$p_{\epsilon}(\boldsymbol{\theta}|\boldsymbol{y}^{\star}) \propto p(\boldsymbol{\theta}) \prod_{i=1}^{n} \left\{ \int p(y_{i}|y_{1:i-1}^{\star}, \boldsymbol{\theta}) \mathbb{1}_{\left\{ \|s_{i}(y_{i})-s_{i}(y_{i}^{\star})\| \leq \varepsilon \right\}} \, dy_{i} \right\}$$
(1)

Take $s_i(y_i) = y_i$ for now. Standard ABC cannot target this approximate posterior, because the probability that $||y_i - y_i^*|| \le \varepsilon$ for all *i* simultaneously is exponentially small w.r.t. *n*. But it does not depend on some summary stats *s*, and $p_{\epsilon}(\theta|\mathbf{y}^*) \to p(\theta|\mathbf{y}^*)$ as $\epsilon \to 0$ (one level of approximation). The EP-ABC algorithm computes a Gaussian approximation of (1). In order to do so, it essentially runs *n* ABC algorithms, each treating separately the constraint $||y_i - y_i^*|| \le \varepsilon$. EP (Minka, 2001)

Consider a generic posterior:

$$\pi(\boldsymbol{\theta}) = p(\boldsymbol{\theta}|\boldsymbol{y}) \propto p(\boldsymbol{\theta}) \prod_{i=1}^{n} l_i(\boldsymbol{\theta})$$
(2)

where the l_i are n contributions to the likelihood. Aim is to approximate π with

$$q(\boldsymbol{ heta}) \propto \prod_{i=0}^{n} f_i(\boldsymbol{ heta})$$
 (3)

where the f_i 's are the "sites". To obtain a Gaussian approximation, take $f_i(\theta) \propto \exp\left(-\frac{1}{2}\theta^t Q_i \theta + \mathbf{r}_i^t \theta\right)$, so that:

$$q(\boldsymbol{\theta}) \propto \exp\left\{-\frac{1}{2}\boldsymbol{\theta}^{t}\left(\sum_{i=0}^{n} \mathbf{Q}_{i}\right)\boldsymbol{\theta} + \left(\sum_{i=0}^{n} \mathbf{r}_{i}\right)^{t}\boldsymbol{\theta}\right\}$$
(4)

where \mathbf{Q}_i and \mathbf{r}_i are the site parameters.

Site update

We wish to minimise $KL(\pi || q)$. To that aim, we update each site (Q_i, r_i) in turn, as follows. Consider the hybrid:

$$h_i(\boldsymbol{ heta}) \propto q_{-i}(\boldsymbol{ heta}) l_i(\boldsymbol{ heta}), \quad q_{-i}(\boldsymbol{ heta}) = \prod_{j \neq i} f_j(\boldsymbol{ heta})$$

and adjust (Q_i, r_i) so that $KL(h_i || q)$ is minimal. One may easily prove that this may be done by moment matching, i.e. calculate:

$$\boldsymbol{\mu}_{h} = \mathbb{E}^{h_{i}}\left[\boldsymbol{\theta}\right], \quad \boldsymbol{\Sigma}_{h} = \mathbb{E}^{h_{i}}\left[\boldsymbol{\theta}\boldsymbol{\theta}^{T}\right] - \boldsymbol{\mu}_{i}\boldsymbol{\mu}_{i}^{T}$$

set $Q_h = \Sigma_h^{-1}$, $r_h = \Sigma_h^{-1} \mu_h$, then adjust (Q_i, r_i) so that (Q_h, r_h) and $(Q, r) = (\sum_{i=0}^n Q_i, \sum_{i=0}^n r_i)$ (the moments of q) match.

$$oldsymbol{Q}_i \leftarrow oldsymbol{\Sigma}_h^{-1} - oldsymbol{Q}_{-i}, \quad oldsymbol{r}_i \leftarrow oldsymbol{\Sigma}_h^{-1} oldsymbol{\mu}_h - oldsymbol{r}_{-i}.$$



- Convergence is usually obtained after a few complete cycles over all the sites.
- We use the Gaussian family for q, but one may take another exponential family.
- Feasiblity of EP is determined by how easy it is to compute the moments of order 1 and 2 of the hybrid distribution (i.e. a Gaussian density q_{-i} times a single likelihood contribution l_i).



Going back to the EP-ABC target:

$$p_{\epsilon}(\boldsymbol{\theta}|\boldsymbol{y}^{\star}) \propto p(\boldsymbol{\theta}) \prod_{i=1}^{n} \left\{ \int p(y_{i}|y_{1:i-1}^{\star}, \boldsymbol{\theta}) \mathbb{1}_{\left\{ \|y_{i}-y_{i}^{\star}\| \leq \varepsilon \right\}} dy_{i} \right\}$$
(5)

we take

$$l_i(\boldsymbol{\theta}) = \int p(y_i|y_{1:i-1}^{\star}, \boldsymbol{\theta}) \mathbb{1}_{\{\|y_i-y_i^{\star}\|\leq \varepsilon\}} dy_i.$$

In that case, the hybrid distribution is a Gaussian times I_i . The moments are not available in close-form (obviously), but they are easily obtained, using some form of ABC for a single observation.

EP-ABC site update

Inputs: ϵ , y^* , i, and the moment parameters μ_{-i} , Σ_{-i} of the Gaussian pseudo-prior q_{-i} .

- **1** Draw *M* variates $\theta^{[m]}$ from a $N(\mu_{-i}, \Sigma_{-i})$ distribution.
- 2 For each $\boldsymbol{\theta}^{[m]}$, draw $y_i^{[m]} \sim p(y_i | y_{1:i-1}^{\star}, \boldsymbol{\theta}^{[m]})$.
- 3 Compute the empirical moments

$$M_{acc} = \sum_{m=1}^{M} \mathbb{1}_{\left\{ \|y_i^{[m]} - y_i^{\star}\| \le \varepsilon \right\}}, \quad \widehat{\mu}_h = \frac{\sum_{m=1}^{M} \theta^{[m]} \mathbb{1}_{\left\{ \|y_i^{[m]} - y_i^{\star}\| \le \varepsilon \right\}}}{M_{acc}}$$
(6)
$$\widehat{\Sigma}_h = \frac{\sum_{m=1}^{M} \theta^{[m]} \left\{ \theta^{[m]} \right\}^t \mathbb{1}_{\left\{ \|y_i^{[m]} - y_i^{\star}\| \le \varepsilon \right\}}}{M_{acc}} - \widehat{\mu}(h_i) \widehat{\mu}(h_i)^t.$$
(7)
Return $\widehat{Z}(h_i) = M_{acc}/M, \ \widehat{\mu}(h_i) \text{ and } \widehat{\Sigma}(h_i).$

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We are turning a deterministic, fixed-point algorithm, into a stochastic algorithm, hence numerical stability may be an issue. Solutions:

- We adjust dynamically *M* the number of simulated points at a given site, so that the number of accepted points exceeds some threshold.
- We use Quasi-Monte Carlo in the ${m heta}$ dimension.
- Slow EP updates may also be used.



In the IID case, $p(y_i|y_{1:i-1}, \theta) = p(y_i|\theta)$, and the simulation step $y_i^{[m]} \sim p(y_i|\theta^{[m]})$ is the same for all the sites, so it is possible to recycle simulations, using importance sampling.

An IID univariate model taken from Peters et al. (2010). The observations are alpha-stable, with common distribution defined through the characteristic function

$$\Phi_X(t) = \begin{cases} \exp\left\{i\delta t - \gamma^{\alpha} \left|t\right|^{\alpha} \left[1 + i\beta \tan\frac{\pi\alpha}{2} \operatorname{sgn}(t)(|\gamma t| - 1)\right]\right\} & \alpha \neq 1\\ \exp\left\{i\delta t - \gamma \left|t\right| \left[1 + i\beta\frac{2}{\pi} \operatorname{sgn}(t) \log|\gamma t|\right]\right\} & \alpha = 1 \end{cases}$$

Density is not available in close-form. Data: n = 1200 AUD/GBP log-returns computed from daily exchange rates.

Results from alpha-stable example



Marginal posterior distributions of α , β , γ and δ for alpha-stable model: MCMC output from the exact algorithm (histograms, 60h), approximate posteriors provided by EP-ABC (40min, solid line), kernel density estimates from MCMC-ABC based on summary statistic of Peters et al (50× more simulations, dashed line).

The stochastic Lotka-Volterra process describes the evolution of two species Y_1 (prey) and Y_2 (predator):

$$\begin{array}{cccc} Y_1 & \stackrel{r_1}{\rightarrow} & 2Y_1 \\ Y_1 + Y_2 & \stackrel{r_2}{\rightarrow} & 2Y_2 \\ Y_2 & \stackrel{r_3}{\rightarrow} & \emptyset \end{array}$$

We take $\theta = (\log r_1, \log r_2, \log r_3)$, and we observe the process at discrete times. Model is Markov, $p(y_i^*|y_{1:i-1}^*, \theta) = p(y_i^*|y_{i-1}^*, \theta)$.

Simulated data





Results





PMCMC approximations of the ABC target (histograms) for $\epsilon = 3$ (top), EP-ABC approximations, for $\epsilon = 3$ (top) and $\epsilon = 1$ (bottom).

Third example: reaction times

Subject must choose between k alternatives. Evidence $e_j(t)$ in favour of choice j follows a Brownian motion with drift:

$$au de_j(t) = m_j dt + dW_t^j.$$

Decision is taken when one evidence "wins the race"; see plot.





1860 Observations, from a single human being, who must choose between "signal absent", and "signal present".









For simplicity, I considered cases where the *n* factors were simple enough to allow (a) to take $s_i(y_i) = y_i$; and (b) to use rejection-ABC at each site. But the same approach may be used to combine more complex factors. Opens the door to applications on repeated experiments and hierarchical models.

More generally, to obtain factorisable likelihoods, one may:

- include latent variables in θ;
- work conditionally on some hyper-parameter;
- use composite likelihood approximations (at the price of an extra level of approximation).

EP-ABC on an HMM composite likehood

Consider a Hidden Markov model:

$$x_{t+1}|x_t, \theta \sim p(x_{t+1}|x_t, \theta), \quad y_t|x_t, \theta \sim p(y_t|x_t, \theta).$$

A possible CL approximation of the true likelihood is

$$p_{CL}(\boldsymbol{y}|\boldsymbol{\theta}) = p(y_{1:L}|\boldsymbol{\theta}) \times p(y_{L+1:2L}|\boldsymbol{\theta}) \times \cdots$$

where the L-dim marginals may be computed as:

$$p(y_{t+1:t+L}|\theta) = \int p(x_{t+1}|\theta) \prod_{k=2}^{L} p(x_{t+k}|x_{t+k-1},\theta) \prod_{k=1}^{L} p(y_{t+k}|x_{t+k},\theta) dx_{t+1:t+L}$$

and $p(x_{t+1}|\theta)$ is the stationary dist. of Markov chain (x_t) . It is easy to sample from this likelihood factor.

Numerical illustration



Alpha-stable stochastic volatility model, n = 120, results obtained in one minute (vs 3 days with PMCMC-ABC). Note that complexity of EP-ABC-CL is O(n), vs $O(n^2)$ for PMCMC-ABC.



CL is often used in certain class of spatial models; however some of these models (e.g. spatial extremes) are such that higher-order marginals are intractable. EP-ABC could be used here as well.

Conclusion



- EP-ABC offers a principled way to combine *n* local ABC approximations (provided the likelihood may be cut into *n* pieces).
- EP-ABC cannot be used in all ABC scenarios, but on the other hand, it can be used in situations where standard ABC is not suitable.
- In certain cases, we may get rid of summary stats entirely.
- EP-ABC is fast (minutes), because it integrates one data chunk at a time (not all of them together). Typically, gain is $\times 100.$
- EP-ABC also approximates the evidence.
- Convergence of EP-ABC is an open problem (Mike?)

Quote, references

• ENSAE

"It seems quite absurd to reject an EP-based approach, if the only alternative is an ABC approach based on summary statistics, which introduces a bias which seems both larger (according to our numerical examples) and more arbitrary, in the sense that in real-world applications one has little intuition and even less mathematical guidance on to why $p(\theta|s(y))$ should be close to $p(\theta|y)$ for a given set of summary statistics."

- Barthelmé, S. and Chopin, N. (2011). ABC-EP: Expectation Propagation for Likelihood-free Bayesian Computation, ICML 2011 (Proceedings of the 28th International Conference on Machine Learning), L. Getoor and T. Scheffer (eds), 289-296.
- Barthelmé, S. & Chopin, N. (2011). Expectation-Propagation for Summary-Less, Likelihood-Free Inference, arxiv:1107.5959.