



RESEARCH ARTICLE

10.1002/2016WR019550

Posterior population expansion for solving inverse problems

C. Jäggli¹ , J. Straubhaar¹, and P. Renard¹

¹Centre for Hydrogeology and Geothermics, University of Neuchâtel, Neuchâtel, Switzerland

Key Points:

- The paper introduces PoPEX, a new ensemble-based Bayesian inversion method
- PoPEX is designed to identify discrete-type models (geological facies)
- Numerical tests show that PoPEX is around 10 times more efficient than iterative spatial resampling

Correspondence to:

C. Jäggli,
christoph.jaeggli@unine.ch

Citation:

Jäggli, C., J. Straubhaar, and P. Renard (2017), Posterior population expansion for solving inverse problems, *Water Resour. Res.*, 53, doi:10.1002/2016WR019550.

Received 22 JUL 2016

Accepted 12 MAR 2017

Accepted article online 17 MAR 2017

Abstract Solving inverse problems in a complex, geologically realistic, and discrete model space and from a sparse set of observations is a very challenging task. Extensive exploration by Markov chain Monte Carlo (MCMC) methods often results in considerable computational efforts. Most optimization methods, on the other hand, are limited to linear (continuous) model spaces and the minimization of an objective function, what often proves to be insufficient. To overcome these problems, we propose a new ensemble-based exploration scheme for geostatistical prior models generated by a multiple-point statistics (MPS) tool. The principle of our method is to expand an existing set of models by using posterior facies information for conditioning new MPS realizations. The algorithm is independent of the physical parametrization. It is tested on a simple synthetic inverse problem. When compared to two existing MCMC methods (iterative spatial resampling (ISR) and Interrupted Markov chain Monte Carlo (IMCMC)), the required number of forward model runs was divided by a factor of 8–12.

1. Introduction

Since the early days of groundwater modeling, inverse methods play a key role in hydrogeology [*de Marsily et al.*, 2000; *Zhou et al.*, 2014]. They allow inferring the spatial distribution of aquifer parameters (e.g., hydraulic conductivities) from indirect measurements (e.g., piezometric records or the concentration of natural tracers in groundwater). Furthermore, they can also be used to constrain recharge rates or boundary conditions. Inverse modeling is therefore a fundamental step in most quantitative studies since the identification of the parameters is a prerequisite for any site-specific model. However, despite its importance and despite more than 50 years of research on this topic, solving the inverse problem still remains one of the hardest challenge. Groundwater flow and transport are often controlled by physical structures that present a high degree of heterogeneity. In particular, the underground may contain discrete structures with sharp contrasts of hydraulic properties, such as channels, faults, karst conduits, or lenses. In this case, it can be essential to identify their location very precisely [*Gómez-Hernández and Wen*, 1998; *Feyen and Caers*, 2006; *Linde et al.*, 2015]. On the other hand, when inverse methods are specifically designed to consider such geologically realistic and highly complex features, their computational effort often becomes extremely demanding. This problem and the inherited limitations are not specific to the field of hydrogeology, but are present in most geophysical applications [*Linde et al.*, 2015].

The aim of this paper is to present a new method named PoPEX to overcome a part of those difficulties. But before entering into the description of this method, let us introduce first the general context. The modeling of any geophysical system often requires a complete mathematical description and full parametrization. Solving those equations is referred to solving the forward problem. The solution exists and is unique if the boundary conditions and initial conditions are known. However, in hydrogeology and geophysics, most often the parameters are only known partially and an exhaustive knowledge of their values is lacking. Inverse problems start from a sparse set of observations of the state variables and aim to find the underlying set of physical parameter values. Neither existence nor uniqueness of a solution is guaranteed and therefore, inverse problems are ill posed. The general theory presented by *Mosegaard and Tarantola* [2002] and *Tarantola* [2005] characterizes the solution of an inverse problem as a conjunction of states of information. More precisely, the solution is defined as a measure function over a given model space. If this posterior measure function describes a probability distribution, their formulation reduces to the commonly used *Bayesian* approach [e.g., *Tarantola*, 2005, section 1.5; *Box and Tiao*, 1973]. In this paper, we only consider problems where both approaches are equivalent. In general, it is very hard or even impossible to find an analytical expression for the solution of an inverse problem.

A possibility for characterizing the posterior probability distribution is to perform an extensive exploration of the model space. One family of pseudorandom exploration schemes is formed by the Markov chain Monte Carlo (MCMC) methods. The mathematical theory for MCMC methods is widely developed and it can be shown that they are asymptotically ergodic [Robert and Casella, 2004; Benaim and Karoui, 2005; Winkler, 2012]. Although they are extensively investigated [Oliver et al., 1997; Fu and Gómez-Hernández, 2008; Hansen et al., 2008; Tonkin and Doherty, 2009; Mariethoz et al., 2010a; Hansen et al., 2012; Valakas and Modis, 2016], it is very challenging to design efficient MCMC schemes. In short, they are general but their applicability is often drastically restricted by the computational costs. Among the alternative families for solving inverse problems, a very prominent one uses gradient-based optimization of an objective function that may be formulated within a Maximum Likelihood (ML) framework. This family of approaches is often used for addressing groundwater [Doherty, 2003; Alcolea et al., 2006; Zhou et al., 2011; Li et al., 2012; Xu et al., 2013] or petroleum engineering problems [Gu and Oliver, 2007; Chen and Oliver, 2013; Melnikova et al., 2015]. These methods are very efficient to generate models that match observed data [Chen and Zhang, 2006; Zhou et al., 2011; Xu et al., 2013]. Unfortunately, they require a linear (continuous) model space. Furthermore, the solution strongly depends on the model parametrization [Mosegaard and Tarantola, 2002; Tarantola, 2005]. This becomes most important whenever a system under study is described by a Jeffrey parametrization. Jeffrey's parameters are strictly positive physical quantities, as, for example, permeability, speed, and frequency. They are equivalent to their inverses, i.e., resistivity, slowness, and period. It is important that the choice of a specific parametrization for a given inverse problem (e.g., permeability or resistivity, speed or slowness, and frequency or period) must not affect the solution. For a detailed discussion of Jeffrey's parameters see Mosegaard and Tarantola [2002].

In this paper, we propose a new ensemble-based method, named posterior population expansion (PoPEX) that explores a geologically realistic discrete model space and accounts for an efficient and accurate solution of inverse problems. The discrete random fields are obtained by a multiple-point statistics (MPS) technique. In general, MPS stands for a pixel-based [Strebelle, 2002; Mariethoz et al., 2010b; Straubhaar et al., 2011] or pattern-based [Zhang et al., 2006; Arpat and Caers, 2007; Honarkhah and Caers, 2010; Hezarkhani and Sahimi, 2012; Mahmud et al., 2014] modeling of complex spatial structures derived from a training image (TI). It allows to generate geological patterns that honor imposed data information. The main idea of PoPEX is to expand iteratively an existing set of geological models by using randomly sampled posterior pattern information. In each iteration, the ensemble of models is used to learn, in a statistical sense, the relation between model parameters and state variables. From this point of view, it is inspired by the ensemble Kalman filter (EnKF) [Burgers et al., 1998; Evensen, 2003, 2006; Chen and Zhang, 2006] but the method neither computes covariances nor any derivatives of some operator. Both computations can be problematic when working with discrete model parameters [Linde et al., 2015]. PoPEX is independent of any parametrization and applicable with any conditional geostatistical simulation tool. It is tested in this paper on a synthetic groundwater flow problem that allows the comparison with a proper reference solution. Comparing the performance to the one of the MCMC schemes presented in Mariethoz et al. [2010a], we show that our algorithm provides a slightly better representation of the posterior information while reducing the number of forward model runs by a factor of 8–12. As a counterpart, the property of ergodicity is lost, which means that some region of the model space may not be sampled. Additional tests show that this becomes most important whenever the real spatial structures are poorly captured by the TI.

The paper is organized as follows. Section 2 recalls the formulation of an inverse problem and presents the methodology of our algorithm. An illustrative example is presented in section 3. It aims to highlight the workflow and to show the evolution of the posterior ensemble for the PoPEX algorithm. Then, we empirically analyze the impact of the input parameters and compare the performance of the method with two existing MCMC schemes. Section 4 finally discusses the advantages and limitations of the methodology and provides some conclusions.

2. Methodology

In this section, we present the new ensemble-based method, that explores a complex geological model space and accounts for an efficient and accurate characterization of a given posterior density function. Let

us start with some definitions of the terminologies used in this work (section 2.1), before we explain the general concepts (section 2.2) and the details of the new algorithm (section 2.3).

2.1. Inverse Problem Formulation

Solving an inverse problem usually aims to infer information from a given set of observations $\mathbf{d}=\{d_1, \dots, d_m\}$ called **data**. Usually, these data represent measurements of state variables such as hydraulic heads, production data, contaminant concentration, and may include some measurement errors. *Mosegaard and Tarantola* [2002] and *Tarantola* [2005] formulate the inverse problem as the characterization of the posterior probability distribution

$$\sigma_M(\mathbf{m})=c \rho_M(\mathbf{m})L(\mathbf{m}), \quad (1)$$

where

c is a normalization constant;

$\rho_M(\cdot)$ denotes the prior probability distribution;

$L(\cdot)$ is the likelihood function.

In this context, the model $\mathbf{m}=\{m_1, \dots, m_n\}$ is a finite set of parameters that fully describes the physical system under study. Usually the choice of a finite parametrization requires a “simplification of reality.” Such parameters can cover boundary conditions, hydraulic conductivity (or resistivity) fields, specific storage, recharge time series, etc. Each model \mathbf{m} is a point in a measurable model space \mathcal{M} . The conceptual choice of the parameters m_i corresponds to the definition of a parametrization of \mathcal{M} . It is clear that this parametrization (i.e., the coordinate system) is not necessarily unique. By definition, the prior probability distribution ρ_M in equation (1) describes any available information on the model parameters, that is independent of the observations \mathbf{d} . The likelihood function, on the other hand, describes the correlations between model parameters and data. It is understood as an indicator of how good a model explains the data and usually involves physical theories that allow to predict the outcome of physical experiments. We assume that the observable set of data corresponding to a model \mathbf{m} can be predicted through the so called forward operator $\mathbf{d}=\mathbf{g}(\mathbf{m})=\{g_1(\mathbf{m}), \dots, g_m(\mathbf{m})\}$. It is possible that the data set $\mathbf{d}=\{d_1, \dots, d_m\}$ includes direct measurements of some model parameters in $\mathbf{m}=\{m_1, \dots, m_n\}$. Although, the proposed method in this paper does not include this kind of data, it is straightforward to extend it to cases where such observations are available. The remaining components can be predicted by solving a set of partial differential equations (describing for example groundwater flow) that is fully defined through the model parameters in \mathbf{m} . Therefore, the components g_i usually include numerical schemes for the solution of differential problems. These numerical approximations together with the finite parametrization of the system can be a critical source of error. Moreover, due to imperfect measuring devices, the data set itself suffers from uncertainties. It is important that the likelihood function L in equation (1) encloses both modeling uncertainties and observational uncertainties. Since the PoPEX algorithm is presented for the first time, we consider a case where the modeling uncertainties are negligible and assume the space of observable data to be linear such that the likelihood function becomes [*Tarantola, 2005*]:

$$L(\mathbf{m})=\rho_D(\mathbf{g}(\mathbf{m})). \quad (2)$$

The probability distribution ρ_D describes any uncertainties and error sources resulting from the act of observing $\mathbf{d}=\{d_1, \dots, d_m\}$.

2.2. General Concepts

This section provides an overview of the general concepts and assumptions used for defining our algorithm. We assume in this paper that the model \mathbf{m} describes spatial petrophysical properties and can be modeled by a pixel-based MPS algorithm. However, the proposed algorithm is not restricted to MPS and can be applied with many other types of geostatistical models. Pixel-based algorithms require a spatial division of the computational domain into a finite number of $n \in \mathbb{N}$ homogeneous grid elements (pixels) within which the petrophysical properties are constant. Each pixel $j \in \{1, \dots, n\}$ will be referred to by its center position \mathbf{x}_j . A model $\mathbf{m}=\{m_1, \dots, m_n\}$ is a set of n parameters where m_j denotes a constant petrophysical property associated to the element \mathbf{x}_j . The set of all pixels is called the simulation grid. The MPS algorithm allows to generate realizations of a random variable $Z=Z(\mathbf{x}_j)$ by reproducing spatial patterns contained in a training

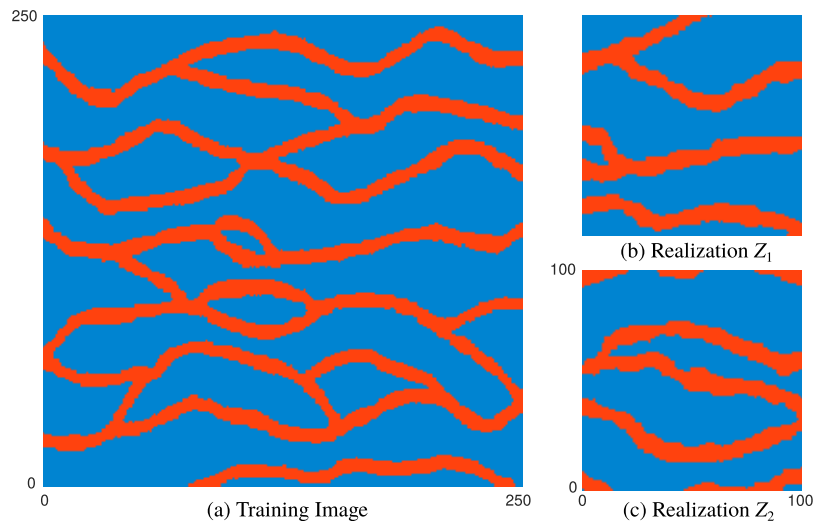


Figure 1. Training image for the MPS simulations together with two different realizations.

image. It is possible to condition MPS realizations at a given set of positions $\{\mathbf{x}_{i_1}, \dots, \mathbf{x}_{i_N}\}$ to a set of values $\{z_1, \dots, z_N\}$ such that $Z(\mathbf{x}_{i_j}) = z_j$ for all $j = 1, \dots, N$. In the literature, the collection $HD = \{(\mathbf{x}_{i_1}, z_1), \dots, (\mathbf{x}_{i_N}, z_N)\}$ is commonly called hard conditioning data.

In this work, we assume that the random variable Z is discrete, i.e., the set of possible values for $Z(\mathbf{x}_j)$ is contained in a finite subset of real values $\mathcal{F} = \{f_1, \dots, f_s\}$. The values f_k for $k = 1, \dots, s$ are called facies values or simply facies. Realizations of the random variable Z are linked to the model parameters such that there is a bijection between the model space \mathcal{M} and the set of all possible MPS realizations. For $j = 1, \dots, n$, the model parameter m_j denotes then the petrophysical property that corresponds to the facies value of Z at \mathbf{x}_j . Figure 1 shows the training image of *Strebelle* [2002] defined on a grid of 250×250 pixels and two possible MPS realizations for a grid of 100×100 pixels. The facies values are represented by two different colors (blue for f_1 and red for f_2) and can be associated to two different values of some petrophysical properties (e.g., permeability, specific storage, and porosity). If, for example, we want to use this two-facies setup for modeling spatial groundwater permeability maps, we choose a set of two different permeability values $\{K_1, K_2\}$ and define the one-to-one correspondence

$$K_i \leftrightarrow f_i, \quad i = 1, 2.$$

Thanks to this bijection between model parameters and facies values, the petrophysical model \mathbf{m} is uniquely defined by the facies map of an MPS realization and vice versa. It is for this reason that in the following, we will interchangeably use the terminologies “realization” and “model” by referring to their spatial map defined in the simulation grid. The concept of a pixel-based indicator function for each facies value will be important. Thus, for any model \mathbf{m} , we define the characteristic indicator function $\mathbf{1}_{f_i}$ at each pixel \mathbf{x}_j such that

$$\mathbf{1}_{f_i}(\mathbf{m}; \mathbf{x}_j) = \begin{cases} 1 & \text{if } m_j \leftrightarrow f_i \\ 0 & \text{otherwise.} \end{cases} \quad (3)$$

Henceforth, the explicit notation of the pixel position \mathbf{x}_j will be omitted. Therefore, the indicator functions in equation (3) and any inherited quantity can be interpreted as maps that are defined on the simulation grid and are constant within each pixel.

The main idea of the posterior population expansion (PoPEX) algorithm is to expand an existing set of models $\mathcal{M}^k = \{\mathbf{m}_1, \dots, \mathbf{m}_k\}$ by using facies information that is weighted by the posterior measure function in equation (1). For each model \mathbf{m}_j in \mathcal{M}^k , we compute the corresponding posterior information $\sigma_M(\mathbf{m}_j)$ and form the set $\tilde{\Sigma}^k = \{\tilde{\sigma}_M(\mathbf{m}_1), \dots, \tilde{\sigma}_M(\mathbf{m}_k)\}$ where

$$\tilde{\sigma}_M(\mathbf{m}_j) = \frac{\sigma_M(\mathbf{m}_j)}{\sum_{r=1}^k \sigma_M(\mathbf{m}_r)}, \quad j=1, \dots, k$$

are the normalized values of the posterior information. For a facies value f_i , we define its posterior probability map p_i^k by

$$p_i^k = \sum_{j=1}^k \mathbf{1}_{f_i}(\mathbf{m}_j) \tilde{\sigma}_M(\mathbf{m}_j). \quad (4)$$

Similarly, for each facies type f_i , we suppose to know prior probability maps q_i . Usually it is possible to approximate the prior probability maps from a sufficiently large number of unconditioned (i.e., without any hard-conditioning data) and independent MPS realizations. The key is then to compare the two probability distributions $P^k = \{p_1^k, \dots, p_s^k\}$ and $Q = \{q_1, \dots, q_s\}$ by means of the Kullback-Leibler divergence (KLD) [Kullback and Leibler, 1951], denoted by $D(P^k||Q)$ and reading

$$D(P^k||Q) = \sum_{i=1}^s p_i^k \log \left(\frac{p_i^k}{q_i} \right). \quad (5)$$

Remember that p_i^k , q_i , and therefore $D(P^k||Q)$ are maps defined on each pixel in the simulation grid. Roughly speaking, the Kullback-Leibler divergence of P^k from Q provides a measure of how different or “surprising” the posterior facies probabilities in P^k are with respect to the prior probabilities in Q . The idea is then to deduce a set of N_C hard conditioning data from which one new MPS realization will be generated. First, the conditioning locations \mathbf{x}_i are sampled from a probability density function that is proportional to the KLD map $D(P^k||Q)$. Then, for each location, we sample a conditioning value z_j from the restricted posterior probabilities $p_i^k(\mathbf{x}_i)$. After the generation of a new realization conditioned to the collection $HD = \{(\mathbf{x}_i, z_1), \dots, (\mathbf{x}_i, z_N)\}$, it is added to the existing set of models \mathcal{M}^k and the posterior measure σ_M is computed. Then, the entire procedure is restarted. An illustrative example of the workflow is presented in section 3.4 in Figure 3.

2.3. Posterior Population Expansion (PoPEX)

The approach described above assumes to know an existing set of models $\{\mathbf{m}_1, \dots, \mathbf{m}_k\}$. Therefore, at the very beginning, we have to generate at least one initial realization. But it is clear that it can be advantageous to start from a larger number of $N_I > 1$ unconditioned and independent initial models. We will see in section 3 that not only N_I but also the number of conditioning data N_C play an important role. Both parameters are predefined by the user and stay unchanged during the whole procedure.

Let us now define the PoPEX algorithm:

- 1: **Input:** $N_I \in \mathbb{N} \setminus \{0\}$ and $N_C \in \mathbb{N}$
- 2: Initialization: Generate N_I unconditioned models
- 3: Set: $k = N_I$ and $\mathcal{M}^k = \{\mathbf{m}_1, \dots, \mathbf{m}_k\}$
- 4: Compute: $\tilde{\Sigma}^k$, P^k and $D(P^k||Q)$
- 5: **while** stopping condition == false **do**
- 6: Choose N_C conditioning data pairs from P^k and $D(P^k||Q)$
- 7: Generate one conditioned realization \mathbf{m}_{k+1}
- 8: Set $\mathcal{M}^{k+1} = \mathcal{M}^k \cup \{\mathbf{m}_{k+1}\}$
- 9: Compute $\tilde{\Sigma}^{k+1}$, P^{k+1} and $D(P^{k+1}||Q)$
- 10: Update stopping condition
- 11: $k = k + 1$
- 12: **end while**

Note that $\tilde{\Sigma}^k$ is the normalized posterior information in \mathcal{M}^k and therefore, this algorithm is independent of the normalization constant c in equation (1). For this reason, the posterior information $\sigma_M(\mathbf{m})$ can be computed by simply setting $c = 1$. Furthermore, the Kullback-Leibler divergence in equation (5) is well defined for $q_i > 0$ for all $i = 1, \dots, s$. If there is $i \in \{1, \dots, s\}$ and a pixel \mathbf{x}_j such that $q_i(\mathbf{x}_j) = 0$, then the prior measure of the set $\{\mathbf{m} : Z(\mathbf{m}; \mathbf{x}_j) = f_i\}$ is equal to zero and therefore $p_i^k(\mathbf{x}_j)$ must vanish as well. In this case, the

corresponding terms in equation (5) are put to zero. For an illustration of the workflow applied to the synthetic problem introduced in the section 3, consult Figure 3.

Let us look in more detail at the most important steps. The two main inputs of this algorithm are the number of unconditioned initial models N_i and the number of conditioning data N_c . [2] Initially, N_i unconditioned and independent models are generated. Note that at this point we suppose to know the prior facies probability maps in $Q = \{q_1, \dots, q_s\}$. If such maps are unavailable and N_i is large enough, they may be approximated from the initial set of unconditioned realizations. Then, with the posterior information of each model, we compute the probability map P^k and update the corresponding Kullback-Leibler divergence $D(P^k||Q)$ (cf. equations (4) and (5)). [6] The central point of the PoPEX algorithm is the way of fixing a hard-conditioning data set $HD = \{(\mathbf{x}_{i_1}, z_1), \dots, (\mathbf{x}_{i_{N_c}}, z_{N_c})\}$ that guides the generation of a new model. For this purpose, we choose the locations \mathbf{x}_{i_j} randomly from a probability distribution proportional to $D(P^k||Q)$. This preferentially selects conditioning locations where the posterior probability P^k has a high information content with respect to the prior probability Q . The values z_j that are imposed at \mathbf{x}_{i_j} are then picked according to the probability values of P^k at \mathbf{x}_{i_j} . Large values of the KLD map $D(P^k||Q)$ show locations where the approximated posterior facies distribution diverges a lot from its prior counterpart. By imposing facies values within such pixels, we expect to increase the probability of generating models with high posterior measure. In steps [8] and [9], the model space \mathcal{M}^k is expanded to \mathcal{M}^{k+1} before the posterior information set $\tilde{\Sigma}^{k+1}$, the facies probability map P^{k+1} and the Kullback-Leibler divergence $D(P^{k+1}||Q)$ are computed. [10] There are different possible stopping criteria, each of which has its justifications and can be chosen according to the needs. As the forward operator, and therefore the computation of the posterior information, can be very expensive in terms of computational cost, we may want to restrict the runtime of the algorithm. Thus, an obvious stopping condition is to set a maximum size of the final population. Sometimes, one may want to use an acceptance/rejection criterion based on the value of the likelihood function $L(\mathbf{m})$ to generate a fixed number of accepted models. A third criterion is the convergence of the posterior facies probability distribution map P^k . In this case, at every step $k > N_i$, the distribution P^k is compared to P^{k-j} , for a $j \geq 1$, and the algorithm is stopped as soon as the difference is small enough.

A very important feature of this algorithm is its independence of any physical parametrization. The only random variables involved are characteristic indicator functions, and therefore, the algorithm is independent of the facies values and all the physical parameters they are associated with. As every new model is depending on all the previous ones, however, there is a risk of exploring only a restricted subregion of the model space. But, we can increase the research area in the model space by increasing the number of unconditioned initial realizations and/or lower the number of conditioning data. An empirical analysis of the choice of N_i and N_c is provided in the section 3.4.

3. Synthetic Case Study

As this paper introduces the PoPEX algorithm for the first time, it is a prerequisite to test it under simple and well-defined conditions where a reference solutions can be computed. This is why we borrowed the two-dimensional groundwater flow problem from *Mariethoz et al.* [2010a]. This small problem is briefly explained in the following section.

3.1. Problem Setting

The mathematical model of a two-dimensional (stationary) groundwater flow problem is described by the Poisson equation:

$$-\text{div}(k\nabla h) = f. \tag{6}$$

The solution $h : D \rightarrow \mathbb{R}$ is usually defined in a bounded, open, and Lipschitz domain $D \subset \mathbb{R}^2$, and describes the hydraulic head level of the groundwater. Together with reasonable boundary conditions, the problem (6) is well posed. As in *Mariethoz et al.* [2010a], the spatial models were defined by channelized structures simulated from the training image in Figure 1a. The two facies types represent uniform transmissivity (k) values of 10^{-2} (m²/s) (channel) and 10^{-4} (m²/s) (matrix), respectively. For modeling the spatial structures, we used the DeeSse implementation [Straubhaar, 2011] of the MPS direct sampling (DS) method [Mariethoz et al., 2010b]. The realizations were generated on a two-dimensional simulation grid

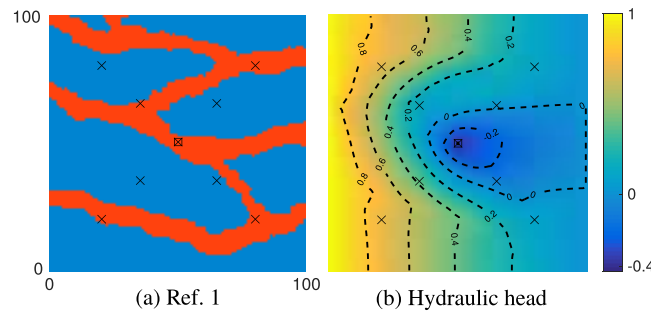


Figure 2. Reference domain Ref. 1 and the hydraulic head values.

containing 100 by 100 pixels and representing a 100 m by 100 m computational domain. The model space was set to be the space of all possible models generated by the DS method. On the upper and lower boundaries, no-flow boundary conditions applied, while fixed head values of 1 m (left) and 0 m (right) were imposed on the lateral boundary parts. One realization with an arbitrary seed has been generated and considered to be the reference domain (cf. Figure 2a). A pumping

well extracting 3 L/s was placed in the center of the domain (square), while at nine locations (crosses), we extracted the hydraulic head values of the numerical reference solution (cf. Figure 2b); these measurements of the groundwater level were the only data constraints used for conditioning the inverse problem. We set the prior distribution ρ_M in equation (1) to be uniform. As in this case, the prior information is constant for any model \mathbf{m} , the PoPEX algorithm only depends on the value of the likelihood function L . Using again the fact that the posterior information in equation (1) can be multiplied by any positive constant without changing the behavior of the algorithm, the likelihood function can be rewritten such that

$$L(\mathbf{m}) = \exp\left(-\frac{\text{RMSE}(\mathbf{m})^2}{2\sigma^2}\right), \quad (7)$$

where $\text{RMSE}(\mathbf{m})$ denotes the root-mean-square error between the predictions and the reference values. The standard deviation is set to $\sigma=0.05$ m, what reasonably matches measurement errors met in practice.

3.2. Illustration of the PoPEX Algorithm

Before starting the analysis of the algorithm let us use the previously defined problem for illustrating the key steps of our algorithm. We fix the input parameters to $N_I = 200$ and $N_C = 15$. Figure 3 shows the evolution of the different maps. It is separated into multiple parts. The two figures in the top row are the fixed prior probabilities for each facies type. For this synthetic example, the maps q_1 and q_2 take constant values of 0.72 and 0.28, respectively. Then, the first two columns of the matrix on the bottom illustrate the posterior probability maps p_1 and p_2 at the iterations $k = 200, 500, \text{ and } 2000$. The third column is the normalized Kullback-Leibler divergence $\tilde{D}(P^k||Q)$. During each iteration, we use the probability density $\tilde{D}(P^k||Q)$ for sampling N_C hard conditioning locations. Red dots are used to indicate the locations that have been picked at iteration $k = 200, 500, \text{ and } 2000$, respectively. After having fixed the conditioning locations $\{\mathbf{x}_{i_1}, \dots, \mathbf{x}_{i_{N_C}}\}$, conditioning facies values z_j are sampled from the localized facies probability maps $P^k(\mathbf{x}_j) = \{p_1^k(\mathbf{x}_j), p_2^k(\mathbf{x}_j)\}$, for $j=1, \dots, N_C$. The last column shows the new model \mathbf{m}_{k+1} that was generated from the hard-conditioning data set $\{(\mathbf{x}_{i_1}, z_1), \dots, (\mathbf{x}_{i_{N_C}}, z_{N_C})\}$ (indicated by the black dots). Note that, due to the definition of the prior probability maps, high probability values in the map p_2 contain more information in the sense that they are more surprising with respect to the prior probability distribution than high probability values in p_1 . As mentioned earlier, $\tilde{D}(P^k||Q)$ can be interpreted as a measure of information contained in P^k with respect to Q .

3.3. Description of the Test Procedures

The synthetic test problem described above has been chosen because it allows to compute an empirical reference set of 300,000 models that represents a good approximation of the entire model space. From this large set of models, any quantity of interest can be computed and will be considered as the exact solution. If, for instance, we are interested in the true posterior expectation of a quantity represented by a function $f(\mathbf{m})$, we use this set of models and compute the reference solution such that

$$\sum_{i=1}^{300,000} f(\mathbf{m}_i) \tilde{\sigma}_M(\mathbf{m}_i). \quad (8)$$

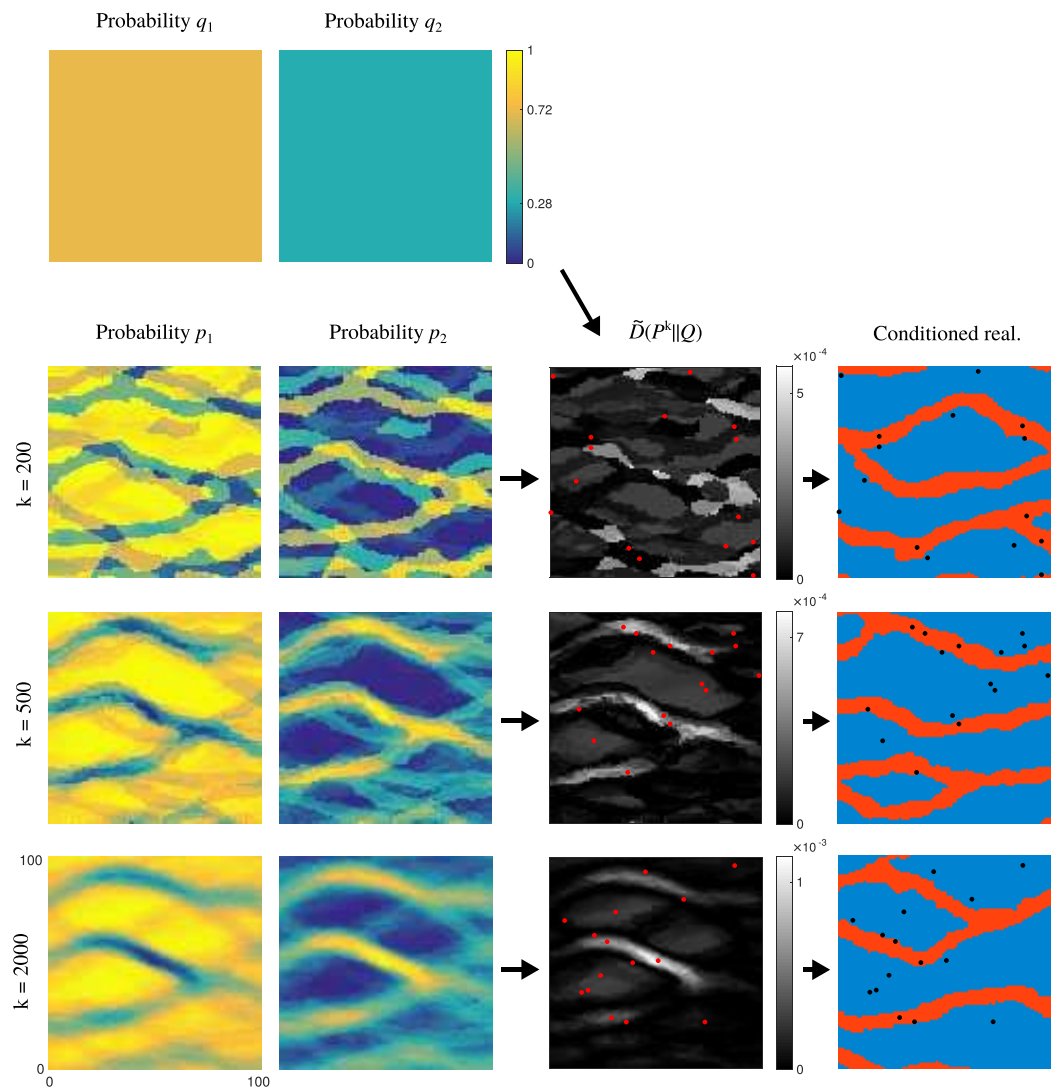


Figure 3. Workflow of the PoPEX algorithm applied to a synthetic two-facies problem. The prior and posterior facies probability maps together with the resulting Kullback-Leibler divergence map $\tilde{D}(P^k||Q)$ are shown for the iterations $k = 200, 500,$ and 2000 . The last column to the right shows the new realization that has been conditioned at the locations indicated by dots.

Again, $\tilde{\sigma}_M$ denotes the normalized posterior information. For an evaluation of the PoPEX algorithm, we formulated four different test procedures. Before presenting some results let us explain each experiment in detail.

3.3.1. Test I: Influence of the Input Parameters N_I and N_C

The goal of this first test is to empirically analyze the influence of the number of unconstrained initial models N_I and the number of conditioning data N_C . We were interested in the diversity of the generated models and therefore on how well the algorithm is able to explore the model space. Equation (8) together with equation (3) are used for computing the reference posterior probability maps $P^{ref} = \{p_1^{ref}, p_2^{ref}\}$. Then, for different numbers N_I and N_C , we run the PoPEX algorithm until 4000 conditioned realizations have been generated. As a measure of the exploration capability, we computed the mean value of the KLD map $D(P^k||P^{ref})$. In other words, if this mean value is low, the posterior facies probabilities in P^k are close to the reference ones and therefore, the algorithm reasonably sampled the most “important subregions” of the model space. In this context, “important” stands for areas where the posterior measure σ_M is sufficiently large. We were mostly interested in the regions explored by the conditioned realizations (i.e., for $k > N_I$), and therefore, P^k was computed without the N_I initial models.

The next two tests are dedicated to compare the PoPEX algorithm with two existing Markov Chain Monte Carlo (MCMC) schemes.

3.3.2. Test II: Comparing the Exploration Capabilities

There are different MCMC techniques available for solving inverse problems in a geostatistical prior model space. The ones presented in *Mariethoz et al. [2010a]* were entitled iterative spatial resampling (ISR) and interrupted Markov chain Monte Carlo (IMcMC). Central for both algorithms is the definition of a likelihood function L as in equation (7). The ISR method uses an MPS technique for the generation of a chain of models $(\mathbf{m}_1, \dots, \mathbf{m}_n, \dots)$. At every instance $n > 0$, it extracts facies values from \mathbf{m}_n and uses them as hard conditioning data for the generation of a candidate model \mathbf{m}^* . This model is then accepted with a probability of $\min\{1, L(\mathbf{m}^*)/L(\mathbf{m}_n)\}$. Conversely, the IMcMC method accepts a new model whenever $L(\mathbf{m}^*) \geq L(\mathbf{m}_n)$ and interrupts and restarts the chain according to a suitable stopping condition. For both MCMC methods, *Mariethoz et al. [2010a]* fixed a number of 100 conditioning points. As suggested, the burn in period in the ISR method was set to be the first 200 accepted realizations, while the IMcMC chain was interrupted whenever

$$RMSE(\mathbf{m}_i) \leq 0.07 \text{ m.} \quad (9)$$

This corresponds to the 95% confidence interval of the data distribution defined by nine independent observations with Gaussian errors.

For comparing the exploring skills, we considered the first 4000 realizations generated by ISR after the burn in time. There is no particular initial stage in the IMcMC method, so we took all the realizations into account. As in the first test, for $k=1, \dots, 4000$ and for each algorithm, we form the weighted facies probability map P^k and compare it to P^{ref} by the KLD map $D(P^k||P^{ref})$. Again, a low mean value of the latter is interpreted as a good exploration of the important regions in the model space.

3.3.3. Test III: Comparing the Efficiency and Data Predictions

Depending on the computational cost of a prediction, it can be very expensive to compute the corresponding random variable for a large number of models. Therefore, we often evaluate it only on a representative subset of models. Using Markov chain Monte Carlo methods, one usually fixes the size of a characteristic (representative) set and stops the algorithm as soon as enough models have been accepted. For analyzing the efficiencies of the methods, we generated a representative set of 200 models satisfying the condition in equation (9) and compared the total numbers of forward simulations needed.

Groundwater production problems often involve the prediction of the capture zone within a given time $T > 0$. Therefore, we defined the random variable $Z_T = Z_T(\mathbf{m}; \mathbf{x}_j)$ to be a characteristic indicator function such that $Z_T(\mathbf{m}; \mathbf{x}_j) = 1$, if a water particle starting at \mathbf{x}_j reached the pumping well in a time no longer than T , and $Z_T(\mathbf{m}; \mathbf{x}_j) = 0$ otherwise. The posterior pumping area was defined as

$$A_T = \sum_{\mathbf{m}} Z_T(\mathbf{m}) \tilde{\sigma}_M(\mathbf{m}).$$

For $T = 20$ h and based on 300,000 unconditioned realizations, we computed A_T^{ref} and compared it to the posterior pumping areas computed for the representative sets of 200 models satisfying equation (9).

The last test aims to discover the applicability and some limitations of the method.

3.3.4. Test IV: PoPEX Solutions for Different Reference Domains

The performance of an inverse method can depend very much on the unknown geology. Therefore, it is important to run the algorithm with data sets (observations) coming from different reference domains. To this end, we generated four additional reference maps and kept the differential problem and the observation locations unchanged. The performances are mainly compared by the number of forward simulations needed in order to generate a representative set of 200 models satisfying equation (9).

3.4. Results

This section presents the results obtained from the four tests described above. Note that the results have been obtained by running each experiment 5 times, starting from five different initial sets. We then show their average performances.

3.4.1. Test I

When we fix the number of conditioning data N_C and vary the number of unconstrained initial models $N_I \in \{100, 200, 500, 1000\}$, we clearly observe a better examination of the model space for higher values of N_I (cf. Figures 4a and 4b). Comparing the two figures we conclude also that in general we had better performance for the weaker conditioning (i.e., for $N_C = 30$). This becomes even clearer when considering Figures

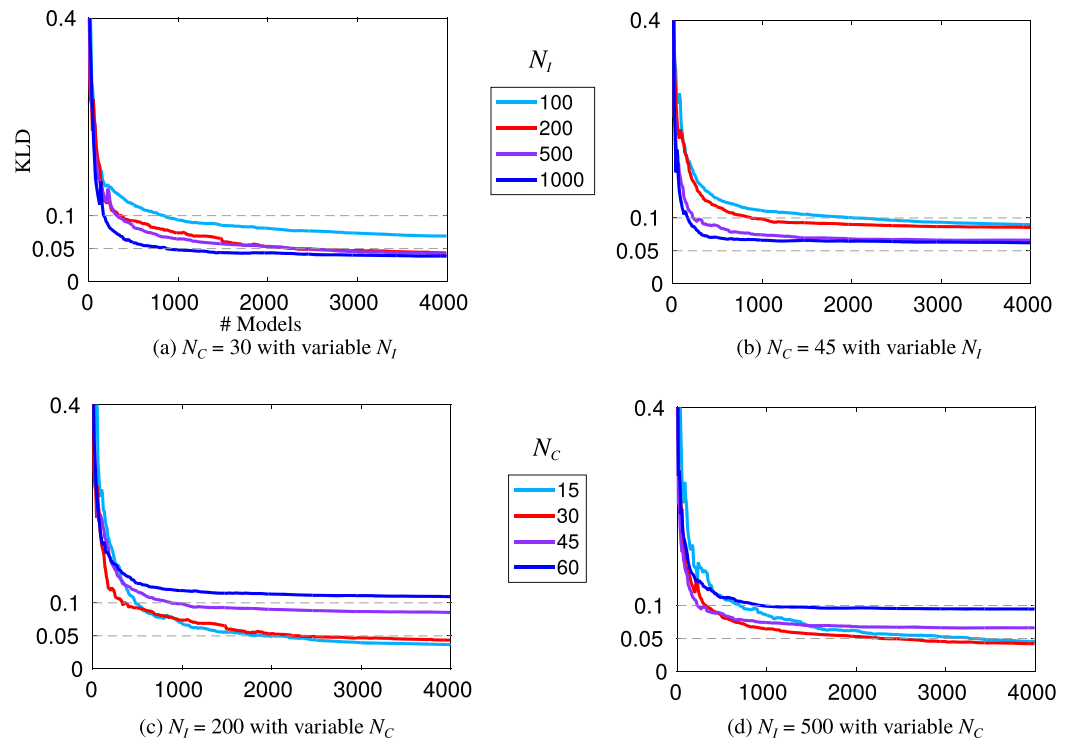


Figure 4. Approximation of the posterior facies probability map for (top) variable N_C and fixed N_I , resp. and (bottom) fixed N_I and variable N_C .

4c and 4d, where the number of unconditioned initial models N_I was fixed and we changed the number of conditioning data $N_C \in \{15, 30, 45, 60\}$. However, a higher number of conditioning points resulted in a faster convergence in the beginning and the posterior probability maps became stationary after a smaller number of iterations. We finally suggest that for a fast convergence we should not choose less than 30 conditioning points, but in order to reasonably examine the model space, we should start with at least 200 unconditioned initial realizations.

3.4.2. Test II

According to the previous test, a reasonable choice for the PoPEX algorithm was $N_C = 30$ and $N_I \in \{200, 500\}$. The PoPEX and the ISR methods showed very similar behavior in approximating P^{ref} , while the IMcMC took slightly more time to converge to a stationary level (Figure 5). Although all the interrupted chains in the IMcMC method are independent of each other, this method was not able to reach the approximation level of the PoPEX algorithm. When we computed the reference posterior probability of the channel facies (p_2^{ref}) and compared it to the maps p_2^k obtained after 4000 simulations, we observed significant differences (Figure 6). The sharp contrasts of the reference map (Figure 6a) were almost entirely missing in the

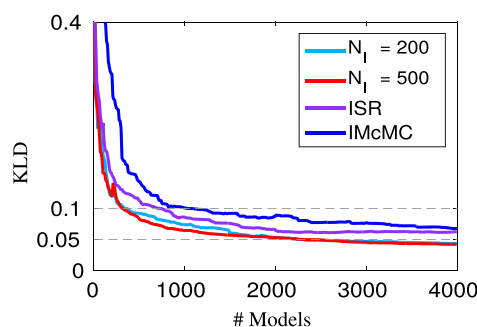


Figure 5. KLD convergence during 4000 realizations for two different settings of the PoPEX algorithm compared to ISR and IMcMC.

IMcMC map (Figure 6d). The ISR picture (Figure 6c) mainly shows three parallel downward structures. The lesser contrasted small bifurcations in the right part of the figure could only be discovered by the PoPEX algorithm ($N_I = 500$, cf. Figure 6b). Therefore, although the differences in Figure 5 seemed to be small, it was easy to see that the PoPEX algorithm clearly generated the best approximation of the reference facies probability map.

3.4.3. Test III

Setting again $N_C = 30$, we observe that in average the two PoPEX algorithms only needed 1705 ($N_I = 500$) resp. 1935 ($N_I = 200$) simulations, while the MCMC methods required 15,698 (ISR) and 21,052 (IMcMC) forward

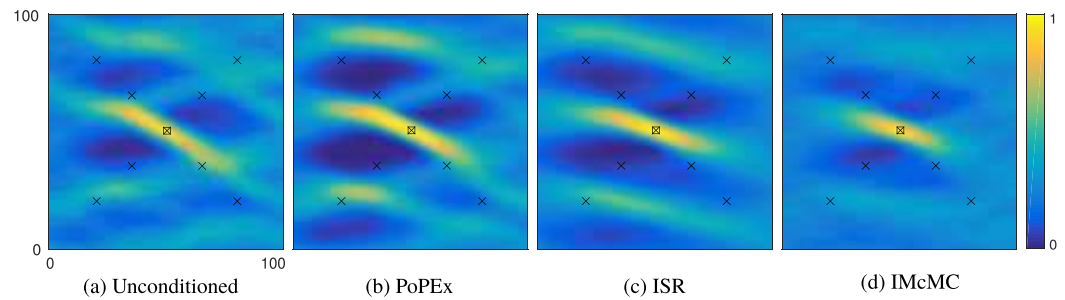


Figure 6. Posterior probability maps p_2^k obtained after 4000 realizations.

simulations, respectively (cf. Figure 7). The generation of unconditioned realizations can be interpreted as a simple rejection sampler and required 42,136 simulations. As suggested by *Mariethoz et al.* [2010a] in the Markov chains, we only considered realizations that are at a distance of at least 12 accepted models. The results in this section showed that for generating a slightly better approximation of the posterior facies probabilities (cf. Figures 5 and 6), the PoPEX algorithms were roughly 8–9 (resp. 11–12) times more efficient than ISR (resp. IMcMC) and more than 20 times faster than rejection sampling (cf. Figure 7). The overall acceptance rates of the PoPEX algorithms were 1 : 8.5 ($N_I = 500$) resp. 1 : 9.7 ($N_I = 200$), while they reached 1 : 6.1 and 1 : 8.7, when considering only the conditioned realizations.

As all of the three algorithms (PoPEX, ISR, and IMcMC) generated characteristic sets with sufficient variability of the models, they all produced accurate predictions of the reference regions and the true capture zone (cf. Figure 8). Nevertheless, we still observe some differences. The predictions of the PoPEX and the ISR algorithm most differ in the 5% region but both were sufficiently close to the reference map. The 5% and 25% regions of the IMcMC method were slightly too broad. Recalling the results obtained in the previous test, this was not surprising, as IMcMC showed the worst approximation of the posterior facies probabilities.

3.4.4. Test IV

The structures in the first two additional domains (Ref. 2 and Ref. 3 in Figures 9a and 9b) correspond well to the ones in the training image (cf. Figure 1a). The third (Ref. 4 in Figure 9c) shows two interrupted channels near the pumping well. As the training image does not contain any disconnected channels, it was very unlikely to generate such models by an MPS method. In the fourth domain (Ref. 5 in Figure 9d), no channel pass through the pumping location. From a physical point of view, this means that 3 L of water are extracted every second from a low-permeable material, which would be absurd. As before we use the hydraulic head values extracted from the reference solution as data constraints for solving the inverse problems. According to the previous analysis, we generated $N_I = 500$ unconditioned initial models and used $N_C = 30$ conditioning points, until 200 models satisfied (9). The structures in the reference domains 1 and 2 (Figures 2a and 9a) show comparable geological patterns. Both are dominated by three interconnected and bifurcated main channels, linking the left to the right boundary part. For solving the inverse problems, comparable numbers of forward simulations (1705, resp. 2087) were needed (cf. Table 1). It turned out that the problem corresponding to the third reference domain (Ref. 3

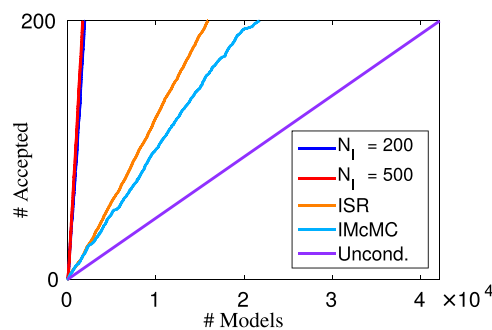


Figure 7. Comparison of the efficiencies for generating a set of 200 accepted models.

in Figure 9b) was relatively easy to solve. The separated and mostly parallel channels match the structures of the training image quite well. It follows that, after only 1206 models, the algorithm was able to find 200 satisfying models. Also, the minimum and the median RMSE values are considerably low (cf. Table 1). Both of the posterior channel probability maps p_2^k (Figures 9e and 9f) describe fairly well the main structures of the corresponding reference domains (Ref. 2 and Ref. 3) but still show sufficient variability in other regions of the computational domain (where the posterior probabilities are close to the prior probabilities).

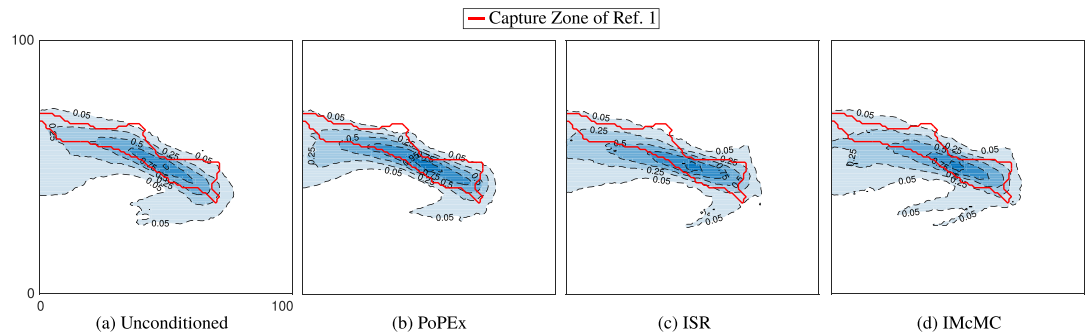


Figure 8. Posterior predictions of the capture zone after 20 h of pumping. The contours are understood as the percentage coverage of a certain region by the 200 representative models.

For revealing some limits of the PoPEX algorithm, we chose the uncommon reference domains Ref. 4 and Ref. 5. The large number of simulations (Table 1) needed for solving the inverse problem resulting from Ref. 4 (Figure 9c) was directly related to its interrupted channel structures. As there are no such patterns contained in the training image, it is very unlikely to generate good candidate models. Although the method was able to detect this unusual structure (Figure 9g), the number of total simulations and the acceptance rate were unacceptable (Table 1). This highlighted the importance of a reliable training image that represents well the geological features. On the other hand, extracting 3 L of groundwater per second from a low-permeable region (Figure 9d) is physically not very plausible. The hydraulic head of the reference solution at the pumping well is -19.1 m, from what follows that the range of the head values is significantly larger. Working with the same (absolute) acceptance tolerance (equation (9)) leads to accept only small relative errors and therefore explains the slower acceptance rate in Table 1 (Ref. 5) and the smaller variability of the posterior models (Figure 9h). The high values of the corresponding minimum and median RMSE also indicate the difficulties to reach the same (absolute) approximation level for a larger range of head values. A stopping criterion based on a minimum number of accepted realizations can require a large number of forward simulations and therefore, significantly grows the computational costs for solving an inverse problem. We conclude that the PoPEX algorithm was very efficient and accurate in solving inverse problems with facies-type prior models. However, unreasonable stopping conditions and/or a nonrepresentative training image result in unacceptable high computational costs.

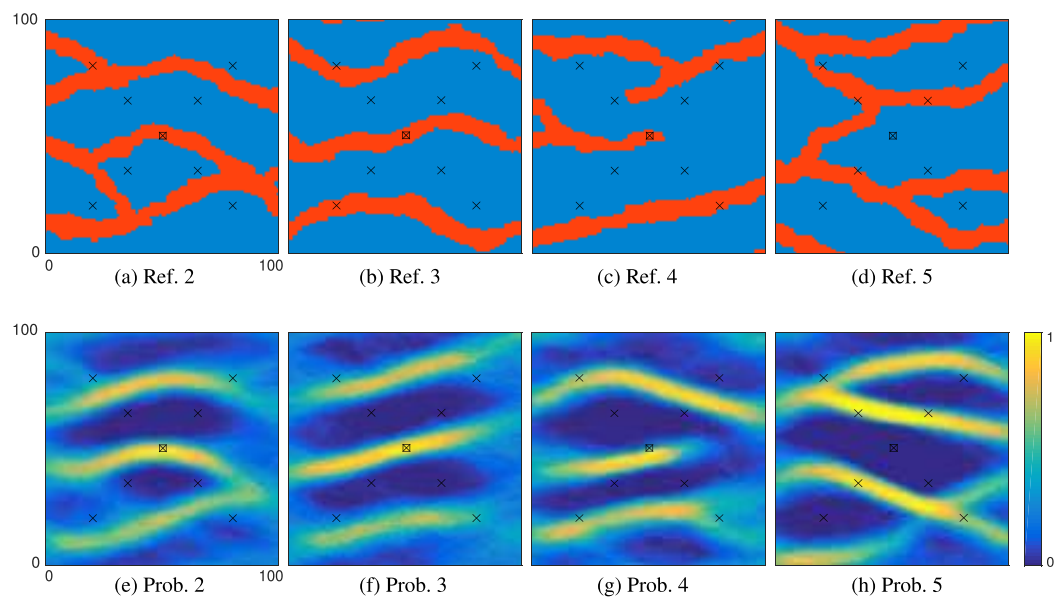


Figure 9. Reference domains 2–5 and their corresponding posterior channel probability maps of 200 accepted models (using PoPEX with $N_f = 500$ and $N_c = 30$).

Table 1. Performances of the PoPEX Algorithm With $N_i = 500$ and $N_c = 30$ for Different Reference Domains

Ref.	Min RMSE	Median RMSE	Max RMSE	Acc. Rate (After N_i)	Simulations
1	0.0316	0.0580	0.0699	1 : 6.1	1,705
2	0.0328	0.0604	0.0700	1 : 8.1	2,087
3	0.0215	0.0560	0.0699	1 : 3.7	1,206
4	0.0318	0.0595	0.0697	1 : 150.4	30,182
5	0.0482	0.0623	0.0697	1 : 55.3	11,560

4. Discussion and Conclusions

In this paper, a new ensemble-based method, entitled posterior population expansion (PoPEX), is proposed. We show on a simple and synthetic example that it efficiently sampled the most important regions (with respect to the posterior information) of a complex and discrete model space. Comparing our method to two existing MCMC schemes, we showed that PoPEX explored the posterior probability distribution more accurately and considerably reduced the computational costs. The small number of input parameters and their intuitive influence on the behavior of the method makes its usage very easy. The entire procedure is independent of any model parametrization. However, we showed also that the quality of the training image and the stopping condition are very important.

A broad range of existing methods for solving inverse problems that are based on the minimization of a misfit function are particularly efficient if three main assumptions are fulfilled: the model space and the data space are linear, their uncertainty is described by a Gaussian probability distribution and they are connected through a linear forward operator [Arulampalam *et al.*, 2002; Mosegaard and Tarantola, 2002; Tarantola, 2005]. In the hydrogeological framework, however, usually none of the assumptions are satisfied. In order to overcome these requirements, nonlinear transformations into Gaussian spaces [Zhou *et al.*, 2011; Li *et al.*, 2012; Xu *et al.*, 2013; Xu and Gómez-Hernández, 2015], linear approximations of the forward operator [Chen *et al.*, 2009] and simplified parametrizations from Gaussian subspaces [Doherty, 2003; Alcolea *et al.*, 2006; Tonkin and Doherty, 2009] have been extensively investigated. Unfortunately, it is not possible in general to meet all of the three assumptions. The core of the PoPEX algorithm however, has been designed for cases in which the model space is discrete and well adapted to account for prior geological knowledge which can be expressed via an MPS or any other conditional geostatistical simulation tool. MPS methods were chosen because they have proven to be a very powerful tool for modeling complex and heterogeneous geological environments in real applications [Caers *et al.*, 2003; Liu *et al.*, 2004; Okabe and Blunt, 2007; Ronayne *et al.*, 2008]. Overall, the proposed algorithm is potentially able to solve sophisticated inverse problems. In this work, we only considered spatial uncertainties that represented different rock types. Nevertheless, it is possible to acknowledge any kind of uncertainties that can be modeled by conditional simulations. The same complexity of the model space can be covered by MCMC methods [Alcolea and Renard, 2010; Mariethoz *et al.*, 2010a; Hansen *et al.*, 2012; Laloy *et al.*, 2016]. The ergodicity of Markov chains ensures an asymptotic exploration of the true posterior information. In practice, however, the convergence of MCMC methods is slow.

The PoPEX algorithm, on the other hand, does not fulfill the property of ergodicity. Assume that $\mathcal{M}^k = \{\mathbf{m}_1, \dots, \mathbf{m}_k\}$ is a sufficiently large subset of the model space \mathcal{M} sampled from a probability measure function $\sigma_M : \mathcal{M} \rightarrow \mathbb{R}$. An unbiased estimator [Durrett, 2010] of the first moment (with respect to σ_M) of a random variable $f : \mathcal{M} \rightarrow \mathbb{R}$ is given by

$$\hat{\mu} = \frac{1}{k} \sum_{i=1}^k f(\mathbf{m}_i). \quad (10)$$

Likewise, if \mathcal{M}^k represents an uniformly distributed subset of \mathcal{M} , the first moment can be approximated by the weighted sum [Robert and Casella, 2004]

$$\hat{\mu} = \sum_{i=1}^k f(\mathbf{m}_i) \bar{\sigma}_M(\mathbf{m}_i). \quad (11)$$

In the PoPEX algorithm, the equation (4) used for computing the posterior probability maps are of the form of expression (11) above. The distribution of the PoPEX realizations, however, is clearly not uniform for

$k > N_i$. If a large number of conditioned realizations has been generated, we expect that the models in \mathcal{M}^k are distributed according to a density that is close (in some sense) to the posterior measure σ_M . Therefore, using weighted sums as in equations (4) and (11) overestimates regions of high posterior information (see e.g., fundamental identity of importance sampling in Robert and Casella [2004]). In the early iterations of the PoPEX method, the number of conditioned models is small and the slight overestimation helps to accelerate the algorithm. In the long term, however, it results in a reduced variability of the posterior models (cf. Figures 6a and 6b).

Let us briefly comment on our choice of the prior probability measure function. The sequential construction of the spatial models by a DS technique depends on the uniformly distributed random paths that run through the pixels. If N denotes the number of pixels and s the number of facies types, there are $N!$ different paths but no more than s^N different models. Therefore, for large N , the map sending a path onto the corresponding model is not injective (as $N! > s^N$). It follows that there are different paths that produce the same realization. By defining an appropriate distance between the models and the training image, we may observe that models with “common” structures are “closer” than others. We expect that such “common” realizations have a higher probability of occurrence. Thus, the MPS algorithm does not produce different models with uniform probability. A distance between the TI and the models could be used for the definition of a suitable prior distribution. However, defining a reasonable distance for facies-type models is far from being trivial. This is why, for this work, we assumed uniformity of the prior distribution.

Although the presented algorithm showed promising behavior on a synthetic problem, let us remark that a complete analysis should involve a more complex field study (with a number of model parameters on the order of $10^6 - 10^8$). In such cases, modeling uncertainties and nonuniformity of the prior distribution usually can no longer be neglected. Both are matters that should be further investigated.

Acknowledgments

The authors would like to thank Michael Pircz, the two anonymous reviewers, and the Editors for their many helpful suggestions. They have greatly helped to improve the presentation of this paper. This work was funded by the Swiss National Science Foundation through the grant 153637. The data and codes used to generate the results of this paper can be obtained from the corresponding author (christoph.jaeggli@unine.ch).

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