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Abstract

Numerical simulations use past reservoir behavior to calibrate models used to predict future performance. Traditionally, this process is carried out deterministically through history matching and most current approaches focus on developing probabilistic procedures, called data assimilation, whereby reservoir simulation models are calibrated to reproduce plausible performance under different operating conditions.

The output of different data-assimilation strategies can over-reduce the variability by having several highly-similar scenarios. Consequently, the need to ensure the variability of simulation models arises, to consider multiple possible solutions. In this vein, we introduce a visual analytics approach, based on phylogenetic trees, as a means to evaluate the variability of numerical reservoir simulation models throughout the probabilistic data assimilation process. Phylogenetic trees arrange simulation results based on similarity and visually convey match quality through color encoding.

We applied our methodology to two scenarios: (i) a synthetic scenario to exemplify the properties of the phylogenetic tree for the analysis of simulation models; and (ii) two different ensembles of simulation models, each representing a data-assimilation iteration, from the UNISIM-I-H benchmark case based on the Namorado Field, Campos Basin, Brazil.

Our strategy is intuitive and easy-to-use, allowing the user to assess the similarity of the numerical reservoir scenarios, ensemble variability, and match improvement during data assimilation iterations.

Introduction

Despite efforts to develop new sustainable energy sources, oil is still one of the most important sources for energy. The management of oil reservoirs requires reliable models that must reproduce past reservoir behavior to estimate the dynamic behavior of the field, for reservoir management and to forecast oil production.

Creating a numerical simulation requires the generation of a reservoir model that contains the reservoir characteristics. However, the lack of information to correctly characterize the reservoir generates uncertainties about the properties, and, consequently, the selected parameters may not represent the actual reservoir. Therefore, it is necessary to develop a process capable of obtaining models with estimates that represent the reality of the field.

Traditionally, this process is carried out deterministically through what is known as history matching, where a single numerical model is generated, from which model uncertainties are evaluated. However, this approach is somewhat limited, as the process has characteristics of inverse problems, where multiple inputs can generate results of the same quality. Thereby, existing efforts focus on probabilistic approaches where multiple scenarios are evaluated together and uncertainties are updated in what we know as data assimilation, which involves information from observations and numerical scenarios to reduce the uncertainties and increase the reliability of forecast estimations (Jahanbakhshi et al., 2018).

There are many methodologies used to perform data assimilation, such as Kalman filter (Jazwinski, 1970), Kalman smoother (KS, Jazwinski, 1970), Ensemble-based methods (Evensen, 2009b), Optimal Interpolation (Daley, R., 1991), 3D/4D Variational Data Assimilation (Lewis and Derber, 1985; Talagrand and Courtier, 1987; Rabier and Courtier, 1992; Errico et al., 1993; Courtier, 1997; Lewis et al., 2006), of which the ensemble Kalman filter (EnKF) and the ensemble Kalman smoother (EnKS) are the most popular examples. Nonetheless, in practical applications, some probabilistic methodologies can greatly reduce the variability of uncertainties, achieving at the end of the assimilation, several scenarios matched that present equal properties parameters, collapsing the uncertainties to the same point. Ensuring the variability of simulation models is vital to consider multiple possible solutions, especially when the focus is on the probabilistic forecast.

Reliable reservoir simulation should be transparent and empower decision-makers rather than create a black box (Islam et al., 2010). Uncertainties are the key elements that largely impact the decision-making process based on modeling (Caers, 2011). In this context, Schiozer et al. (2015) proposed a 12-step methodology to improve the decision-making process. In Step 5, it is highlighted the importance of the data assimilation through a reduction of scenarios on the closed-loop process.

Many authors propose strategies to reduce the scenarios to be considered without running the costly flow simulations. Some automatic techniques are based on ranking (Ballin et al., 1992; Steagall and Schiozer, 2001; Schiozer et al., 2004; Sarma et al., 2013; Meira et al., 2016), based on certain objective functions and dependent on the property selected. These methods sort the simulation models based on a given measure and, then, may select models in the top, medium and/or bottom of the ranking. The main problem with this approach is that if the measure has no correlation with the reservoir production, then the selected models will not represent the variability of the uncertainties. Probability-based techniques

(Rahim and Li, 2015) are also applied to find an optimal subset of simulation models. However, they are computationally time-consuming for a large set of models and sensitive to the presence of outliers. These strategies do not provide an overview of the simulation model distribution.

Other authors have proposed projection maps to represent the similarity space of simulation models, whereby each point represents a simulation model, by analyzing how the models are different or similar to each other to select representative ones. Distance functions have also been proposed, such as the Hausdorff distance (Suzuki et al., 2008; Suzuki and Caers, 2008) and the EnKF metric (Caers and Park, 2008; Park, 2011). Other authors, see Sahaf et al. (2018) and Scheidt and Caers (2009), have suggested applying a clustering method on the projection map and, subsequently, selecting a representative model from each cluster. The drawback of these strategies is that models are significantly reduced considering just the similarity between them and not the objective functions.

In general, these strategies, despite giving some clues about uncertainty, fail to (1) assess the variability of the simulation models in the uncertainty reduction process; (2) see a global view; (3) consider similarity between simulation models or the number of objective functions within an accepted range; and (4) evaluate the collapse of reduction of uncertainties. The main contribution of the present work relies upon a visual approach to evaluate the variability of numerical reservoir simulation models throughout a probabilistic well data-assimilation process, and also to understand the reduction of uncertainties. The contribution of the proposed method is related to steps 4 and 5, which are related to scenario generation and reduction, of the unified 12-step methodology proposed in Schiozer et al. (2015).

In summary, we introduce a visual analytics approach, based on phylogenetic trees, to evaluate the variability of numerical reservoir simulation models, that supports visualizing, in a single representation, the similarity of reservoir properties and well-matching quality through color encoding. This proposed solution is an interdisciplinary result of computer scientists and petroleum engineers. It is intuitive and easy-to-use, allowing the user to efficiently assess ensemble variability and match improvement during data-assimilation iterations. The described solution can also be used to evaluate the spatial movement of fluids.

As modern reservoir management is usually described as a continuous process that optimizes the interaction between data and decision making during the life cycle of a field (Saleri, 2005), our visual data analysis approach can be used iteratively, by generating a visualization at each data-assimilation iteration, giving an overview of how data is converging, where users may make decisions and/or adjustments.

Scope/Objective

We introduce a visual approach to evaluate the variability of numerical reservoir simulation models throughout the probabilistic well data assimilation process. The main contribution of our method is the definition and generation of a visual representation to convey: (i) similarity of simulation models and (2) well-matching quality through color encoding, to assess variability.

Methodology

Figure 1 depicts an overview of the workflow. From a model ensemble (a), we define the acceptance range, from which matching quality is calculated to obtain the color mapping (b). We define the metric to be applied between models to calculate the dissimilarity matrix (c). The visualization of a phylogenetic tree depicts the similarity and matching quality of the simulation models (d).

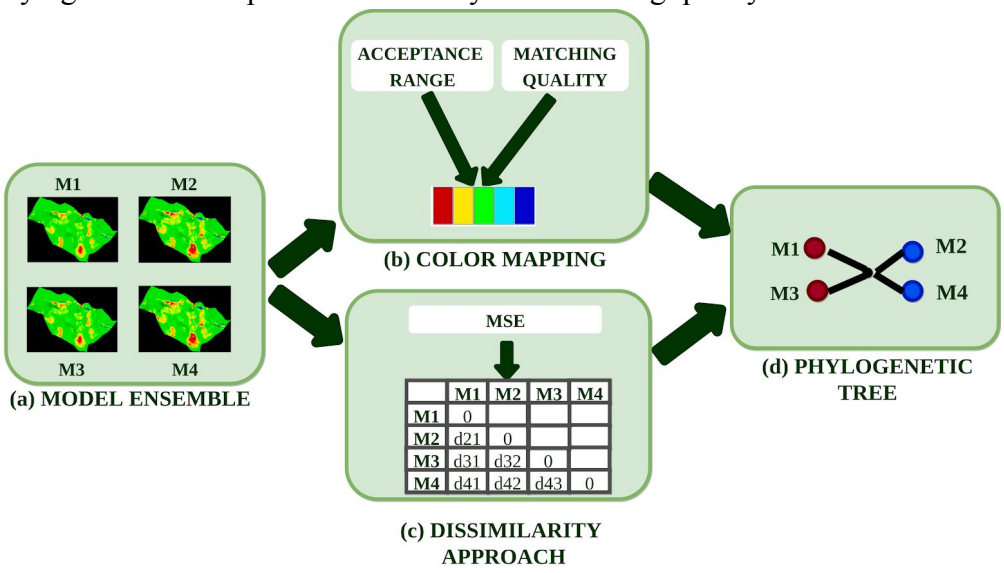


Fig. 1 – Flowchart of the proposed methodology to visualize the variability of numerical simulations.

Model Ensembles, Data Assimilation, and Objective Functions

We validated this procedure against the benchmark UNISIM-I-H (see Figure 1.a), a synthetic reservoir based on structural, facies, and petrophysical models using geological and rock/fluid data from a real Brazilian pos-salt reservoir field (Avansi and Schiozer, 2015a). This dataset is composed of synthetic 4D seismic data and 500 reservoir simulation models, where each model corresponds to a particular combination of all reservoir uncertainties. We used the set of models, which have a horizontal grid of 58×81. More details about the seismic data generation can be found in Davolio and Schiozer (2019).

We adopt the probabilistic data-assimilation procedure proposed by Almeida, et al. (2019) to reduce the number of scenarios from the initial set. This data assimilation procedure is based on the methodology introduced in Maschio and Schiozer (2016), but spatial uncertainties are treated through a regionalized co-simulation. The metric employed to measure the deviation between the scenarios estimations and historical data is the Normalized Quadratic Deviation with Sign quality indicator (NQDS) presented by Avansi et al. (2016). NQDS (Equation 1) measures, for a variable and a generated model, the misfit of the variable in the model.

$$NQDS = \frac{\left(\sum_{i=1}^{n}(Sim_i - Obs_i)\right)}{\left|\sum_{i=1}^{n}(Sim_i - Obs_i)\right|} * \frac{\sum_{i=1}^{n}(Sim_i - Obs_i)^2}{\sum_{i=1}^{n}(Obs_i * Tol + C)^2}, \quad 1$$

where i corresponds to a certain time instant, Sim_i and Obs_i are the simulated and the observed data measured at the time i, Tol is the percentage of tolerance for variables be considered good with respect

to historical data, and C is a constant to prevent division by zero, in case the production rate is zero. The closer to zero NQDS is, the more similar the two (history and simulated) data points are. NQDS equaling zero means that they are coincident. The NQDS strategy supports the definition of matching-quality levels, to identify models with equivalent matching quality for one or more variables.

Acceptance Range and Global Matching Quality

We used the NQDS indicator to evaluate multiple local objective functions, for each output variable considered in the data-assimilation process and for each model generated. We considered 78 local Objective Functions (OFs): oil rate (Qo), water rate (Qw), gas rate (Qg), and bottom-hole pressure (BHP) for 14 producers (4 OFs × 14 producers = 56 OFs) and water injection rate (Qwi), and BHP for 11 injectors (2 OFs × 11 injectors = 22 OFs).

We calculated the number of NQDS of the local Objective Functions (#OFs) within a certain cut-off value (acceptance ranges), adjustable by the user, to identify different models with similar matching quality, considering that there is no unique solution for a data-assimilation problem. Depending on the purpose, we could consider all local objective functions to analyze the models considering the entire reservoir, or locally considering only the objective functions of producers and injectors in a certain region. Different acceptance ranges will create different matching qualities.

Once (#OFs)-values are computed for all simulation models, we can assign a categorical color scale to indicate different levels of quality (see Figure 1.b). With this purpose, we selected a color scale as defined in Figure 2 from red to blue in which red represents models with small number of OFs (worst matching quality), cyan, green and yellow represent models with greater sequential number of OFs, and blue represents models with a great number of OFs (good well matching). Color is used to convey well data matching quality (fluid rates and pressure) of each simulation model in the phylogenetic tree.

Fig. 2—Categorical color scale from red to blue.

The Dissimilarity of Simulation Models

To calculate the dissimilarity of simulation models of an ensemble at a data-assimilation iteration, we used a well-known cost function: the Mean Squared Error (MSE), see (Tillier et al., 2013) for details on this cost function. We calculated the MSE-values between pairs of numerical simulation models to obtain the differences between them as:

$$MSE(M_A, M_B) = \frac{1}{n} \sum_{i=1}^{n} (M_A[i] - M_B[i])^2 \ , \qquad 2$$

where M_i is the *i-th* reservoir simulation model, n is the number of cells in the grid of each simulation model, and $M_A[i]$ is the value of the cell i.

The result of comparing all reservoir simulation models is a lower triangular dissimilarity matrix (see Figure 1.c), which does not duplicate information. Numerous other dissimilarity functions could be selected and would be compatible with our proposed method. The resulting dissimilarity matrix is used as an entry to organize the simulation models in the phylogenetic tree.

Phylogenetic Trees

To represent the global similarity, we use the concept of phylogeny (see Figure 1.d), which is widely applied by biologists to support the construction of viable evolutionary relationships that exist between species (Swofford and Sullivan, 2003). The result of this process is a phylogenetic tree (phylo-tree) used to represent evolutionary distances, facilitating the assessment of sequence diversity within and between groups of species. Phylo-trees are usually represented by acyclic graphs with leaves representing species and topology indicating ancestry relationships. In our case, species are simulation scenarios, where their relationships are defined through similarity of saturation maps, using the dissimilarity matrix, as described in the previous section.

Of the different phylogeny methods, the most important are those based on distance matrix methods (Swofford and Sullivan, 2003). The most popular heuristic approach used to reconstruct phylo-trees from distance matrices is Neighbor-Joining (NJ) (Saitou and Nei, 1987), a bottom-up strategy that builds a rootless tree. In this work, we rely upon the NJ implementation introduced by Cuadros et al. (2007) to reflect the similarity of multiple scenarios.

The NJ approach begins with a star tree, where all scenarios are connected (simulations in our case). Then, it iteratively identifies pairs of closest scenarios (those with the smallest distance values), defined as neighbors, by selecting the smallest value in calculating the sum of the distances between the branches, using the equation:

$$S_{ij} = \frac{1}{2(n-2)} \sum_{k \neq i,j}^{n} (D_{ik} + D_{jk}) + \frac{1}{2} D_{ij} + \frac{1}{n-2} \sum_{(k,\, l \neq i,j) \wedge (k<l)}^{n} D_{kl}, \qquad 3$$

where i and j are the indices of the scenarios to be compared, D_{ij} is the matrix value in the position (i, j). k represents all scenarios except i and j, and n is the number of scenarios.

Once the pair of neighboring scenarios to be grouped is chosen, a new virtual node X is created to connect them. The selected pair of scenarios is removed from the dissimilarity matrix and replaced by the new virtual node. The distance between the new node and the other scenarios is calculated as:

$$D_{i-j,k} = \frac{D_{ik} + D_{jk}}{2}, \qquad 4$$

where $k \leq n$ excluding the scenarios i and j.

At each iteration, the number of instances is reduced by one unit and the process is repeated to find another pair of neighboring scenarios. The iterative process is performed up to have three instances.

Pairs of similar scenarios are arranged on branches that link them according to similarity. The resulting visual representation is colored using the color scale established for the matching-quality of each scenario, conveying well data matching quality (fluid rates and pressure).

To analyze the variability of scenarios, we look at the formed branches. A well-formed branch

containing circles with similar colors represents a set of similar numerical reservoir scenarios in terms of well matching and spatial fluid similarity.

Results

We applied our methodology to two different case studies. The first is a synthetic case, which exemplifies the properties of the phylogenetic tree for the analysis of simulation models. The second case considers two different ensembles of simulation models regarding the UNISIM-I-H benchmark, each of which represents a data-assimilation iteration.

Synthetic case

We created a synthetic case, illustrated in Figure 3. This dataset comprises three different groups of similar maps. We assigned a different hypothetical quality matching for these groups, represented by red, blue and green. A reasonable visualization should highlight that the first and second rows are different despite being a reflection along the cross-diagonal.

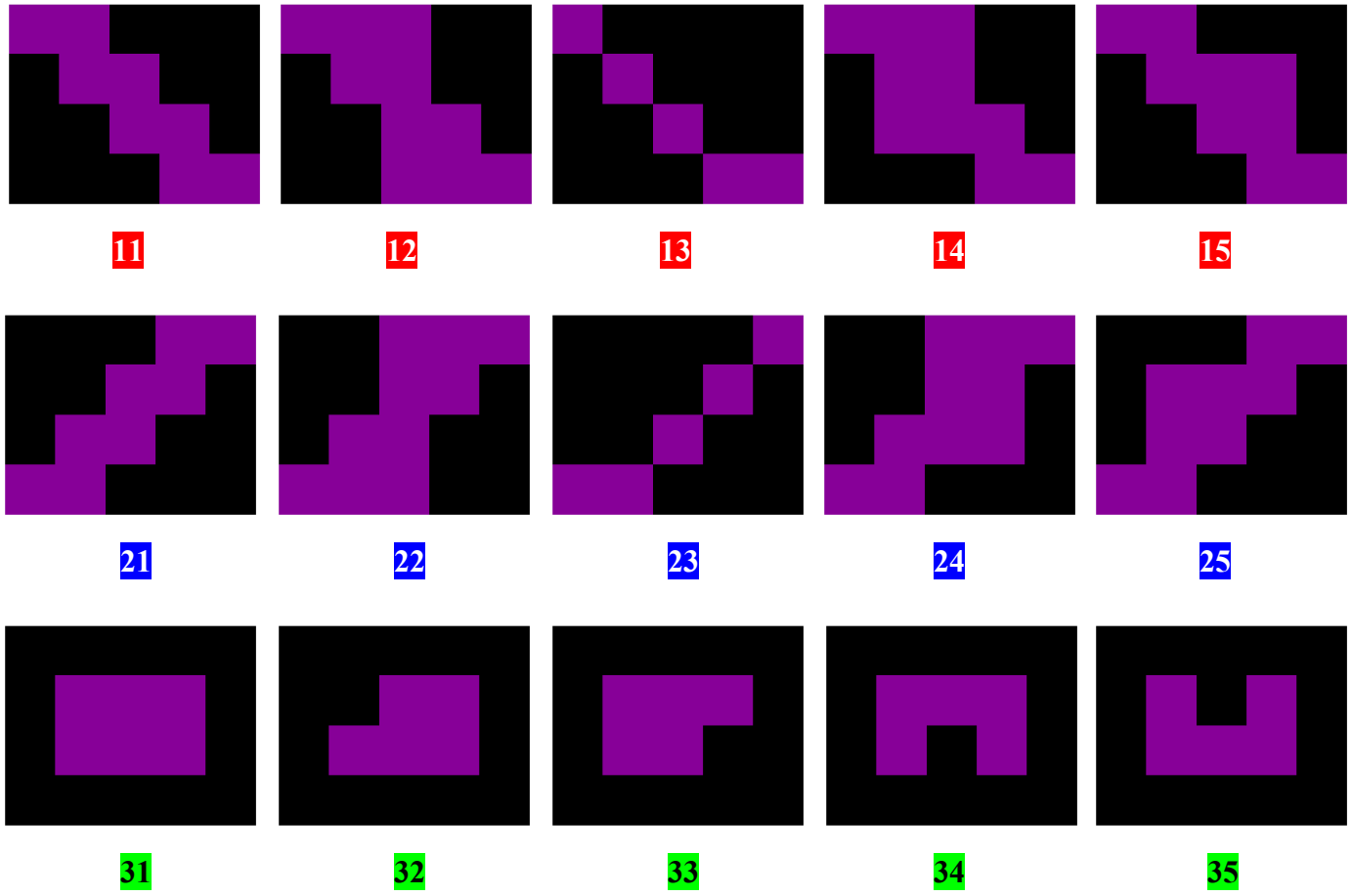


Fig. 3—Simplified scenario exemplifying properties of the phylogenetic tree.

Figure 4 depicts the phylo-tree for the synthetic scenario. Because of the MSE nature (the average of the sum of squared differences), the first group and the second are more similar to the third than among them. Therefore, the elements of the first row are placed at the bottom, clearly separated from the elements of the second row (upper part). The elements of the different groups are placed together. Note that the positions of the elements are affected by the selection of the dissimilarity metric.

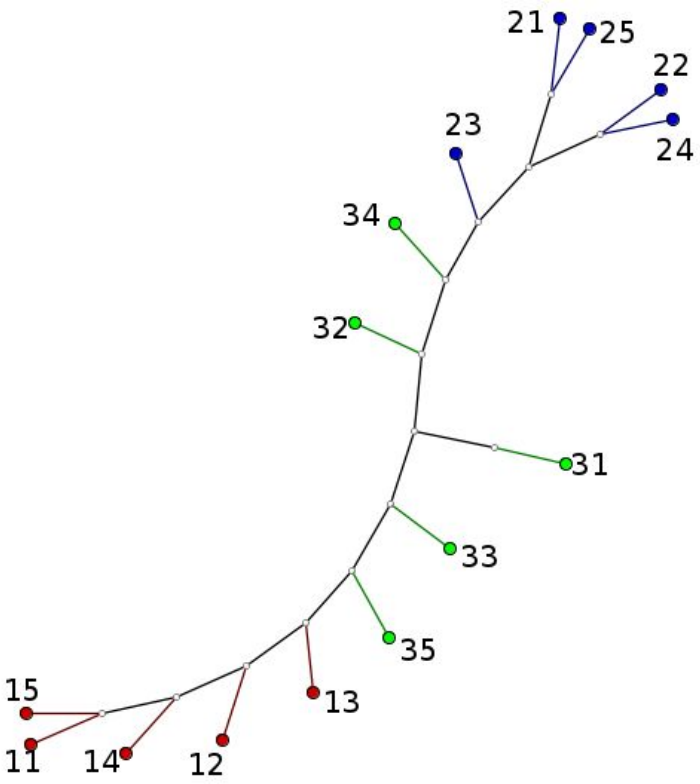


Fig. 4—Phylogenetic tree resulting from the synthetic case.

Model ensembles at different data-assimilation iterations

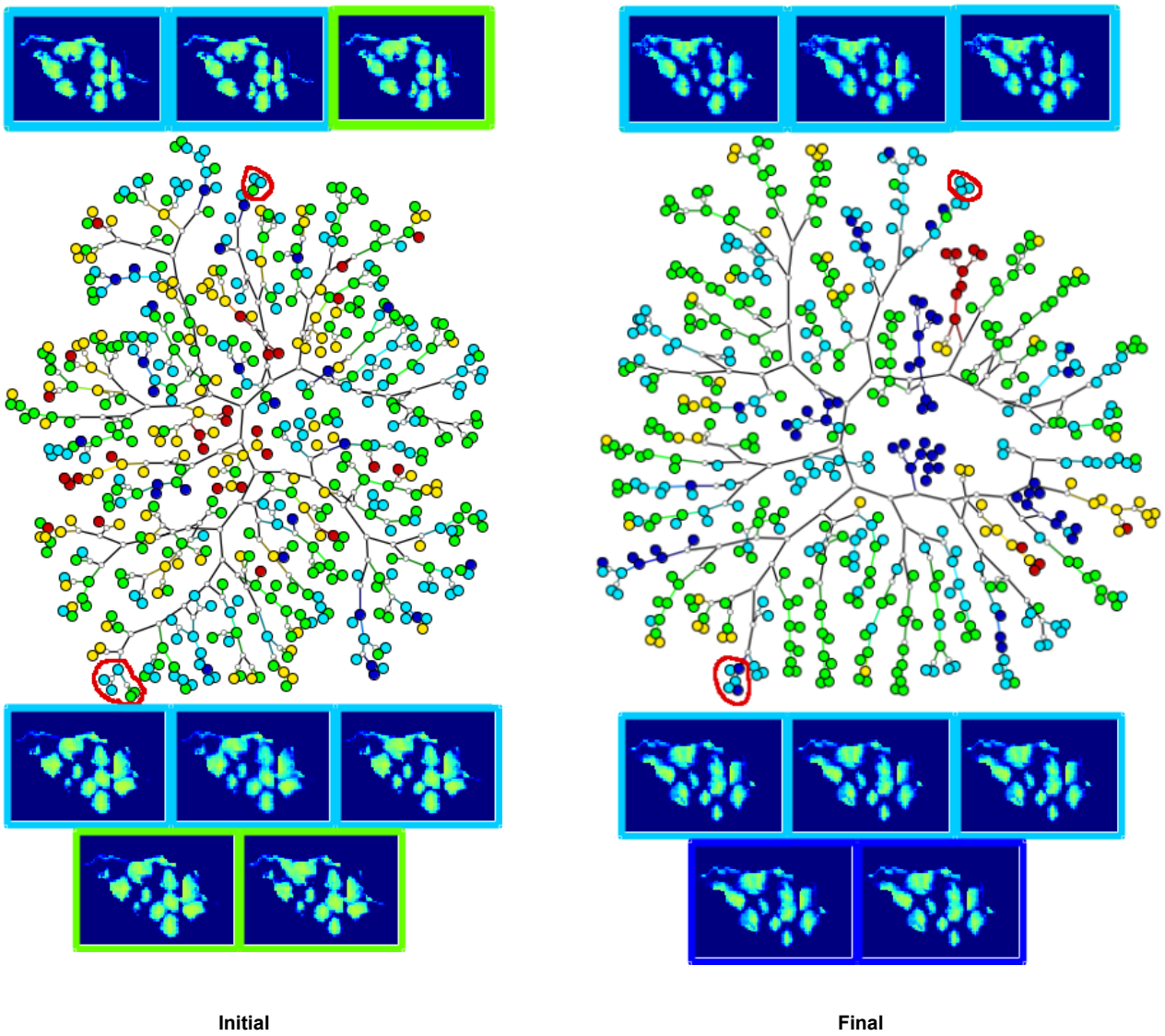
We now explore data from the benchmark UNISIM-I-H, previously described, for two different time instants. Figure 6 shows phylo-trees at those two-time assimilation instants. Each model is represented by a colored circle. The closer the circles are to each other, the more similar the water saturation maps. The global quality matching is defined as the number of OFs that present errors inside the cutoff value [-5,5]. The colors represent the global quality matching of the well based on 78 local objective functions (OFs): Qo, Qw, Qg, and BHP for 14 producers, and Qwi and BHP for 11

injectors. Models shown in blue represent good well matching (#OFs≥65), while models with the worst matching quality (#OFs<50) are shown in red. The resulting color scale is defined in Figure 5.

Fig. 5— Color scale to represent the well matching based on the number of OFs. Models shown in blue represent a good well matching, while models with the worst matching quality are shown in red.

Figure 6 shows 500 simulation models from two data-assimilation iterations, initial and final, with detailed views. If we select sub-branches of equivalent quality (similar color) but in different places of the phylo-trees, as shown in Figure 6, we can see that models with similar matching quality color and in the same branch present very similar spatial distributions.

Also, the phylo-tree visualization allows seeing an improved well matching (fewer red models) and less variability (close model clusters) on the final iteration. We observe that, after data-assimilation, the best models are grouped in a few branches, which is a good indication that the procedure kept some spatial variability, represented here by the similarity of saturation maps.



Initial Final

Fig. 6— Visual variability analysis of 500 simulation models from two data-assimilation iterations (initial on the left, final on the right). The global quality matching is defined as the number of OFs that present errors inside the cutoff value [-5,5]. Detailed views of some branches of two data-assimilation iterations. Each model is represented by a colored circle.

By selecting a branch, we can see its simulation models. In Figure 7, we selected three groups of elements belonging to different sub-branches from the final iteration: A-models with good matching quality (blue circles), B-models with regular quality matching (green circles), and C-models with bad quality matching (red circles).

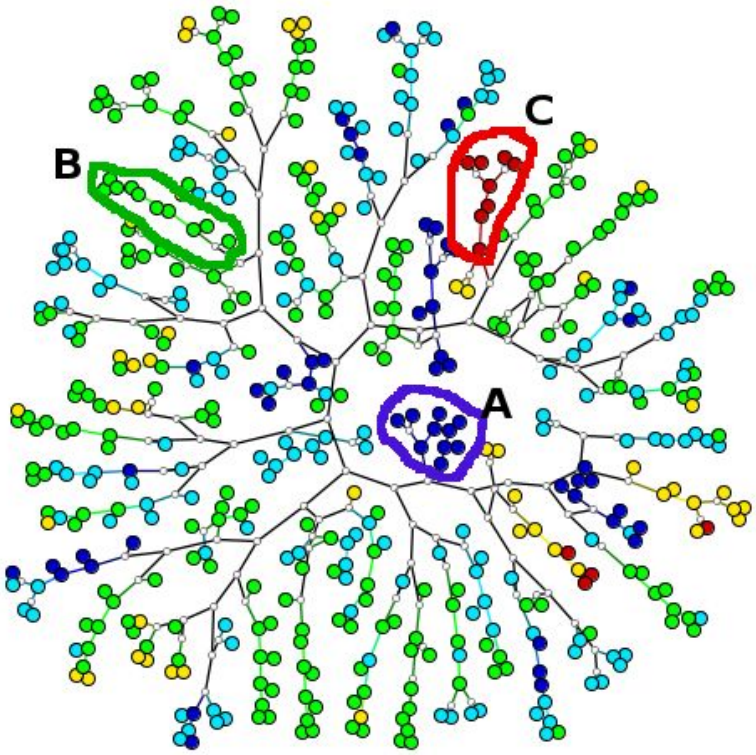


Fig. 7— Three selected groups: A-models with good matching quality, B-models with regular quality matching, and C-models with bad quality matching.

We also explore the similarity of these simulation models related to cumulative graphics for producer 08 in the dataset. The selected scenarios, which are in the same branch, present similar forecast production. We see that good models match the forecast very well. Also, we observe that group B (regular) seems to give a worse fit than group C (bad). This fact could be due to maybe some of those OFs are more important than others. Other strategies to represent the matching quality can be used, in which some OFs could have more relevance than others.

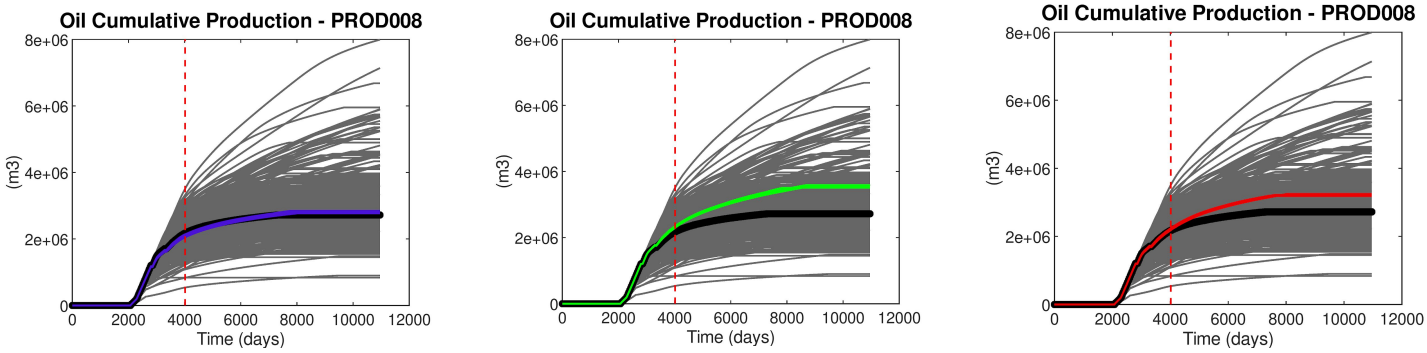


Fig. 8— Cumulative graphics of three groups of elements belonging to different sub-branches from the final iteration.

The analysis using phylo-trees can be also performed locally from subregions of interest, considering just the OFs belonging to the wells considered in those subregions. That analysis could support

engineers worried about a few wells that do not history-match, even if they can get the overall match.

Conclusions

In this work, we presented a visual analysis approach to evaluate the variability and matching quality of numerical simulations at different data-assimilation iterations. Our visualization allows the validation of spatial fluid similarity. The novelty of this work is the adaptation of phylogenetic-tree analysis and visualization for reservoir simulation model assessment.

Our method takes advantage of human perception through the visualization of well-formed branches of models representing coherent relationships of similarity. All visual representations can be generated in an acceptable amount of time.

As a validation of the methodology, we applied it to a synthetic scenario to exemplify properties of the phylogenetic tree and a realistic case considering different ensembles of simulation models, each representing a data-assimilation iteration. The phylogenetic-tree design effectively represents the variability and quality of scenarios. It allows one to (i) analyze the similarity of maps (proximity of circles in the tree) and the matching quality (circle colors); and (ii) compare iterations to evaluate the matching quality improvement (fewer reds) and the model variability (several branches).

The methodology is flexible and can be applied to reservoirs at different stages of their lifetime, facilitating the inclusion of variability analysis into the decision-making process. It can also help to identify more representative models in a given task. Future work will include the integration of the approach into the process of uncertainty reduction to check and ensure that a certain degree of variability is kept.

Nomenclature

BHP	=	Bottom Hole Pressure
C	=	Constant to prevent division by zero
DA	=	Data-assimilation process
M_j	=	Reservoir Simulation Model number j at a certain data-assimilation iteration
MSE	=	Mean Squared Error
NJ	=	Neighbor-joining
NQDS	=	Normalized Quadratic Deviation with Sign
Obs_i	=	Observed data measured at the time i
OF	=	Objective Function

#OF	=	Number of Local Objective Functions inside a cutoff value
Phylo-tree	=	Phylogenetic tree
Qg	=	Gas rate
Qo	=	Oil rate
Qw	=	Water rate
Qwi	=	Water injection rate
Sim_i	=	Simulated data measured at the time i
Tol	=	Percentage of tolerance

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