Inversion and Prediction-Focused Approach (PFA) imaging of multiple loops Surface Nuclear Magnetic Resonance (SNMR) data

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Appendix C

Deterministic inversion: Resolution matrices

A way to assess the ability of the model to retrieve correct data in a deterministic way is to compute the associated resolution matrix. To do so, Müller-Petke and Yaramanci proposed in 2008 an approach based on the singular-value decomposition (SVD) of the forward operator:

$$\mathbf{d^{obs}} = \mathbf{Gm} = \mathbf{USV}^T\mathbf{m} \tag{C.1}$$

They suggested the use of the Picard conditions (linked to Picard plots) to assess the right truncation to apply to the decomposed problem in order to avoid noise propagation in the model. The use of the Picard condition is supposed to account for the noise level and avoid noise propagation, similarly to regularization parameters in the QT inversion (Müller-Petke & Yaramanci, 2008). It states that the value of :

$$a_i = |\mathbf{u_i}^T\mathbf{d}|/\sigma_i \tag{C.2}$$

where,

- $\mathbf{u_i}^T$ is the transpose of the i^th column of the matrix U
- $\mathbf{d}$ is the data (here, the amplitude at t=0 to comply with the linearity of the problem)
- σ_i is the i^th singular value (diagonal of S)

should remain more or less constant or decrease with the value of the index i (Fedi, Hansen, & Paoletti, 2005).

From the Picard plot, it is possible to establish a reasonable truncation. In this work, it has been chosen to use a simple algorithm to compute the "best" truncation index:

1. Compute the means of the a_i values from $i - 10$ to i
2. Compute the relative increment of each mean value
3. Find the first relative increment larger than 25%

Then, the resolution matrices were computed using:

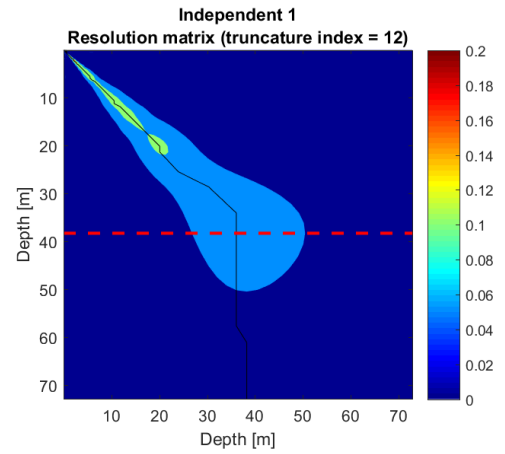
$$\mathbf{R_m} = \mathbf{V}_p \mathbf{V}_p^T \tag{C.3}$$

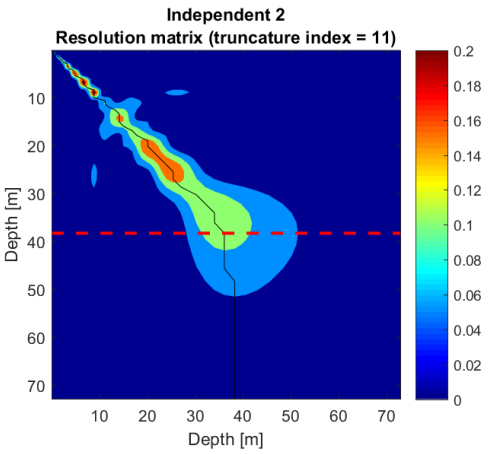
with p, the truncation index ($\mathbf{V}_p$ is the matrix constituted of the p first columns of the $\mathbf{V}$ matrix from the SVD) (Müller-Petke & Yaramanci, 2008).

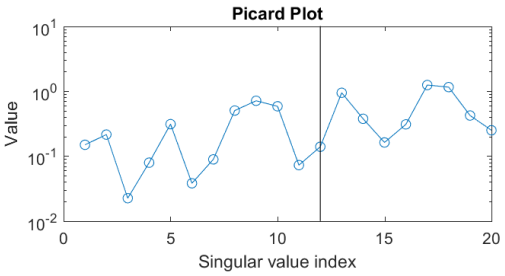
This process has been applied to all the inversions presented in the Subsection 7.3.2 (Chapter 7). The results of such analyses are presented in Figure C.1.

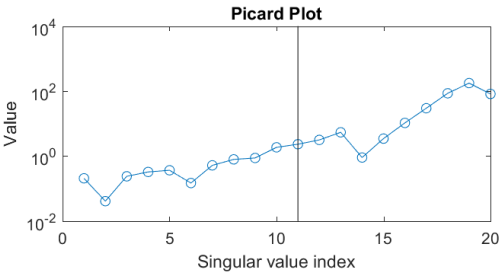
From those matrices, it is interesting to point out that the "Independent 1" and "Independent 5" datasets (hence the same transmitter/receiver) are producing the clearest resolution matrices with a very narrow resolution at the top and a spreading with depth. The other inversions are susceptible to a larger spreading of the resolution, even at low depth. However, the "depth of confidence", marked with the dashed red line, is changing with the type of transmitter/receiver couple in the "Independent" inversions, whereas this depth is not significantly changing with the "Joint" and "General" inversions. The use of the "Joint" and, to a larger extent, the "General" inversions tends to decrease the spreading of the resolution matrix along the diagonal, hence to recover the behavior of the classical inversions.

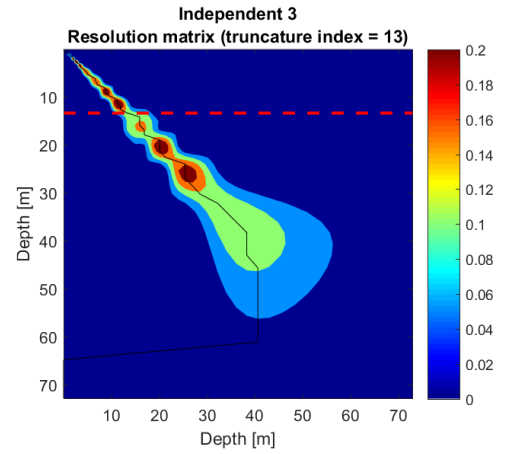
The use of the 10 m loop is also questionable from the analysis of the observation of the resolution matrices. Actually, it seems that the corresponding "Independent 3" and "Independent 6" are the ones that lead to smaller confidence depths (respectively 13.5 and 30.5 m) compared to the classical inversions. It is also observed that the "Independent 4" (30 m transmitter but 50 m receiver) resolution matrix has a large spreading around 20 m, which limits the confidence depth to 21.0 m. However, contrary to the two other limited resolution cases, the resolution of this model shows very few spreading around the diagonal above this confidence depth, which ensures a better model.

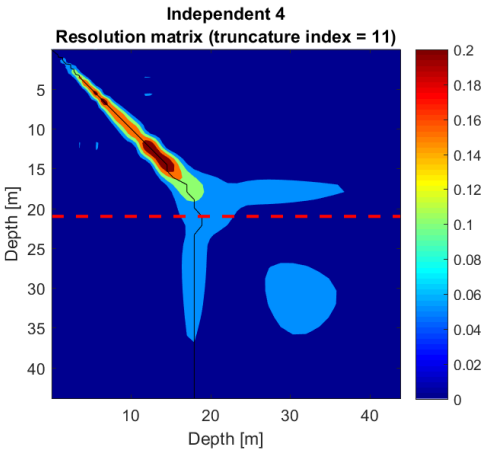

Independent 1
Resolution matrix (truncature index = 12)
Depth [m]
Depth [m]

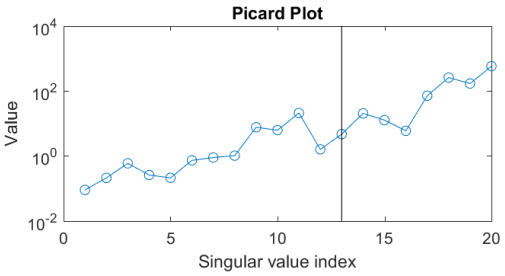

Independent 2
Resolution matrix (truncature index = 11)
Depth [m]
Depth [m]

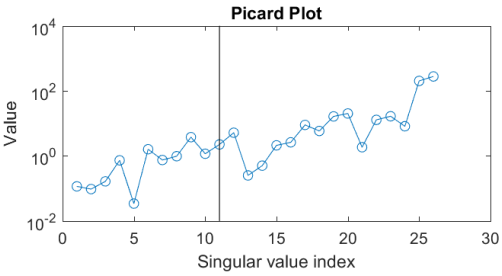

Picard Plot
Value
Singular value index

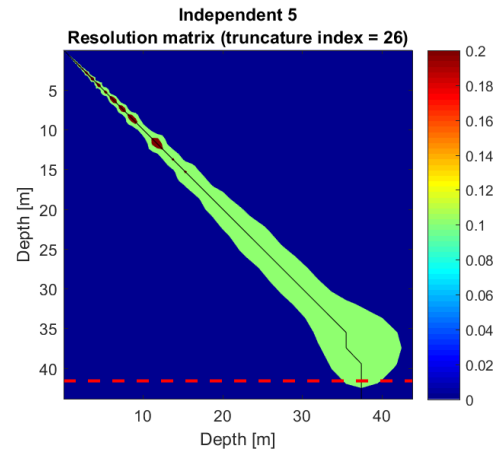

Picard Plot
Value
Singular value index

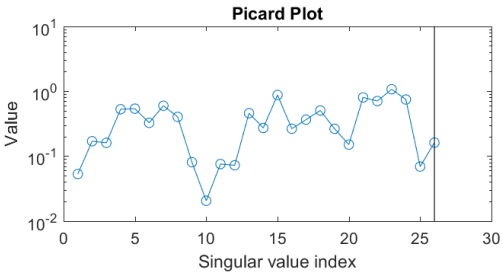

Independent 3
Resolution matrix (truncature index = 13)
Depth [m]
Depth [m]

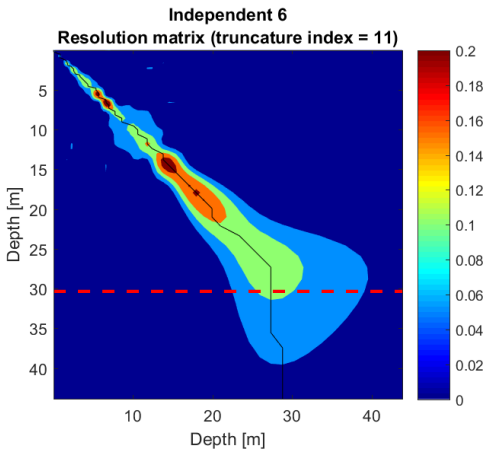

Independent 4
Resolution matrix (truncature index = 11)
Depth [m]
Depth [m]

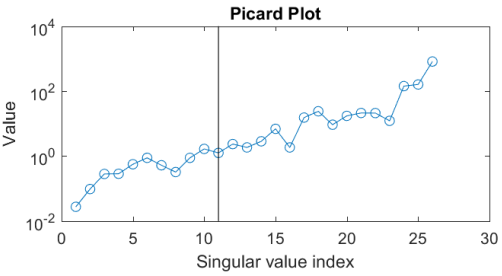

Picard Plot
Value
Singular value index

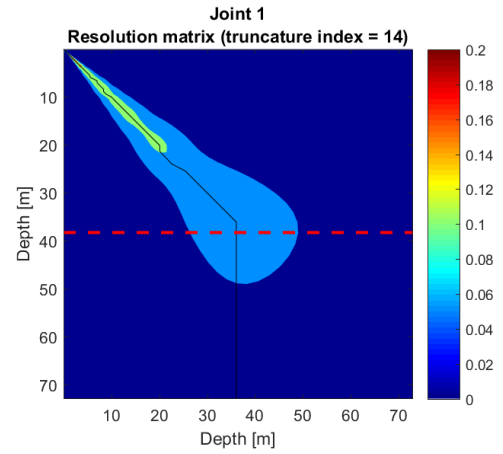

Picard Plot
Value
Singular value index

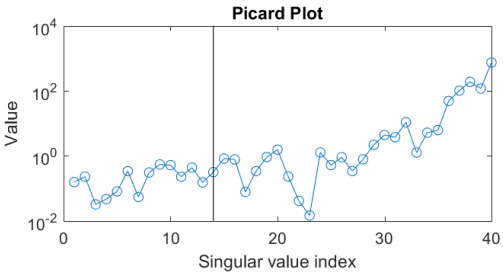

Independent 5
Resolution matrix (truncature index = 26)
Depth [m]
Depth [m]

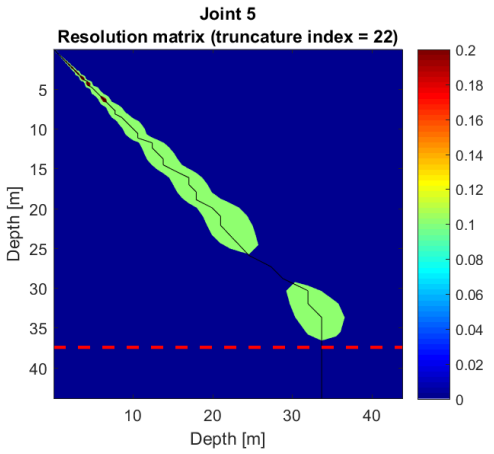

Picard Plot
Value
Singular value index

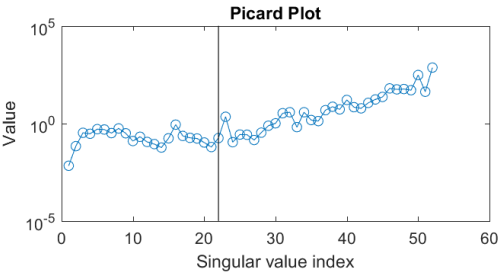

Independent 6
Resolution matrix (truncature index = 11)
Depth [m]
Depth [m]


Picard Plot
Value
Singular value index


Joint 1
Resolution matrix (truncature index = 14)
Depth [m]
Depth [m]


Picard Plot
Value
Singular value index


Joint 5
Resolution matrix (truncature index = 22)
Depth [m]
Depth [m]


Picard Plot
Value
Singular value index

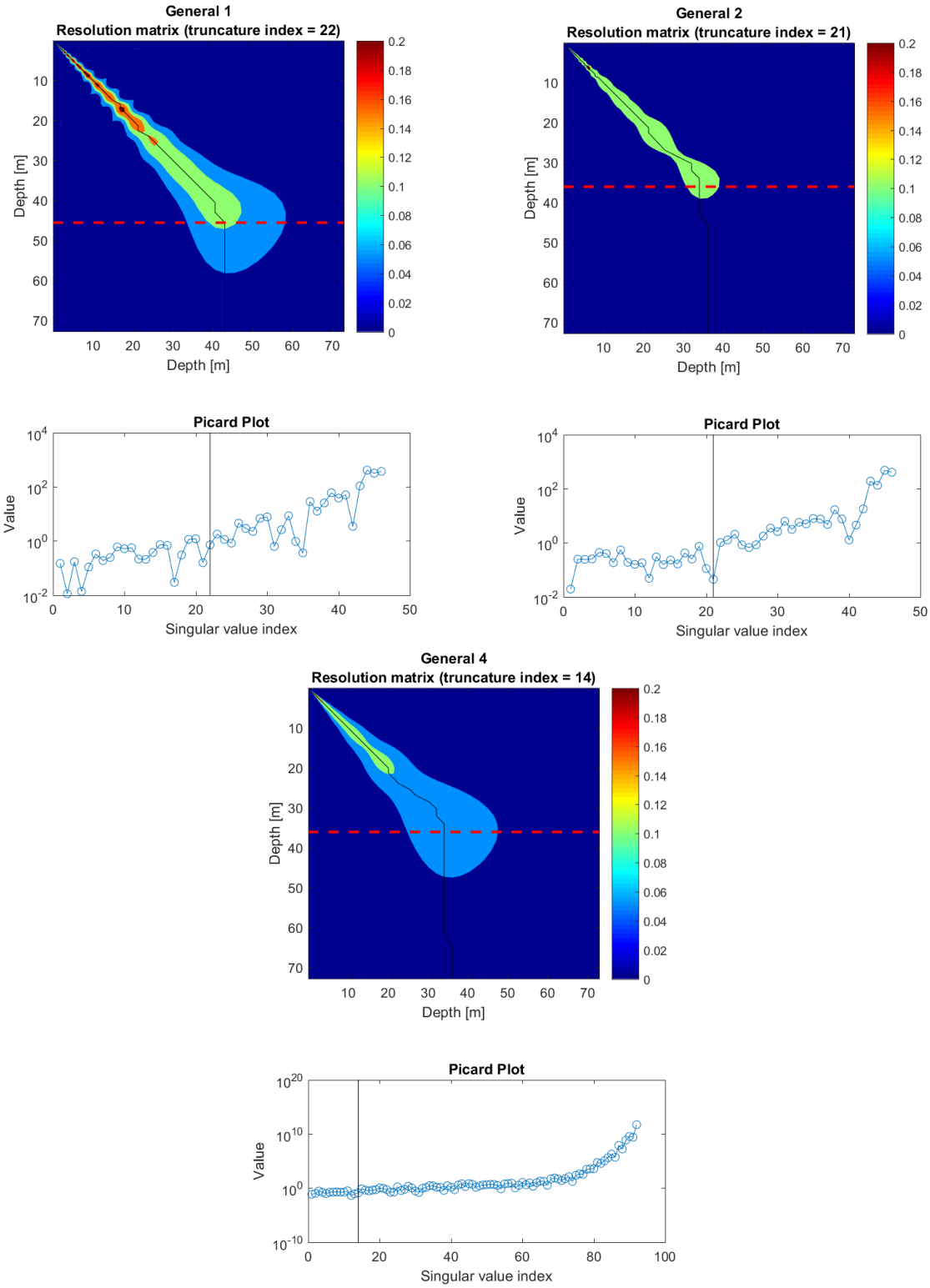


Figure C.1: Resolution matrices (absolute value) and Picard plots for the different inversions proposed in the Subsection 7.3.2. The black line represents the maximum of resolution and the dashed red line represents the maximal depth where the deviation from the diagonal is less than 10% (Müller-Petke & Yaramanci, 2008).