Self Consistent Inverse Pronlem With Cross Validation

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1 Introduction and Motivation

The mathematical term well-posed problem stems from a definition given by Jacques Hdamard. He believed that mathematical models of physical phenomena should have the properties that.

1. A solution exists.

2. The solution is unique.

3. The solution's behavior changes continuously with the initial conditions.

Problems that are not well-posed in the sense of Hadamard are termed ill-posed. Inverse problems are often ill-posed.

Continuum models must often be discretized in order to obtain a numerical solution, while solutions may be continuous with respect to the initial conditions, they may suffer from numerical instability when solved with finite precision, or with erros in the data. Even if a problem is well posed, it may still be ill-conditioned, meaning that a small error in the intial data can result in much larger errors in the answers.

In order to solve the ill-posed problem, regularization method is introduced. A simple form of regularization applied to integral equations, generally termed Tikhonov regularization, is essentially a trade-off between fitting the data and reducing a norm of the solution.

Ill-posed inverse problem with the regularization method can give out a very good reconstructed result compared to the exact result, but only if the measured value and the model is accurate enough.

In order to solve the ill-posed inverse problem which the measure value or the model is not accurate enougth to give out a good reconstructed result, we introduce the self consistent regularization method With Cross Validation.

2 Generalized Cross Validation

The fitness is calculated as:

$$\min_{\lambda} ||Ax_{\lambda} - b^{exact}||_2^2 \tag{1}$$

However, we can't calculate it since b^{exact} is not available. Generalized Cross Validation is a classical statistical technique that comes into good use here [1].

Using Generalized Cross Validation(GSV), the fitness can be calculated as:

$$\min_{\lambda} \frac{||Ax_{\lambda} - b||_2^2}{\left(m - \sum_{i=1}^{n} \varphi_i^{[\lambda]}\right)^2} \tag{2}$$

3 Cellular Evolutionary Algorithm

Usually EAs assume that the strucutre of the population is panmictic, which means that any inidividual may interact with any other individual in the population. However, this need not be always the case: we often see population sin the biological and social world in which individuals only interact with a subset of the rest of the population. This situation can usefully be depicated by using the concept of a population graph [2].
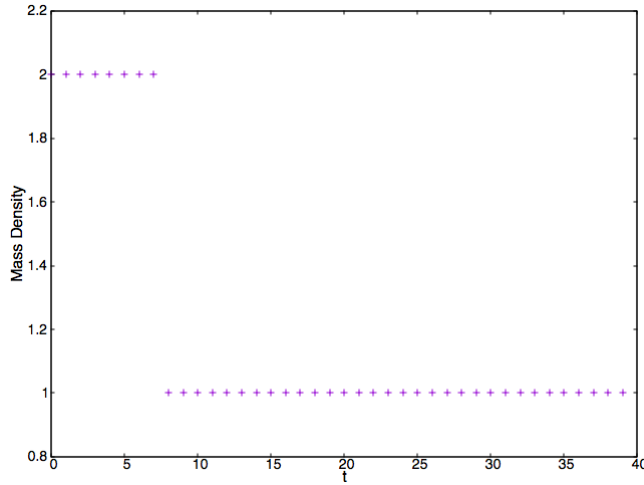
4 Result

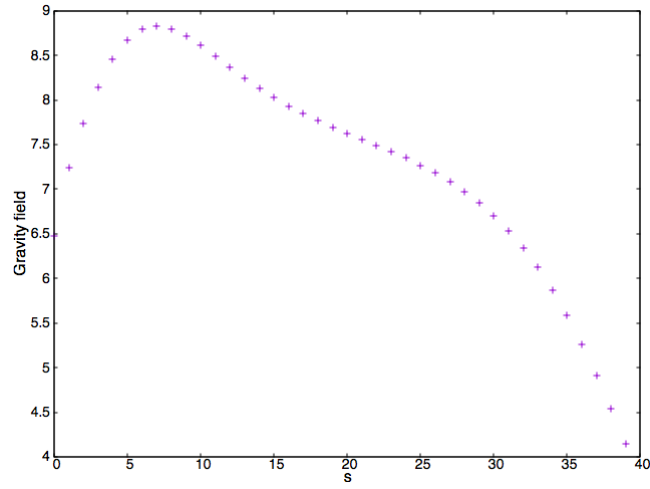
Figure 1: Exact f function (mass density distribution)
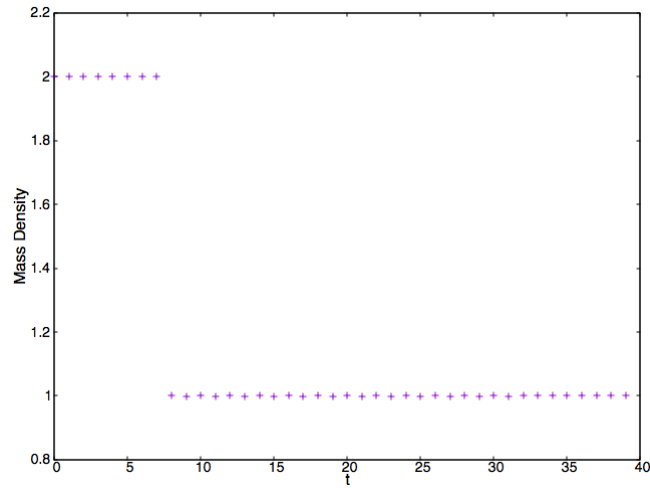
Figure 2: Exact signal g (the gravity field)

Figure 3: The Reconstructed function f(the mass density distribution) after self-consistent genetic algorithm, at $\lambda = 10^{-12}$, GSV value = 1.65e-25

References

[1] Per Christian Hansen. *Discrete inverse problems: insight and algorithms*, volume 7. Siam, 2010.

[2] Alfons G Hoekstra, Jiri Kroc, and Peter MA Sloot. *Simulating complex systems by cellular automata*. Springer, 2010.
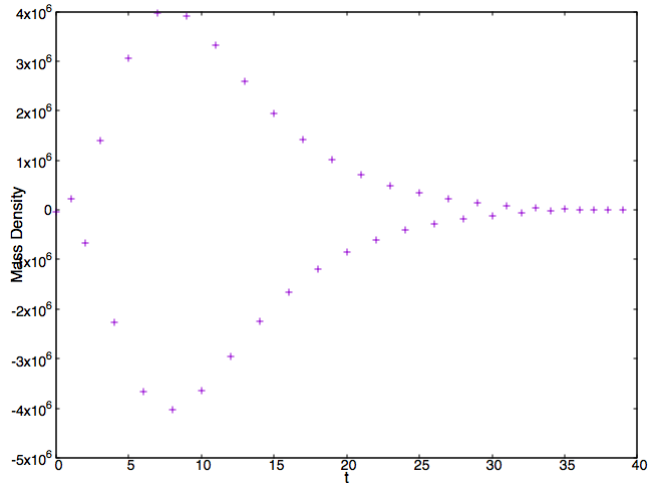
Figure 4: The Reconstructed function f(the mass density distribution) without self-consistent genetic algorithm, at $\lambda = 10^{-12}$, GSV value = 7.22e-10