A GENETIC ALGORITHM FOR PHASE UNWRAPPING ERRORS CORRECTION IN THE SBAS-DINSAR APPROACH

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ABSTRACT

The Differential Synthetic Aperture Radar Interferometry (DInSAR) remote sensing technique permits to investigate the temporal behaviour of the detected displacements through the generation of the deformation time-series. In this scenario the Phase Unwrapping (PhU) is a crucial point where several errors could occur since the problem is intrinsically ill-posed. In this paper we present a technique to correct unavoidable PhU errors and limit their impact in the final deformation time-series. The proposed approach works pixel-by-pixel and is based on the combination of an L1-norm inversion for the identification of the possible PhU errors and a genetic algorithm (GA) for the search of the best fitting solution. We include the technique in the Small Baseline Subset (SBAS) DInSAR processing chain to correct the results of the Extended Minimum Cost Flow algorithm, but in principle it can be used as a correction step after a generic PhU procedure used in SBAS. Results from MonteCarlo simulations are shown in this paper while real data cases will be presented at the conference.

Index Terms— Phase Unwrapping, Genetic Algorithm, L1-norm, DInSAR, SBAS

1. INTRODUCTION

Differential Synthetic Aperture Radar Interferometry (DInSAR) is a remote sensing technique with important applications for geological and anthropic processes studies, thanks to its capability to generate very spatially dense ground displacement maps with centimetre to millimetre accuracy. In particular, starting from an appropriate sequence of differential interferograms, it is possible to study the temporal evolution of the detected displacements through the exploitation of advanced DInSAR approaches, able to generate deformation time-series.

In this context, one of the most difficult tasks for the retrieval of displacement information is represented by the Phase Unwrapping (PhU) step. The PhU operation consists of the reconstruction of the original (unwrapped) phase starting from its analytical restriction (wrapped phase) in the $[-\pi, \pi]$ interval [1]. Such a thing entails that the PhU problem is

affected by a strong ambiguity in the spatial and temporal excursion of the phase. Proper addition or subtraction of a number of 2π corrections for each pixel of the interferometric phase map would solve the above mentioned ambiguity. It is evident that the solution of this problem is not trivial, especially in presence of fast deformation phenomena or in area affected by decorrelation noise [2].

In this work we present an algorithm that aims to identify the PhU errors of the Extended Minimum Cost Flow (EMCF) algorithm [3] exploited in the Small Baseline Subset (SBAS) approach [4]. The proposed algorithm works on a pixel-by-pixel basis and is developed as a cascade of two steps: an L1-norm inversion, that identifies the interferograms likely affected by PhU errors, and a guided scanning of the possible solutions given by a genetic algorithm (GA) [5], to retrieve the corrections of 2π values.

The proposed algorithm is very useful because it permits to manage sets of integers representing the multiples of 2π that have to be added to the phase values. The resulting solution is so coherent with the discrete nature of the phase unwrapping problem itself.

2. TECHNIQUE PROCESS FLOW

Let us start our analysis by considering the SBAS approach. After a generic procedure of phase unwrapping carried out on the whole stack of the interferometric phase maps, the resulting unwrapped interferograms can be inverted by means of a pseudo-inverse matrix in order to generate the corresponding temporal evolution of the phase, which correspond to the displacement time series generation [4]. Comparing by subtraction couples of images from the time series, the wrapped interferograms can be reconstructed. The phase difference between the wrapped original interferograms and the reconstructed ones from the time series is bigger (in absolute value) for interferograms where the probability of a phase unwrapping error is higher. The pseudo-inverse matrix inversion is based on an L2-norm minimization criterion, which smears the possible reconstruction errors in a large temporal region of the time-series images, so making difficult the identification of PhU errors.

The present algorithm is mainly divided in two separates steps. The first one concerns the identification of the PhU errors by means of an L1-norm minimization technique of inversion [6], followed by the application of a GA to evaluate the PhU corrections to be applied.

2.1. L1-norm minimization

The L1-norm minimization technique for the interferograms inversion represents a valid identification of the PhU errors. It is a well-known result of the compressed sensing, which is based on the hypothesis of few sparse errors (i.e. an L0-norm of the error vector very low).

Acting independently for every single pixel of the displacement time series, the algorithm compares the unwrapped interferograms reconstructed from the corresponding displacement time series obtained through an L1-norm inversion technique, with the starting phase unwrapping solution of the pixel itself. The interferograms where the difference between these two solutions in module is higher than a fixed threshold will be considered in the correction procedure as a gene of the GA chromosome.

2.2. Genetic Algorithm solution search

The Genetic Algorithm is a well-known multivariate analysis technique [5] that simulates the natural mechanism of evolution. It results in a guided scanning of all the possible combinations for the values of a given set of variables. The possible values of the variables are considered as genes of a chromosome. The goodness of the solutions is identified by a fitness function that consequently characterizes the chromosome itself.

The GA creates a large number of chromosomes, starting from the first one evaluated from the L1 inversion. Every chromosome is created by mutations of single genes and crossing over between two parent chromosomes (from the second generation one). The former is based on a Poissonian distribution, since the allowed values of the genes are integers to be considered as 2π multiples for the phase unwrapping. Every generation ranks and saves the most performing chromosomes from whom a new generation is created until convergence. Convergence is reached when a chromosome keeps on staying in the first position of the rank for a certain number of generations, whose value depends on the chromosome length [6].

The objective function for the rank of the GA procedure is given by the temporal coherence [3] of the pixel, which is evaluated after the L2-norm inversion of the new unwrapped solution of the GA procedure. It is defined as

$$t_{coh} = \frac{1}{N_{int}} \sum_{i=1}^{N_{int}} e^{j(\phi_{reco,i} - \phi_{orig,i})} \quad (1)$$

where N_{int} is the number of interferograms, $\phi_{reco,i}$ is the reconstructed interferogram phase and $\phi_{orig,i}$ is the start phase

value before the inversion. The temporal coherence is a value ranging between [0,1] by definition, and represents a quality factor related to the goodness of the retrieved PhU solution.

It is important to point out that the temporal coherence is calculated using all the interferograms of the temporal stack, despite the correction algorithm works only on the interferograms enhanced by the L1-norm inversion as a potential source of errors.

The proposed algorithm is intended as an unwrapped phase correction technique for a generic PhU procedure. So a displacement time series point with a high amount of PhU errors (corresponding to a low temporal coherence value) is automatically excluded from the GA correction to avoid reaching a solution with no physical meaning. This kind of solution could be characterized by a high temporal coherence value coming from an algebraic artefact. According to the accuracy provided by our DInSAR algorithm, we reject all points with a temporal coherence value lower than 0.7.

In other words, according with the hypothesis of sparse L0-norm of the error required by the use of the L1-norm inversion, we consider pixels where the number of wrong unwrapped solutions is reasonably low with respect to the number of interferometric pairs.

In our case, we apply the correction technique to a solution obtained through the well-known EMCF (Extended Minimum Cost Flow) approach [3], based on a temporal and spatial phase unwrapping procedure, but, in principles, the presented algorithm can be applied to any other phase unwrapping procedure with a different quality factor function instead of the temporal coherence..

The flow chart in figure 1 summarizes the correction procedure of the algorithm.

The above-mentioned correction is applied at the end of the whole phase unwrapping procedure pixel by pixel separately. This spatial independence of the algorithm allows an extreme parallelization of the whole process, which is extremely important to reduce the processing time from an unaffordable duration.

Figure 1. Description of the correction procedure starting from the solution of the EMCF phase unwrapping. Third, fourth and fifth steps are depicted in separate blocks because the flow parallelization separates the set of points to be analysed in different subsets according with the calculation power.

3. RESULTS

We apply the correction technique to simulated data. We simulate several models of ground deformation for a single pixel: linear, sinusoidal, sigmoidal and logarithmic profile of deformations. We divide the deformation profile in several steps representing our acquired images, and then we simulate the creation of interferograms. The interferometric phase so obtained is modified by adding the known sources of noises as spatial and temporal decorrelation, atmosphere interference and general gaussian white noise. Then we added a fixed amount of phase unwrapping errors, also varying the percentage rate of them.

We apply the GA correction to those data, and evaluate the goodness of the correction by considering the RMS distance of the reconstructed point of the time-series w.r.t. the original ground displacement (known by the model). The parameters of the GA have been tuned according with the SBAS DInSAR technique, after a testing phase with simulated data.

As long as the introduced phase unwrapping error percentage is lower than 10% the GA improves the average RMS distance of 30%. In addition we observe that, comparing our correction technique with respect to a standard L1-norm corrected solution for retrieving phase unwrapping errors, the algorithm reduces the false alarm probability from 8% to 2%. Figure 2 shows the results of a simulation for a single pixel with the four different reproduced deformations of the soil.

The assessment of the procedure with real data is still ongoing and we will show the results obtained on real data during the conference.

The results we obtained so far show that in case of strong deformations the algorithm maximises the temporal coherence resulting in an increasing of the deformation dynamics, according with the known effect of underestimation risk for the phase unwrapping algorithms [8].

Figure 2. Results from the MonteCarlo simulation. The black line is the simulated movement of the pixel in time. Black asterisks are the result of the inversion without the GA correction. Red markers are the result of the inversion after the GA correction. We show 4 cases in which the temporal behaviour is, from top to bottom, linear, logarithmic, sigmoidal and sinusoidal. The presence of PhU errors for this case is set to 5%.

4. CONCLUSIONS

In this paper we present a new technique of correction of Phase Unwrapping errors for the generation of deformation time-series in the DInSAR remote sensing scenario.

The technique is based on an L1-norm minimization approach for the inversion from unwrapped interferograms to time-series images, in order to identify with a sharper precision the potential Phase Unwrapping errors. Then a genetic algorithm is performed on the identified pixels in order to retrieve the error corrections.

Results on MonteCarlo simulated data show an evident improvement of the reconstruction, and also a reduction of false good reconstructed pixels, which is a well-known problem of the L1-norm inversion application.

The whole process is extremely granularized, in order to be run with strong parallelization granularity and to retrieve a significant reduction of the execution time.

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