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A RESIDUE-PAIRING ALOGRITHM FOR INSAR PHASE UNWRAPPING

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Abstract—Phase unwrapping is a key problem to generate digital elevation maps (DEMs) by synthetic aperture radar (SAR) interferometry. A lot of phase unwrapping algorithms have been proposed to solve this problem. However, in noisy region, many unwrapping algorithms are inoperative because of the denseness of residues. In this paper, we propose a path following phase unwrapping method, namely Residue-Pairing (RP) algorithm. The algorithm starts from residues, based on the aggregate of coordinates of each positive residues (or negative residues), to search the nearest opposite polar residue and connect them. Compared to the Goldstein's algorithm, the brunch cuts produced by this algorithm can effectively decrease their total length and contract the isolated region especially in noisy region. With raw data simulation, the results confirm the validity of RP algorithm in dense-residues region.

1. INTRODUCTION

Interferometric Synthetic Aperture Radar (InSAR) imaging is one of the most important developing direction of Synthetic Aperture Radar (SAR) imaging [1–4]. In SAR interferograms, the phase value of a pixel is a function of the terrain height. SAR imaging is the base of the InSAR imaging, and the image phase is critical to InSAR imaging [5, 6]. For variations in the terrain height above the minimum, the phase value wraps by integer multiples of 2π and ambiguities occur. To extract the information about terrain height from the interferogram, we must resolve this ambiguity and focus on the accuracy of the unwrapping phase.

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By far, various methods to estimate a correct unwrapped phase map have been proposed [7, 8]. There are two types of phase unwrapping methods: Path-following methods and the minimum-norm methods. As local method, the former can restrict the error within certain region. As to the latter, the result got from this method is roughly approximate shape of unwrapped phase, so the error is global transferred. In high noisy region, the phase unwrapping is particular difficult because of the dense residues, which generally results in phase errors. Compared to the minimum-norm method, path-following method is more suitable for the characteristic of local transfer, if the integration path is optimally set.

The Goldstein's algorithm is the classic path-following algorithm [7]. It is extremely fast and generally satisfactory. By examining the branch cuts and determining if any appear to be placed poorly or if any isolate a region, the user can usually determine if the algorithm failed. However, the branch cuts do not always indicate when there are problems. So we need to find a scheme which can avoid isolating a region.

In this paper, we propose a path-following phase unwrapping method, namely Residue-Pairing (RP) algorithm. This algorithm is based on the aggregate of coordinates of each positive residues (or negative residues), and search the nearest opposite polar residue within the window of certain size. The size of the window is increasing along with the searching, like an area with the residue in the middle of it overspreading until meet an opposite polar residue.

It is necessary to first describe the residue theorem for phase unwrapping. And then the basic idea and procedures of the RP algorithm will be presented. At last, we will discuss the performance of RP algorithm and make a compare with the Goldstein's algorithm.

2. RESIDUE THEOREM

In the most general and least-restrictive sense, two-dimensional phase unwrapping is an impossible problem. For example, an unknown phase function φ corrupted by noise and wrapped into the interval $(-\pi, \pi]$ is impossible to recover unambiguously. However, certain assumptions of the underlying process can make the phase unwrapping problem tractable. The most common assumption is that the desired unwrapped phase has local phase derivatives that are less than π radians in magnitude everywhere. We assume that we know the phase

ϕ, modulo 2π, on a discrete grid of points:

$$\begin{aligned} \psi_{i,j} &= \phi_{i,j} + 2\pi k,\ k \text{ an integer} \\ -\pi < \psi_{i,j} &\leq \pi,\ i=0,\ldots,M-1,\ j=0,\ldots,N-1 \end{aligned} \tag{1}$$

where $\psi_{i,j}$ and $\phi_{i,j}$ presents the wrapped and the unwrapped phase respectively at the same grid locations. From the wrapped phase $\psi_{i,j}$ we can compute the following wrapped phase differences:

$$\begin{aligned} &\Delta^x_{i,j} = W\{\psi_{i+1,j} - \psi_{i,j}\}, \quad i = 0,\ldots,M-2,\ j = 0,\ldots,N-1; \\ &\Delta^x_{i,j} = 0,\ \text{otherwise} \end{aligned} \tag{2}$$

and

$$\begin{aligned} &\Delta^y_{i,j} = W\{\psi_{i,j+1} - \psi_{i,j}\}, \quad i = 0,\ldots,M-1,\ j = 0,\ldots,N-2; \\ &\Delta^y_{i,j} = 0,\ \text{otherwise} \end{aligned} \tag{3}$$

We assume that the phase differences of the $\phi_{i,j}$ are less than π in magnitude everywhere. In this case ϕ includes the effect of noise, which may be considered as additive, on the unknown phase φ. The noise is one of the matters that cause phase gradients discontinuous which produce residues. In the process of two-dimensional phase unwrapping, there is a residue theorem

$$\oint \nabla_\varphi(r) \cdot dr = 2\pi \times (\text{sum of enclosed phase residue charges}) \tag{4}$$

It is easy to see that when the residue charges are balanced in a region, the line integral around that region is zero for any simple path chosen [12]. Thus consistent unwrapping is possible only if all integration paths do not encircle unbalance residue charges. Once the residue charges are balanced by connecting the residues of opposite polarity with branch cuts, unwrapping can occur along any path that does not cross branch cut.

As we know, the discontinuous phases result in the residues. The residue density in an interferogram, i.e., the number of residues per sample, increases with phase noise. Residues obviously mark the endpoints of line in the interferogram along which the true phase gradient exceeds $\pm\pi$. These lines are often referred to as 'branch-cuts'.

The phase gradient estimate of Equations (2) and (3) has the advantage that its errors are local and come in integer multiples of 2π. High gradients may either be caused by steep terrain slopes or by decorrelation phase noise. In the first case the branch-cuts follow the terrain discontinuity and may extend over many samples, while in the latter case often only single phase gradient estimates are off by $\pm 2\pi$,

i.e., branch-cuts are only one sample long. In either case every branch-cut carries one positive and one negative residue at its endpoints. Generally, the residues appear in pair except for some singular points.

3. RESIDUE-PAIRING ALOGRITHM

3.1. Basic Concept

In many path-following algorithms, the accuracy of the result depends on the path chosen to perform the unwrapping. Goldstein's branch cut algorithm, the classic path-following algorithm, is effective at generating optimal branch cuts, and it is extremely fast. The idea is to connect nearby residues with branch cuts so that the residues are balanced. Residues can also be balanced by connecting them with branch cuts to the image border.

There are other approaches in addition to Goldstein's for generating the branch cut [13, 14]. These algorithms are restricted to dipole cuts. In contrast to this, Goldstein's algorithm generates more general types of branch cuts that can join the residues in 'clumps' rather than pairs. Thus, in noisy region, the branch cuts produced by Goldstein's algorithm may be completely useless. One case is shown in Figure 1. The phase data for this case is shown in Figure 1(a), and the residues are shown in Figure 1(b). The branch cuts produced by Goldstein's algorithm are shown in Figure 1(c). Goldstein's algorithm is designed to minimize the lengths of the branch cuts by connecting the residues to their nearest neighbors regardless of the quality of the phase values. Its nearest-neighbor strategy is not always the best approach.

To solve this problem, we propose the Residue-Pairing algorithm. The placement of branch cuts is based on the consideration of the

(a) (b) (c)

Figure 1. (a) The wrapped phase, (b) the residues, (c) the branch cuts produced by Goldstein's algorithm.

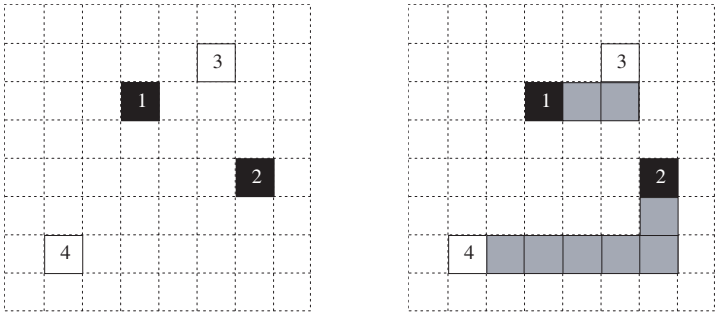


Figure 2. Placement of branch cuts (a) four residues, (b) branch cuts based on RP algorithm.

whole residues. To minimize the sum of the lengths of the cuts, the cuts should connect two opposite polar residues.

And commonly, there are some isolated singular residues left after pairing, because the total charges of whole residues may not be zero. Those residues are connected to the image border finally. For the residues which would be paired, each of them has only one nearest opposite polar residue. However, the nearest one not always is the right one to be connected. Among the whole nearest distances for each residues, those residues which have the shortest distance have the priority to be connect to their nearest opposite residue.

As shown in Figure 2, there are four residues in the image. The dark pixels marked with 1&2 are positive residues. The white pixels marked with 3&4 are negative residues. P_1, P_2, N_3 and N_4 are employed to label those residues respectively. From Figure 2(a), we can find that N_3 is the nearest negative residue to P_1 as well as P_2. Obviously, N_3 can not be connected to two opposite polar residues. One of them must be eliminated. At this moment, the shortest distance to N_3 is used to guide the selection. We select the one which has the shortest distance and place the branch cuts. Thus, P_1 is the one to N_3. The branch cuts based on RP algorithm is shown in Figure 2(b).

From the previous description, we conclude two basic concepts when we place the branch cuts between two residues.

1. The polarities of two residues that connected with branch cuts must be different.
2. Both of the residues that to be connected in pair are the nearest opposite polar residues to each other expect for those which have been connected in pair.

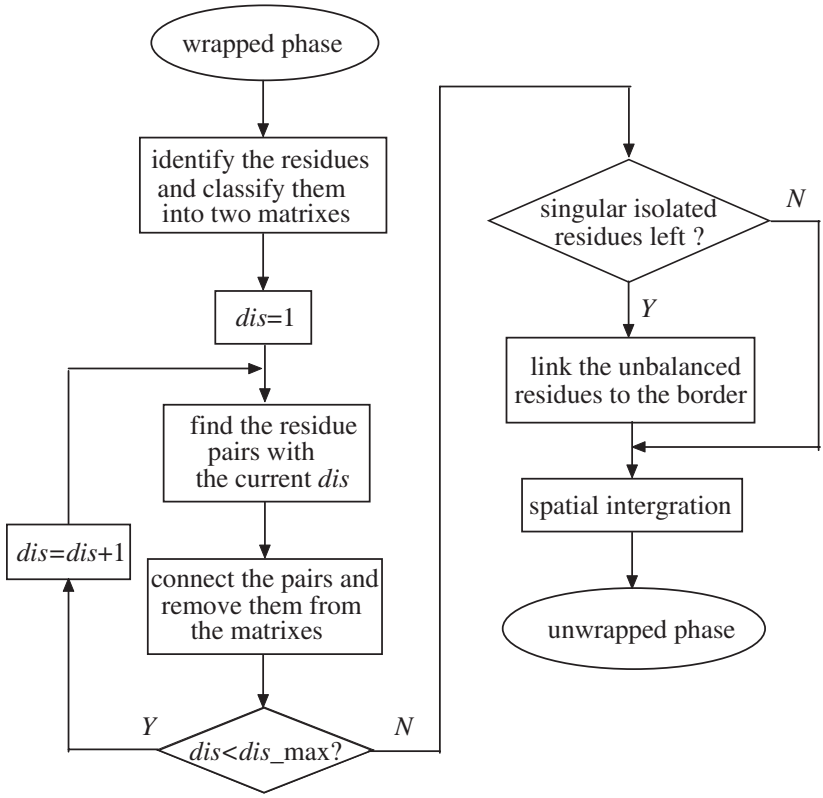


Figure 3. Schematic diagram of RP algorithm.

3.2. Process of RP Algorithm

The key of the RP algorithm is to make sure that the distance of each residue pair to be connected is the nearest among the residues which are not balanced. An additional parameter *dis* which increases step by step is needed to ensure the distance of each residue pair that to be connected is the nearest. A first value for *dis* is required in this algorithm as well as a maximum which we will discuss in the next section.

Since the polarity and coordinates of the residues are necessary information for RP algorithm, two matrixes are needed to place the coordinates of the positive and the negative residues respectively. There must be some singular isolated residues left after the pairing. For those residues we link them to the border of the image finally. Then we can unwrap the phase date after all the residues have been

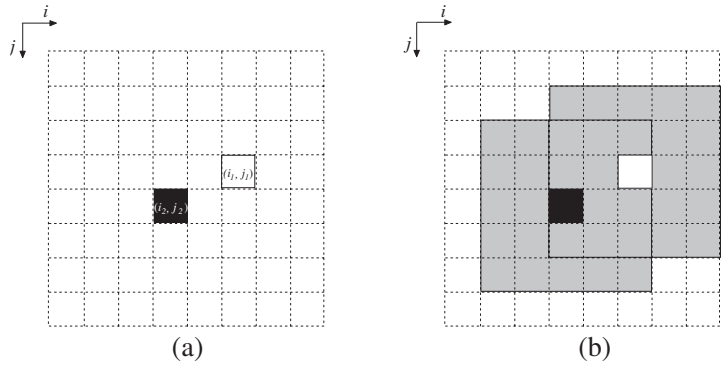


Figure 4. (a) The residue pair, (b) the smallest boxes which centered with each residue and cover another one respectively.

balanced. Figure 3 is a schematic diagram showing the process of the RP algorithm.

3.3. Search Residue Pairs

After the residues identification, we will obtain two matrixes of the coordinates of the residues with opposite polarity respectively. To find nearest residue pairs, an additional parameter *dis* will be used to define current nearest distance.

Now, it is necessary to define how *dis* denotes the distance between two residues (if not mentioned specially, two residues means two opposite polarity residues). The distance of two points generally means the beeline. If we get two residues, (i_1, j_1) and (i_2, j_2), shown in Figure 3(a), the distance would be

$$dis_{1,2} = \sqrt{(i_1 - i_2)^2 + (j_1 - j_2)^2} \tag{5}$$

However, it is not convenient to describe the distance with decimal fraction for the sake of calculation. We choose another function to define the distance

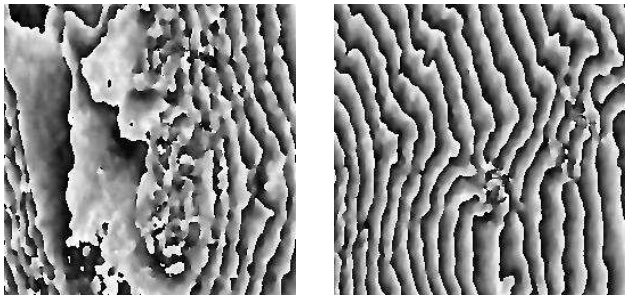
$$dis'_{1,2} = \max(|i_1 - i_2|, |j_1 - j_2|) \tag{6}$$

For the example in Figure 4(a), the $dis'_{1,2}$ is 2 pixels. As shown in Figure 4(b), we can find that the smallest boxes mutually centered with one residue and cover another residue are $(2 \times dis'_{1,2} + 1) \times (2 \times dis'_{1,2} + 1)$ pixels, viz. 5×5 pixels. Thus, it is a new way to comprehend the second basic concept mentioned in Section A.

A first value 1 will be given to *dis*, which means the current nearest distance is 1 pixel. We search the residue pairs with current *dis* from two matrixes and connect them. After that those connected residues should be removed from the matrixes respectively. Thus the current *dis* are not suitable for the rest residues in the matrixes, we need increase the value of *dis*. Each time 1 pixel will be added to the *dis*. However, *dis* requires a maximum threshold, at which point can restrict branch cuts within a proper length. The improper length may result in the encircled region which can not be unwrapped. For a $M \times N$-pixel image we have found that a bound of $\frac{\min(M,N)}{4}$ works well in practice.

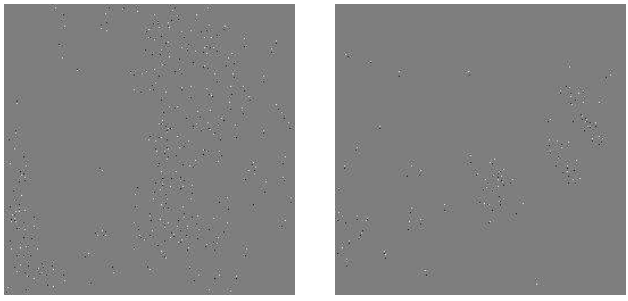
4. RESULTS AND ANALYSES

Once the branch cuts are in place and all the residues are balanced, the phase can be unwrapped along any path that does not cross the branch



(a) (b)

Figure 5. The wrapped phase image.



(a) (b)

Figure 6. The residues maps of Figure 5.

cuts. Many phase unwrapping algorithms which aim at choosing a "good" set of branch cuts encounter difficulty in noisy region. Because there are dense residues, some regions are easily encircled by branch cuts which are not expected. The RP algorithm can solve this problem. In this section, we will compare the performance of RP algorithm with that of the Goldstein's algorithm.

4.1. Raw Data Simulation

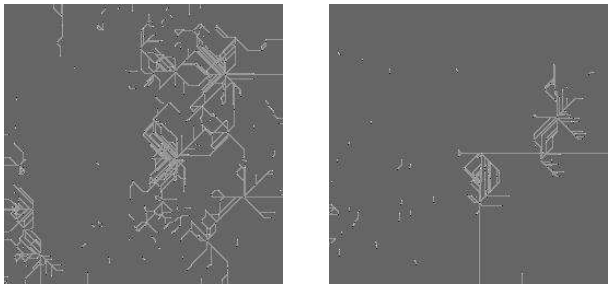
Two images of 256×256 pixels InSAR data reflecting the different density of residues will be employed. Those data are obtained from an E-SAR X-band interferometric phase of Mount Etna. Figure 5 shows the wrapped phase of the two images, and the residues maps of them are shown in Figure 6 respectively. Table 1 shows the residues amounts of those two images. The amount of residues is in an inverse ratio to the quality of the interferometric stripes.

Table 1. The residues amounts of Figure 5.

	Positive residues	Negative residues	Total residues
Figure 5(a)	202	204	406
Figure 5(b)	77	78	155

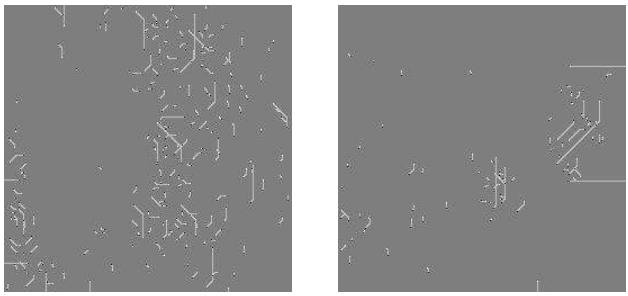
Table 2. The length of branch cuts by using RP algorithm and Goldstein's algorithm.

	Goldstein's	RP
Figure 5(a)	5688	1920
Figure 5(b)	1644	762



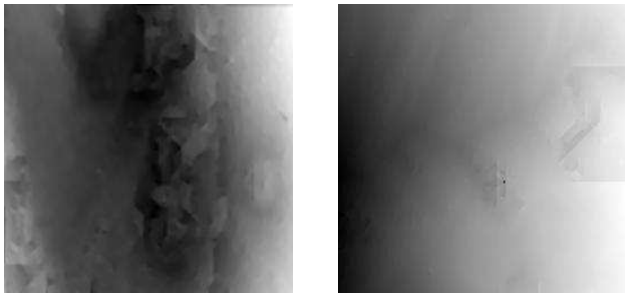
(a) (b)

Figure 7. The branch cuts generated by Goldstein's algorithm.



(a) (b)

Figure 8. The branch cuts generated by RP algorithm.



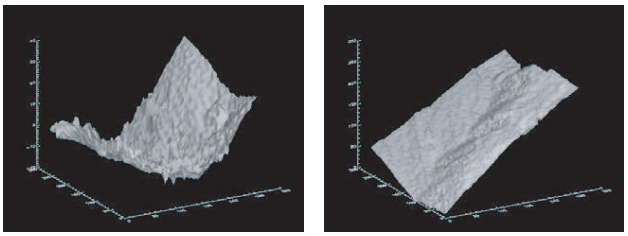
(a) (b)

Figure 9. The unwrapped phase image by RP algorithm.

From the Table 1, we can see that each image contains approximately even amount of the positive and negative residues. It is good for the RP algorithm, because few residues will be left as isolated singular residues after pairing. Figure 7 displays the branch cuts of two images by applying Goldstein's algorithm. Obviously, we can see a mass of isolated region in each image. The branch cuts are confined to the noisy regions which corrupt the unwrapping of the phase. Figure 8 shows the branch cuts generated by RP algorithm. Compare to the results of Goldstein's algorithm, there are scarcely any isolated region in the Figure 8. The lengths of branch cuts by using RP algorithm and Goldstein's algorithm are shown in Table 2. The RP algorithm has a better performance in condensing the length of branch cuts.

From the images in Figure 7 and Figure 8, we can easily find that the branch cuts generated by those two algorithm are almost the same in non-noisy region. For (a), the region is in the left-to-center, while it is in the left for (b). The residues in non-noisy region

usually appear in pairs and the pairs are spread around to each other, so there are no differences to link them together by using those two algorithms. However, in noisy region the residues are dense. When we search for residue, it is natural to find a residue with the same polarity. Then in the Goldstein's algorithm, those two residues will be linked and the search continues which lead to increase the length of the branch cuts. While for the RP algorithm, the residue with the same polarity will be ignored and the search continues until find a residue with opposite polarity. That is why the branch cuts generated by those two algorithms are so different in noisy region. The unwrapped phase images and their 3-D displays are shown in Figure 9 and Figure 10.



(a) (b)

Figure 10. The 3-D display of unwrapped phase by RP algorithm.

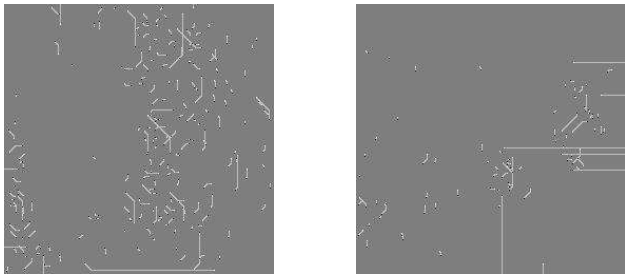
4.2. The Threshold of *dis*

As we have mentioned in the previous section, the optimal threshold of *dis* is $\frac{\min(M,N)}{4}$ for a $M \times N$-pixel image. This threshold determines the amount of isolated singular residues that to be connected to the border of the image. We prefer pairing the residues as many as possible, as well as restricting branch cuts within a proper length.

The threshold, namely *dis*_max, means the longest distance between the residue pairs. If the *dis*_max is too big, the branch cuts that link the residue pairs may cross over the noisy region. It would induce greater chances that generate the encircled regions with the branch cuts that have already been placed. On the other hand, if the length of branch cuts is too long, the unwrapping phases along the both side of branch cut will lack of certain consistency. If the *dis*_max is too small, there are more residues left after pairing. Howeverit is more acceptable for us to connect those extra isolated singular residues in pairs than to the border of the image respectively, because it may increase the total length of branch cuts.

For the simulation in previous section, the *dis*_max we chosen is

64 pixels for the 256 × 256-pixel image. Now, we alter the *dis_*max, 128 pixels for Figure 6(a). and 32 pixels for Figure 6(b). And the final placements of branch cuts are shown in Figure 11. There is a long branch cuts between a residues pair in the underside of Figure 11(a). While in Figure 8(a), two short branch cuts which link to the border of the image instead. Compare Figure 11(b) with Figure 8(b), we can find there are four extra branch cuts that linked to the border of the image in Figure 11(b). Obviously, the lengths of branch cuts in Figure 11 are longer than in Figure 8. Thus a proper threshold of *dis* is very important for the RP algorithm.



(a) (b)

Figure 11. The placement of branch cuts after the alteration of *dis_*max.

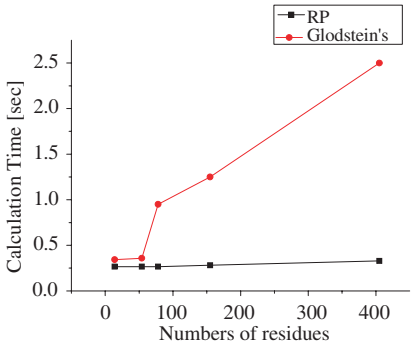


Figure 12. Calculation time versus numbers of residues.

4.3. Calculation Time

Calculation time is another parameter to differentiate unwrapping algorithms. Usually the shorter is the better. We employ five 256×256-

pixel images with different residue density. The number of residues range from 14 to 406. We unwrap them using Goldstein's algorithm and RP algorithm respectively and record the calculation times of branch cuts placements. The results are shown in Figure 12.

The red line and the black line represent the Goldstein's algorithm and the RP algorithm respectively. From the trend of the lines, we can find that the RP algorithm is faster than Goldstein's algorithm. The red line increases sharply when the amount of residues over 70. While the black line climbs gently no matter how many the residues are. The RP algorithm is base on the aggregate of residues which reduces with the removals of residues pairs, while the Goldstein's algorithm needs to search residues through the whole image. The time difference of those two algorithms is increasing with the residues. So in noisy region, the RP algorithm is in the ascendant.

5. CONCLUSION

In this paper we have proposed a path following phase unwrapping algorithm- the RP algorithm. We discuss its basic concepts and the process in detail. Finally several pieces of raw data are employed to verify the validity and the feasibility of this algorithm. Compare to the Goldstein's algorithm, the RP algorithm is good at decreasing the length of branch cuts and contracting the isolated regions. The RP algorithm treats with the aggregate of residues, thus its calculation time is faster than Goldstein's algorithm especially in noisy region.

Additionally, we have also discussed the relationship between the threshold of *dis* and the amount of isolated singular residues. In the RP algorithm, there are unavoidably some isolated singular residues left after pairing. It is not always the best choice to link those residues to the border of the image, because those residues may appear in the middle of the image or the noisy region. In the former case, it produces overlong branch cuts. While in the latter case, it may yield isolated regions with other branch cuts. Both of those two cases are not what we expect, thus how to deal with those isolated singular residues is what we need to study next.

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