



Robust Polarimetric Scatterers Extraction for SAR ATR

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ABSTRACT TITLE

We present a new tool for extracting robust and stable polarimetric scatterers from ground target SAR data with applications to Automatic Target Recognition (ATR). This combination of signal processing algorithms enables us to synthesize the fully polarimetric scatterers information contained in a collection of adjacent SAR images (i.e. looks) and derives the probabilities for individual (or groups of) scatterers to be active and stable over a certain observation angle for the target under test. It is based on an autofocus polarimetric version of the CLEAN-RELAX algorithm, which is followed by a tracking on both the position and polarimetric information of the extracted scatterers over some angular extension (or separate looks). A sub-pixel autofocus and a local relaxation is embedded in the algorithm to achieve a better extraction. Residual translations between focused looks are then estimated through a simple correlation scheme or using the following scatterers tracking. Individual extracted scatterers are tracked from one look to another using a matching criteria based both on the distance and the fully polarimetric magnitudes. We then derive the most probable target signature, which may be used as template for classification purposes. This process may also be very useful when working with target variants, in order to define which part of the target may remain stable and potentially useful for the classification stages. Moreover, this makes a tremendous information compression, which becomes mandatory when working with large data collections. We show an application of the technique on a real dataset that was provided by Qinetiq to Nato SET 053 group for ATR evaluation purposes.

1.0 INTRODUCTION

Synthetic Aperture Radar (SAR) images are highly dependent on target aspect, they contain speckle and not clear edge maps, all of which makes traditional classifiers that compare target signature intensities with references not very efficient. Intensity variations cause significant changes in the image correlation between test and train set. Some studies have worked on the use of local maxima (peaks or elementary scatterers) as classification features, but such features seem quite sensitive to target variations and, furthermore, different targets may have very similar peaks distribution. The four channel polarimetric peaks information can be added to better characterize and separate the target signatures among each other [9]. We propose to increase the robustness of these features by working on "stable" peaks that remain active on a wide angular aspect angle with almost unchanged polarimetric properties. Such peaks bear a stronger probability to be characteristic of the scattering of major parts of the target, which makes them less sensitive to targets variants and, by definition, to aspect angle errors that could be made in the a priori target orientation detection for instance.

We propose to find these stable scatterers by applying several signal processing algorithms to a collection of SAR images (or "looks") representing the target signature over a wide aspect angle (typically up to 10°), each look being coherently formed over a smaller angular aperture. This may correspond to the situation where a radar does some spotlight imaging over a given target.

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Most of these algorithms are original or give polarimetric extensions to existing ones. The analysis is made in three major steps. First, we extract the peaks location and their polarimetric information in each look. This first stage separates the target elementary scatterers from the clutter response: a polarimetric extension of the CLEAN/RELAX peak extraction algorithm is derived to extract both the position and polarimetric magnitudes of elementary peaks within the resolution cells. This iterative processing also includes an embedded "autofocus" to compensate for any sub-pixel residual error done while forming the SAR image. We call "hyperlook" the result of this extraction, i.e. the spatial positions $(X_i, Y_i)_{i=1:N}$ and polarimetric magnitudes¹ $A_i = (A_i^{HH}, A_i^{HV}, A_i^{VH}, A_i^{VV})_{i=1:N}$ of the N extracted peaks. Each hyperlook forms a concise description of the polarimetric target signature at a specific aspect angle. In a second step, we apply a feature-matching algorithm on pairs of hyperlooks through a graduated assignment technique that we have adapted to take into account both the spatial and a "polarimetric" distance between peaks. This algorithm finds the possible connection between a peak (X_i, Y_i, A_i) in one hyperlook and a peak (X_i, Y_i, A_i) in another; this matching scheme is optimized on a one to one basis while preserving the possibility for an "unstable" peak not to connect. In this procedure, we also estimate the residual translation between the different looks and compensate for it. Then, the result of this matching procedure enables us to derive the stability of the individual extracted scatterers by looking at the connection map for each peak and build the most stable peaks distribution that can be used as template for classification purposes.

We will show the application of the major steps of the proposed analysis scheme on real SAR data and its evaluation on a simple classification test.

2.0 POLARIMETRIC STABLE SCATTERERS EXTRACTION

2.1 Autofocus Polarimetric CLEAN/RELAX algorithm

In classical radar imaging, the basic assumption lays in the ideal bright points model (or canonical peaks) of elementary scatterers that compose the scene to be imaged: the discrete data model is usually written as a set of N complex sinusoids with "frequencies" $(X_k, Y_k)_{k=1,\dots,N}$ and amplitude A_k in noise e.

$$H(K_{x},K_{y}) = \sum_{k=1}^{N} A_{k} e^{j(K_{x}X_{k}+K_{y}Y_{k})} + e(K_{x},K_{y})$$
(1)

and the image I(X,Y) is then the 2D spectra of the formatted radar data $H(K_x, K_y)$ with $K_x = 4\pi f \sin\theta/c$ and $K_y = 4\pi f \cos\theta/c$, with frequency f in the radar bandwidth Δf and observation angle θ within $\Delta \theta$. In Synthetic Aperture measurements the angle θ is linked to the observation time T through the relative motion of the target and the radar.

Under this assumption, the extraction problem matches the signal processing formulation of superresolution. An extended analysis of the various spectral estimation methods that can be used is given, from a signal processing view in [1], and applied to SAR imaging in [2]. However, most of the methods require an *a priori* knowledge or estimation of the number of reflectors, which deeply limits their application to SAR imaging and features extraction.

Unlike these, the CLEAN/RELAX algorithm [3][4][5] is an asymptotically statistically efficient estimator that minimizes the following nonlinear least squares criterion:

$$C(X_{k}, Y_{k}, A_{k}, M)_{k=1, \dots, M} = |H - \hat{H}_{M}|^{2}$$
with $\hat{H}_{M} = \sum_{k=1}^{M} A_{k} e^{j(K_{k}, X_{k} + K_{k}, Y_{k})}.$
(2)

¹ H stands for horizontal polarisation, V for vertical ; first letter for emission second for reception



One advantage is that the number of elementary peaks is estimated within the algorithm. CLEAN belongs to a family of iterative methods, which, within each iteration, search for the biggest peak in a complex image and subtract its complex contribution in its corresponding Fourier spectrum. RELAX basically extends the CLEAN algorithm with a relaxation step. See [3][4][5] for a more detailed description of both algorithms and their implementation.

2.1.1 CLEAN/RELAX architecture

CLEAN is a deconvolution technique that can be summarized in the following steps :

- Find the brightest point in the image
- Measure the complex amplitude and the location of the brightest point
- Form a new image by subtracting ("cleaning") the complex contribution of this point in the Fourier spectra of the image
- Repeat the procedure on the next brightest peak, and so on.
- Stop the procedure when the power of last extracted scatterer is below a chosen level or the noise (clutter) level is reached.

The RELAX algorithm simply add a secondary CLEAN cycle to each peak close to a newly estimated one: each peak contribution is then estimated taking into account its neighbourhood by forgetting ("uncleaning") previous estimations and re-estimating them one by one. This adds some robustness to the extraction at the price of an increased computer load.

Adaptation of the CLEAN algorithm to polarimetric data is rather straightforward. Rather than using CLEAN on each polarimetric channel, which would need to reconnect extracted peak between channels, we propose to work on the polarimetric span image I^{span} to first estimate the location of the brightest peak at each step:

$$\mathbf{I}^{\text{span}} = \sqrt{\left(I^{HH}I^{HH^*} + I^{HV}I^{HV^*} + I^{VH}I^{VH^*} + I^{VV}I^{VV^*}\right)}$$
(3)

with I^* being the complex conjugate of I.

Then, the peak magnitude can be measured in each channel separately, and so is done the cleaning process.

2.1.2 Adding autofocus to the peak extraction

Refined image focusing is often neglected although it deeply influences the extraction quality. The image patches we are dealing with are often extracted from larger scene for which an average focusing has been done (presumably up to the radar resolution cell). But small residual motion errors create phase shifts that may slightly distort the peaks response: these errors will eventually be cumulated through the cleaning stage of the CLEAN/RELAX algorithm. In the presence of such errors $\delta R(\theta)$, the data model equation (1) becomes:

$$H(f,\theta) = \sum_{k=1}^{N} A_{k} e^{j4\pi f(X_{k} \sin\theta + Y_{k} \cos\theta + \delta R(\theta))/c} + e(f,\theta)$$
(4)

For rather small frequency bandwidth, angular aperture, and residual errors, this can be approximated at first order to:



$$H(K_{x},K_{y}) = \sum_{k=1}^{N} A_{k} e^{j(K_{x}X_{k}+K_{y}Y_{k})} e^{j\phi(K_{x})} + e(K_{x},K_{y})$$
(5)

This shows that residual errors will mainly distort the cross-range components of the image $I(X, Y) = FT[H(K_x, K_y)]$.

The least square criterion (2) has then to be changed to:

$$C(X_{k}, Y_{k}, A_{k}, M, \varphi)_{k=1, \dots, M} = |H(K_{k}, K_{y}) e^{j\varphi(K_{x})} - \hat{H}_{M}(K_{x}, K_{y})|^{2}$$
(6)

The solution of this problem can be wrapped into the CLEAN/RELAX architecture as shown in [6] and [7]. At each CLEAN extraction step, we obtain an estimation of the phase distortion via:

$$e^{j\hat{\phi}(K_{x})} = \sum_{K_{y}} H^{*}(K_{x}, K_{y}) \hat{H}(K_{x}, K_{y})$$
(7)

which we use to correct the entry data for a completely new CLEAN/RELAX cycle.

When working with polarimetric data, the focusing can be done on each channel separately in case of phase centre mismatch between the different channels.

The autofocus is turned off when the induced changes or the estimated phase variations fall below a certain level.

2.1 Graduated assignment algorithm and softassign

We have applied the polarimetric CLEAN/RELAX extraction on a set of L successive SAR looks. As a result we now have L sets of extracted scatterers described using their position and polarimetric magnitude $[X_i^t, Y_i^t, A_i^t]_{i=1:N_i; l=1:L}$ which we call "hyperlooks". We know want to link the scatterers information over the various aspect angles. But even at nearby aspects, features may shift, disappear or appear: we wish to find a correspondence between two sets of extracted scatterers where some may be missing, added or displaced, in the presence of a global residual translation between the two sets. We also wish a one to one matching. Note that a coarse estimation of the global translation can be found through the spatial correlation of the two reconstructed images once we have applied the known relative rotation between looks. We will use a matching algorithm proposed by Meth in [11] which use a method developed by Gold & al. in [12] and [13] called graduated assignment, which is based on works made in [14][15] and called "softassign".

The graduated assignment technique is a specialized method of efficiently finding good suboptimal solutions for optimization problem that use a match matrix to explicitly denote an assignment between one set of objects and another. Match matrix is a 0-1 matrix with 1 denoting that a given point in one set is assigned to a given point in the other set. Graduated-nonconvexity is used to turn these discrete variables into continuous ones in order to reduce the chances of getting trapped in local minima. Technique is iterative, where at each step, an estimate of the match matrix is made and then "softassign" is used to ensure that the match matrix remains the continuous analog of a true assignment. Softassign is a method employed to satisfy assignment constraints: one feature in one image can match to at most one feature in the other. In practice, one can show that it can be done by an iterative process of alternatively normalizing the rows and columns.

Let us consider two hyperlooks $[X_i^1, Y_i^1, A_i^1]_{i=1:N_i}$ and $[X_j^2, Y_j^2, A_j^2]_{j=1:N_2}$ corresponding up to a translation (t_x, t_y) . A match matrix $M_{i:i}$ is defined such that $M_{i:i} = 1$ if point *i* in first look corresponds to point *j* in



the second look, and 0 otherwise. Up to this point note that the match matrix is a kind of permutation matrix. An extra row and column are added to the match matrix $M_{i:j}$ to hold the slack variable in order to handle spurious or missing links: $M_{i:N_2+1} = 1$ if peak *i* is an outlier, 0 otherwise and $M_{N_1+1:j} = 1$ if point *j* is an outlier, 0 otherwise. $M_{i:j}$ is then a $N_1 + 1$ by $N_2 + 1$ matrix.

An objective function is then formulated [11]&[12]:

$$E(M_{i;j}, t_{x}, t_{y}) = \sum_{i=1}^{N_{i}} \sum_{j=1}^{N_{2}} M_{i;j} \times D_{i;j}(t_{x}, t_{y}) - \alpha \sum_{i=1}^{N_{i}} \sum_{j=1}^{N_{2}} M_{i;j} + \sum_{i=1}^{N_{i}} \mu_{i} \left(\sum_{j=1}^{N_{i}+1} M_{i;j} - 1 \right) + \sum_{j=1}^{N_{2}} \nu_{j} \left(\sum_{i=1}^{N_{i}+1} M_{i;j} - 1 \right) + \frac{1}{\beta} \sum_{i=1}^{N_{i}+1} \sum_{j=1}^{N_{i}+1} M_{i;j} \left(\log M_{i;j} - 1 \right)$$
(8)

With $D_{i:j} = \sqrt{\left(X_i^1 - X_j^2 - t_x\right)^2 + \left(Y_i^1 - Y_j^2 - t_y\right)^2}$ the square Euclidean distance. We modify this distance to take into account the polarimetric dimension. Let us define the normalized polarimetric scalar product as:

$$PSP(A_1, A_2) = \frac{\sqrt{(A_1^{HH} A_2^{HH^*} + A_1^{HV} A_2^{HV^*} + A_1^{VH} A_2^{VH^*} + A_1^{VV} A_2^{VV^*})}{A_1^{span} A_2^{span}}$$
(9)

PSP is closed to 1 if peaks have similar polarimetric response and 0 if the polarimetric scattering mechanisms are completely uncorrelated. Then we can replace $D_{i,j}$ by $D_{i,j}/PSP(A_i^1, A_j^2)$ in (8) to get an objective function that takes both the spatial distance and polarimetric distance into account. Then peaks that are spatially close may not connect if their polarimetric response is very different. The first term in the cost function (8) is then a spatio-polarimetric distance measurement of connected peaks once they have been compensated for the residual translation. The second term is added to encourage the match within a tolerance distance controlled by parameter α . The third and fourth terms contain Lagrange multipliers for the raw and column sums: this imposes the two-way constraints for one to one matching. Last term permits the translation of the problem from a binary formulation to a continuous [0,1] interval: it is similar to a barrier function. This smoothing function pushes the minimum of the objective away from discrete local minimal points by making the objective more convex, with the convexity control parameter β (similar to a relaxation temperature) that may be adjusted to slowly move the matrix closer to 0-1 values.

Minimum of the objective function may then be found by choosing a sequence of increasing β and minimizing the objective at each step. Minimization is done with respect to the matrix elements $M_{i,j}$ and Lagrange multipliers μ_i and ν_i by setting the respective partials to zeros. Minimization with respect to Lagrange parameters is called softassign, which turns to be a simple alternate normalization of the rows and columns of the estimated objective function $\hat{M}_{i,j} = \exp(-\beta \times D_{i,j}(X_i^1, X_j^2, Y_i^1, Y_j^2, \hat{t}_x, \hat{t}_y)/PSP(A_i^1, A_j^2) - \alpha)$.

Please refer to [11] and [12] for a more detailed description of the algorithm implementation.

3.0 AUTOMATIC TARGET RECOGNITION APPLICATION

We will go through the steps described in the first section and see how it can be applied to real SAR data that were provided by QINETIQ UK.

For the demonstration matter, we have taken 3 sets of SAR images, composed each of 5 looks corresponding to the observation of two different targets at the same angular aspect (azimuth and depression angle), target 1 being observed twice in two sets artificially named "test set" and "train set" (see figures 1 to 3). Looks are separated by 2° so the overall rotation is about 10°. Note that the two targets have almost the same size and look roughly similar to the eye.





Figure 1: Target 1 test set raw looks (HH: red; HV/VH: green; VV: blue).



Figure 2: Target 1 train set raw looks.



Figure 3: Target 2 train set raw looks.

We then have extracted the elementary scatterers for each look (see figures 4 to 6). Please note that superresolution by factor 2 was used when reconstructing the images in figures 4 to 6 to allow a better distinction of the individual extracted peaks. Using the graduate assignment we have found the connection maps between peaks of each set. We then have looked for the peaks that were connected in at least three looks over the five, and we have rebuilt their corresponding image (figure 7): we clearly see the similarities of polarimetric stable peaks in the first two sets, while the third one has a quite different distribution. If we finally try to match the stable peaks between the three different sets, we have a 70 to 80% matching (depending on the polarimetric distance level we choose) between the first two, i.e. from same class, and only 15 to 20% matching with the third one (other class).





Figure 4: Target 1 test set: hyperlooks (polar. peaks extraction result of figure 1).



Figure 5: Target 1 train set: hyperlooks of figure 2.



Figure 6: Target 2 train set: hyperlooks of figure 3.



Figure 7: Most stable peaks for target 1 test set (left) target 1 train set (middle) & target 2 train set (right).

We have repeated this experiment using four different targets with about 25 separated "5 looks test sets" (360° round) per target. Each set being tested against all the other targets for the similar observation angles. We are then able to build ROC curves giving the Percentage of Correct Classification against the Percentage of False Alarm obtained using different classification features. We have tested two features: the first one is the maximum of the raw looks image correlation and the second one is the stable



polarimetric scatterers matching percentage obtained using our algorithms. Results are shown figures 8 and 9 and show the advantage of using the stable scatterers rather than the raw image correlation: mean behaviour (dash curve) is almost 20% higher at any PFA level.



Figure 8: ROC curve for classification using maximum of raw look image correlation (Xcoordinate: Percentage of False Alarm; Y-coordinate: Percentage of correct classification).



Figure 9: ROC curve for most stable polarimetric scatterers matching (X-coordinate Percentage of False Alarm; Y-coordinate Percentage of correct classification).

4.0 CONCLUSION

We have presented some new signal processing tools that can be applied to polarimetric SAR images of targets. The autofocus polarimetric CLEAN/RELAX algorithm is useful to precisely extract the



elementary scatterers from the clutter background. Then an assignment method is able to achieve a fine peak matching taking polarimetry into account. We have shown their possible application to extract the most stable polarimetric scatterers from a sequence of SAR raw images, which can be used as a characteristic template for classification purposes. We guess they can have many other usages, such as target analysis, SAR image enhancement ... A more extensive analysis of the scatterers stability within the possible target variants could be investigated using such algorithms.

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