Parallel Algorithm and Hybrid Regularization for Dynamic PET Reconstruction
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Abstract—To improve the estimation at the voxel level in dynamic Positron Emission Tomography (PET) imaging, we propose to develop a convex optimization approach based on a recently proposed parallel proximal method (PPXA). This class of algorithms was successfully employed for 2D deconvolution in the presence of Poisson noise and it is extended here to (dynamic) space+time PET image reconstruction. Hybrid regularization defined as a sum of a total variation and a sparsity measure is considered in this paper. The total variation is applied to each temporal-frame and a wavelet regularization is considered for the space+time data. Total variation allows us to smooth the wavelet artifacts introduced when the wavelet regularization is used alone. The proposed algorithm was evaluated on simulated dynamic fluorodeoxyglucose (FDG) brain data and compared with a regularized Expectation Maximization (EM) reconstruction. From the reconstructed dynamic images, parametric maps of the cerebral metabolic rate of glucose (CMRglu) were computed. Our approach shows a better reconstruction at the voxel level.

I. INTRODUCTION

The extraction of physiological parameters at the voxel level (parametric imaging) is a challenging problem in dynamic PET imaging (space+time). In [1], [2], [3] the authors demonstrated the advantage of taking into account time-frame characteristics during the reconstruction for improving the image quality and the physiological parameter estimation. More recently, the space+time information was used by considering wavelet-frame decompositions [3], [4], [5]. To efficiently deal with such representations, the criterion to minimize often involves a \( \ell_1 \)-norm (regularization term) which leads to a non-differentiable problem. New convex optimization algorithms (within the class of proximal methods) have been developed in [6], [7] aiming at minimizing criteria which are non-necessarily differentiable. The first application combining wavelet-frame representations and proximal algorithms in dynamic PET image reconstruction was suggested by Verhaeghe et al. [3] by considering Forward-Backward (FB) iterations [6] to minimize a criterion involving a Gaussian data fidelity term and a wavelet spline regularization. In [5], the authors performed Temporal Activity Curves (TAC) denoising in the sinogram space before reconstruction by using the Douglas-Rachford (DR) algorithm so as to deal with a Kullback-Leibler divergence as a data fidelity term, which is well-adapted to Poisson noise. To perform simultaneously denoising and reconstruction with wavelet regularization, we previously designed in [8] a nested iterative algorithm (FB-DR algorithm). This method allowed us to improve the reconstruction quality, but its two main drawbacks were (i) a high computational time due to the required subteration and (ii) the presence of artifacts introduced by wavelet regularization. To tackle these problems, we consider in this paper a more recent algorithm called Parallel ProXimal Algorithm (PPXA) [9] which is well-adapted to dynamic PET due to (i) its parallel structure and (ii) the possibility of dealing with hybrid regularization such as the combination of a wavelet-frame penalty and a total variation measure [10]. This method was presented for image deblurring applications in the presence of Poisson noise [11] and its application to dynamic PET is now investigated.

This paper is organised as follows. First, we will present the considered degradation model and the criterion we aim at minimizing. Then, convex optimization tools such as the proximity operator and PPXA will be introduced. The main technical difficulty in this work consists of computing the proximity operator of the data fidelity term. A solution to overcome this difficulty will be proposed. Finally, numerical experiments will be provided by considering simulated and real dynamic PET \([^{18}\text{F}]\)-FDG exams.

II. PROBLEM

We consider a finite parameterization of the original image denoted by \( \mathbf{y}_t = (\mathbf{y}_{i,t})_{1 \leq i \leq N} \) which corresponds to the spatial activity distribution for a time-frame \( t \). These data are observed through the linear system associated with the matrix \( \mathbf{A} = (A_{j,i})_{1 \leq j \leq M, 1 \leq i \leq N} \) where each element \( A_{j,i} \) represents the probability for a voxel \( i \) to be detected in the tube of response (TOR) \( j \). Moreover, during the acquisition process, data are contaminated by Poisson noise. The effect of the noise is denoted by \( \mathcal{P} \). The dynamic PET data \( \mathbf{z}_t = (z_{j,i})_{1 \leq j \leq M} \) are related to the original images by the following degradation model:

\[
(\forall t \in \{1, \ldots, T\}) \quad \mathbf{z}_t = \mathcal{P}(\mathbf{A}\mathbf{y}_t) \quad (1)
\]

where \( T \) denotes the number of time-frame. The reconstruction process requires to find the finite parameterization \( \hat{\mathbf{y}} = (\hat{y}_t)_{1 \leq t \leq T} \) closest to \( \mathcal{P} = (\mathbf{y}_t)_{1 \leq t \leq T} \) from the measured data \( \mathbf{z} = (z_t)_{1 \leq t \leq T} \).

In order to perform this task, we consider a variational formulation where the criterion is made up of a data fidelity term related to Poisson noise, a hybrid regularization term...
algorithm known as PPXA [9] allows us to relax the Lipschitz assumption and to solve any minimization problem formulated as

$$\hat{x} \in \text{Argmin}_{x \in \mathbb{R}^L} \sum_{q=1}^Q f_q(x)$$

where $Q \in \mathbb{N}^+$ and where $(f_q)_{1 \leq q \leq Q}$ are convex, lower semi-continuous and proper functions from $\mathbb{R}^L$ to $]-\infty, +\infty]$. The iterations are recalled in Algorithm 1.

Algorithm 1 General form of PPXA

1. Set $\gamma \in [0, +\infty[$.
2. For every $q \in \{1, \ldots, Q\}$, set $(\omega_q)_{1 \leq q \leq Q} \in [0, 1]^Q$ such that $\sum_{q=1}^Q \omega_q = 1$.
3. Set $(u_{q,0})_{1 \leq q \leq Q} \in (\mathbb{R}^L)^Q$ and $x_0 = \sum_{q=1}^Q \omega_q u_{q,0}$.
4. For $n = 0, 1, \ldots$
   - 4a) For $q = 1, \ldots, Q$
     - $p_{q,n} = \text{prox}_{\gamma f_q} u_{q,n}$
   - 4b) $p_n = \sum_{q=1}^Q \omega_q p_{q,n}$
   - 4c) Set $\lambda_n \in [0, 2]$
   - 4d) For $q = 1, \ldots, Q$
     - $u_{q,n+1} = u_{q,n} + \lambda_n (2p_n - x_n - p_{q,n})$
   - 4e) $x_{n+1} = x_n + \lambda_n (p_n - x_n)$

The convergence of the sequence $(x_n)_{n \in \mathbb{N}}$ generated by Algorithm 1 to a solution $\hat{x}$ of (3) is established under the following assumption.

Assumption III.1

(i) $\lim_{x \to +\infty} f_1(x) + \ldots + f_Q(x) = +\infty$.
(ii) $\bigcap_{q=1}^Q \text{Int dom } f_q \neq \emptyset$.
(iii) $\sum_{n \in \mathbb{N}} \lambda_n (2 - \lambda_n) = +\infty$.

The main difficulty of this algorithm lies in Step 4a) which requires to compute the proximity operator of each function $f_q$. Fortunately, for a large class of functions, this operator takes a closed form [14]. For example, the $\ell_1$-norm proximity operator corresponds to a soft-thresholding. The way to proceed with $tv$ is detailed in [9]: it results that $tv$ can be split in a sum of four functions, denoted by $(tv_i)_{1 \leq i \leq 4}$ when Haar filters are considered. However, a remaining difficulty in using this algorithm for dynamic PET reconstruction is to obtain an explicit form at Step 4a) for $D_{KL}(z_t, A)$. Consequently, we assume that for every $r \in \{1, \ldots, R\}$, $\mathbb{I}_r$ is a partition of $\{1, \ldots, M\}$ in nonempty sets. Additionally, we can write $D_{KL}(z_t, \cdot)$ as a sum of $M$ functions $\Psi_j(t) : \mathbb{R} \to [-\infty, +\infty]$ operating on each $j$-th component $z_{j,t}$ of $z_t$. By regrouping the terms in this sum such that $j \in \mathbb{I}_r$ (for every $r \in \{1, \ldots, R\}$), $\Psi_j(t) = \sum_{j \in \mathbb{I}_r} \Psi_{j,t}(z_{j,t})$. $D_{KL}(z_t, A)$ can be decomposed as a sum of $R$ functions involving reduced-size linear operators $A(r) = (A_{j,i})_{i \in \mathbb{I}_r, 1 \leq i \leq N}$ containing non-overlapping and thus orthogonal rows of $A$. For every $r \in \{1, \ldots, R\}$, $\mathbb{I}_r$ denotes a set of TOR involving distinct pixels. The resulting PPXA iterations are detailed in Algorithm 2.

1Let $\varphi : \mathbb{R}^X \to [-\infty, +\infty]$ be a convex, l.s.c. and proper function, $\text{dom } \varphi = \{u \in \mathbb{R}^X \mid \varphi(u) < +\infty\}$ and the interior of $C \subset \mathbb{R}^X$ relative to its affine hull is the set denoted by $\text{rint } C$.
Algorithm 2 PPXA for dynamic PET reconstruction

1) Set $\gamma \in [0, +\infty[$.
2) Set $\omega_1 = \ldots = \omega_R = \frac{1}{3R}$, $\omega_{R+1} = \ldots = \omega_{R+4} = \frac{1}{16}$ and $\omega_{R+5} = \omega_{R+6} = \frac{1}{4}.
3) Set, for every $q \in \{1, \ldots, R + 6\}$, $u_{q,0} = Fz$ and $x_0 = \sum_{q=1}^{R+6} \omega_q u_{q,0}.$
4) For $n = 0, 1, \ldots$
   4a) For $t = 1, \ldots, T$
      \[ p_{r,t,n} = \text{prox}_{\gamma \omega_k A} \left( u_{r,n} \right) \]
      \[ p_{R+1,t,n} = \text{prox}_{\gamma \omega_k \mathcal{V} \varphi} \left( u_{R+1,n} \right) \]
      \[ p_{R+2,t,n} = \text{prox}_{\gamma \omega_k \mathcal{V} \varphi} \left( u_{R+2,n} \right) \]
      \[ p_{R+3,t,n} = \text{prox}_{\gamma \omega_k \mathcal{V} \varphi} \left( u_{R+3,n} \right) \]
      \[ p_{R+4,t,n} = \text{prox}_{\gamma \omega_k \mathcal{V} \varphi} \left( u_{R+4,n} \right) \]
      \[ p_{R+5,n} = \text{prox}_{\gamma \omega_k \mathcal{V} \varphi} \left( u_{R+5,n} \right) \]
      \[ p_{R+6,n} = \text{prox}_{\gamma \mathcal{C} \mathcal{F}} \left( u_{R+6,n} \right) \]
   4b) Set $n = \sum_{q=1}^{R+6} \omega_q p_{q,n}.$
   4c) Set $\lambda_n \in [0, 2[$
   4d) For $q = 1, \ldots, Q$
      \[ u_{q,n+1} = u_{q,n} + \lambda_n \left( 2p_n - x_n - p_{q,n} \right) \]
   4e) $x_{n+1} = x_n + \lambda_n \left( p_n - x_n \right)$

IV. MATERIALS AND METHODS

A. Simulated data

The method was evaluated on simulated 2D+time data, using one slice of the Zubal brain phantom [15]. A two compartment model with $k_4 = 0$ was used to simulate a dynamic [18F]-FDG brain study, with 16 time frames with a duration varying between 30 seconds for the first time-frames to 5 minutes for the last ones. Moreover, small local variations of $k_i$ were created in the cortex and putamen (see Figure 2, top-left). 288 (radial) × 144 (angles) sinograms with a radial sampling of 2.247 mm were simulated by analytically projecting the phantom and adding Poisson noise. Attenuation, random and scattered coincidences were not simulated in this example. The number of events varies from 48 for the first time-frame to 26804 for the last time-frame.

The PPXA algorithm is implemented in parallel with the OpenMP library and run over 400 iterations of 10s each. The relaxation parameter is here equal to $\lambda_n \equiv 1$ and the stepsize is $\gamma = 6.10^5$. The system matrix is split in $R = 432$ subsets and the function number is $Q = R + 6$. The chosen separable orthonormal wavelets correspond to symmlet filters of length 6 over 3 resolution levels of spatial decomposition. PPXA 1 refers to our approach without temporal regularization and PPXA 2 considers a two-level decomposition with Daubechies-6 wavelets on the interval for temporal decomposition [16]. The latter choice is motivated by the small number of time-frames and aims at avoiding boundary effects. The constraint on the data range is $C \in [0, 10^3] \cdot Bq/cc$. The chosen regularization parameters are $\kappa = 0.1$ and $\vartheta = 10^{-5}$. A limited value of the parameter $\vartheta$ was chosen so as to avoid “cartoon effects”. The proposed solution without temporal regularization in PPXA 1/PPXA 2 is compared with EM-ML and EM-ML with post-smoothing (Sieves). SIEVES 1 denotes a Gaussian filtering optimized to yield the minimum MSE and SIEVES 2 uses a Gaussian kernel leading to a similar noise level than our approach. For EM-ML and SIEVES 1/2, the iteration number is 250. A full width at half maximum (FWHM) of 12 mm x 12 mm (resp. 14 mm x 14 mm) is used for SIEVES 1 (resp. SIEVES 2).

B. Pre-clinical data

We also processed real data resulting from a [18F]-FDG exam on the ecat HR+ scanner (Siemens medical solutions, Knoxville, TN, USA). 284 MBq were injected to a 4.5 kg baboon. The injection was done under camera. A dynamic acquisition was performed with septa extended. The prompt and delayed coincidences were registered separately in 16 frames with a duration varying from 1.5 minutes to 4 minutes. The global exam duration was 54 minutes. Transmission was realized before injection by a rotative source of germanium 57.

We reconstructed prompt data by considering three different approaches: filtered backprojection (FBP), EM-ML reconstruction with Gaussian (12 mm x12 mm FWHM) post-filtering (Sieves) and our approach (PPXA). During the reconstruction process, attenuation effects, normalization effects, and random coincidences have been taken into account. However, scattered coincidences have not been considered (this choice is justified by the septa extended). The system matrix used for SIEVES and PPXA does not model resolution (PSF) effects.

V. RESULTS

A. Simulated data

Figures 1 and 2 display the reconstruction results for different temporal-frames ($t = 4$: 1.5-2 min and $t = 7$: 8-13 min). During first frames when the noise level is particularly high, PPXA 2 restores quite well the brain activity even if artifacts can be observed (for example in the thalamus area).

Table I compares the normalized MSE for different areas of interest such as the cortex, the thalamus and the striatum. It can be observed that PPXA 2 leads to the smallest normalized MSE for the first frames and equivalent normalized MSE for the last ones.

Figures 3, 4, and 5 represent Temporal Activity Curves for individual pixels in different area of interest. This allows us to evaluate the impact of the spatio-temporal reconstruction and the good results obtained with PPXA 2.

Using Pmod software (PMOD Technologies Ltd, Zürich, CH), parametric images of CMRglu were computed from the EM-ML, Sieves, and PPXA reconstructions. The results are shown in Figure 6. The differences between the CMRglu images is not as much important as the TAC results or the reconstructed images. This is mainly due to the Patlak model which essentially uses the last frames for CMRglu computation, which are less sensitive to noise.
Fig. 1. Reconstructed images (in Bq/cc) for \( t = 4 \).

Fig. 2. Reconstructed images (in Bq/cc) for \( t = 7 \).

Fig. 3. TAC in the thalamus.

Fig. 4. TAC in the cortex.

Fig. 5. TAC in the striatum.

Table I

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<th>Thalamus</th>
<th>Striatum</th>
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</table>
B. Pre-clinical data

Figure 7 shows the reconstructed images obtained with the different reconstruction methods for temporal-frames $t = 4$ (4-6 min), $t = 7$ (14-18 min), and $t = 14$ (42-46 min). These results illustrate the good behaviour and the quantitative correctness of the proposed method on real data.

VI. CONCLUSION

We have presented a convex optimization approach to deal with spatio-temporal PET reconstruction. The minimized criterion is composed with different terms: generalized Kullback-Leibler divergence (minus Poisson log-likelihood) term, $\ell_1$-norm for wavelet-based regularization, total variation and dynamic range constraint. To minimize efficiently this criterion, we employed PPXA which is a recent algorithm belonging to the class of proximal methods. The convergence of this algorithm is guaranteed and it is implementable in parallel.

The effectiveness of the proposed approach was demonstrated on simulated and real pre-clinical data.

REFERENCES


