Reconstruction of Short Time PET Scans Using Bregman Iterations

Jahn Müller, Christoph Brune, Alex Sawatzky, Thomas Kösters,
Klaus P Schäfers, Martin Burger

Abstract—We propose a method for reconstructing data from short time positron emission tomography (PET) scans, i.e data acquired over a short time period. In this case standard reconstruction methods deliver only unsatisfactory and noisy results. We incorporate a priori information directly in the reconstruction process via nonlinear variational methods. A promising approach was the so-called EMTV algorithm, where the negative log-likelihood functional, which is minimized in the expectation maximization (ML-EM) algorithm, was modified by adding a total variation (TV) term. To improve the results and to overcome the issue of the loss of contrast we extend the algorithm by an inverse scale space method using Bregman distances, to which we refer as BREGMAN EMTV algorithm. The methods are tested on short time (5 and 30 seconds) FDG measurements of the thorax. We can show that the EMTV approach can effectively reduce the noise, but still introduces an oversmoothing, which is eliminated by the BREGMAN EMTV method, obtaining a reconstruction of comparable quality to the corresponding long time (20 and 7 minutes) scan. This correction for the loss of contrast is necessary to obtain quantitative PET images.

I. INTRODUCTION

IN many applications of positron emission tomography one has to deal with reconstructions from few data. In particular, this is the case when one only a small amount of coincidence events is available, for instance due to tracers with a short radioactive half-life (e.g. radioactive water $H_2{}^{15}O$), a low tracer dose or a short scan time. The latter one is of particular interest, since for instance in the task of motion correction, the whole scan time is divided into short time frames (so-called gates) , which have to be reconstructed separately (e.g. [1]). Also in dymanic PET imaging one has to deal with short time frames.

In the cases above standard reconstruction methods like filtered backprojection or the expectation maximization (ML-EM) algorithm deliver unsatisfactory and noisy results. To improve the reconstruction one would like to make an efficient use of a priori information. Therefore nonlinear variational methods are incorporated into the reconstruction process. A promising approach was the so-called EMTV algorithm [2], [3], [4], where the negative log-likelihood functional, which is

minimized in the ML-EM algorithm, was modified by adding a total variation (TV) term.

TV regularization, first introduced as the so-called ROF model in [5] for image denoising, is already extensively studied in image processing and it is well known that it suppresses noise effectively while preserving sharp edges. The ROF model for denoising an image g is given by

$$\underset{f \in BV(\Omega)}{\arg \min} \left\{ \frac{1}{2} \int_\Omega (f - g)^2 dx + \alpha |f|_{TV} \right\}, \qquad (1)$$

where $|f|_{TV}$ denotes the so called total variation seminorm:

$$|f|_{TV} := \sup_{\substack{\varphi \in \mathcal{C}_0^\infty(\Omega)^d \\ ||\varphi||_\infty \le 1}} \int_\Omega f \nabla \cdot \varphi \, dx. \qquad (2)$$

If f is sufficiently smooth, (2) can be formally rewritten as

$$|f|_{TV} := \int_\Omega |\nabla f| dx. \qquad (3)$$

Unfortunately, TV suffers from a systematic error, namely a loss of contrast in the images. This effect can also be seen in the EMTV algorithm and hence, we propose to extend the algorithm by an inverse scale space method using Bregman distances (cf. [6]) to overcome this issue. This approach has already been successfully applied in optical nanoscopy, where the raw data are also corrupted by Poisson noise [7].

II. METHODS

The basic problem arising in PET reconstruction can be written as

$$Kf = g$$

where g are the measurements outside the body, f is the unknown distribution of the tracer inside the body and K is the PET system matrix. The penalized Maximum Likelihood (ML) estimation then leads to the following variational problem:

$$\underset{f \ge 0}{\arg \min} \int \underbrace{(Kf - g \log Kf)}_{\text{distance measure}} + \alpha \underbrace{R(f)}_{\text{regularization}}, \qquad (4)$$

with the so-called Kullback-Leibler divergence as distance measure, a regularization functional $R(f)$ and a parameter α controlling the strength of regularization.

In the absence of regularization (i.e. $\alpha = 0$), the iterative standard reconstruction scheme for solving (4) is the well known ML-EM algorithm (cf. [8]):

$$f_{k+1} = f_k \frac{K^*}{K^*1} \left(\frac{g}{Kf_k} \right).$$

Applying total variation regularization to emission tomography is not new (cf. [9], [10]). However, there were some issues in computing the minimizer of the functional

$$\arg\min_{f \geq 0} \int (Kf - g \log Kf) + \alpha |f|_{TV} \qquad (5)$$

using the exact definition of the total variation seminorm (2).

A. EMTV

Sawatzky et al proposed in 2008 a nested two step algorithm, which solves the minimization problem (5) in a robust and efficient way [3]. The first step of each iteration is a simple EM iteration step and the second one solves a weighted ROF model:

EM step:

$$f_{k+\frac{1}{2}} = f_k \frac{K^*}{K^*1} \left(\frac{g}{Kf_k} \right)$$

TV step:

$$f_{k+1} = \arg\min_{f \in BV(\Omega)} \left\{ \frac{1}{2} \int_\Omega \frac{K^*1(f - f_{k+\frac{1}{2}})^2}{f_k} + \alpha |f|_{TV} \right\}$$

Note, that the TV step differs from the original ROF model (1) only by the weighting $\frac{K^*1}{f^k}$. Although this approach leads to quite good results (i.e. the noise is well suppressed, while the edges are preserved), we can observe a strong loss of contrast in the reconstructed images (see Fig. 1 (c) and Fig. 3 (c)).

B. BREGMAN EMTV

To overcome the issue of the loss of contrast, we apply the Bregman iteration (cf. [6]) to our problem and hence obtain the following minimization problem:

$$f^{l+1} = \arg\min_{\substack{f \in BV(\Omega) \\ f \geq 0}} \left\{ \int (Kf - g \log Kf) + \alpha D^{p^l}_{|\cdot|_{TV}}(f, f^l) \right\}$$

where the regularization term is the Bregman distance between f and the previous iteration f^l, defined by

$$D^{p^l}_{|\cdot|_{TV}}(f, f^l) = |f|_{TV} - |f^l|_{TV} - \langle p^l, f - f^l \rangle,$$

with p^l being a subgradient of the total variation seminorm at f^l, (i.e. $p^l \in \partial |f^l|_{TV}$). For any fixed $l \in \mathbb{N}$ the minimization can be realized by a slightly modified ROF model and an additional outer iteration with an update variable v.

EM step:

$$f^{l+1}_{k+\frac{1}{2}} = f^{l+1}_k \frac{K^*}{K^*1} \left(\frac{g}{Kf^{l+1}_k} \right)$$

TV step:

$$f^{l+1}_{k+1} = \arg\min_{f \in BV(\Omega)} \left\{ \frac{1}{2} \int_\Omega \frac{K^*1(f - (f^{l+1}_{k+\frac{1}{2}} + f^{l+1}_k v^l))^2}{f^{l+1}_k} \right.$$
$$\left. + \alpha |f|_{TV} \right\}$$

Update:

$$v^{l+1} = v^l - \left(1 - \frac{K^*}{K^*1} \left(\frac{g}{Kf^{l+1}} \right) \right).$$

(a) 20 min - ML-EM   (b) 5 sec - ML-EM
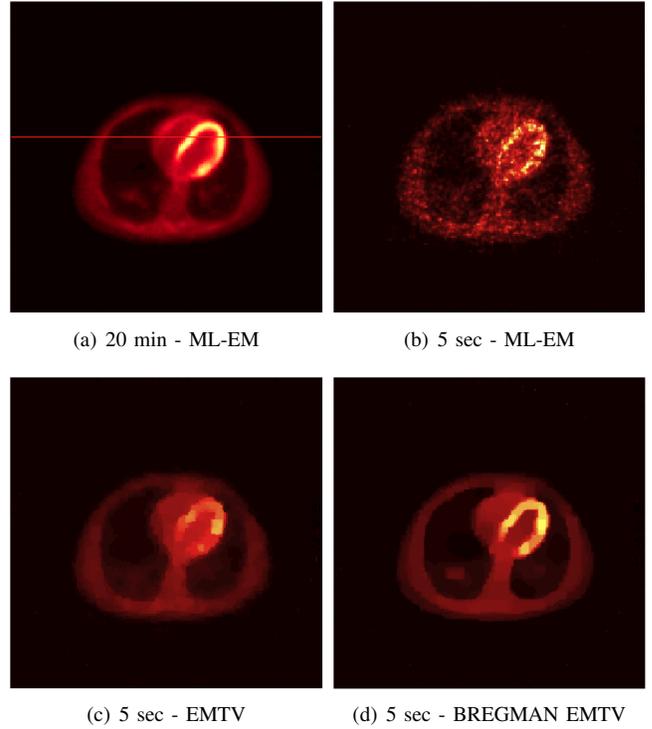
(c) 5 sec - EMTV   (d) 5 sec - BREGMAN EMTV

Fig. 1. 2D slices of F-FDG^{18} reconstructions. (a) 20 minutes of data reconstructed with 20 ML-EM iterations (reference image) (b) as (a) but only 5 seconds of data (c) reconstructed with the EMTV algorithm, 20 iterations, $\alpha = 0.025$ (d) reconstructed with the BREGMAN EMTV algorithm, 7 Bregman iterations, each with 15 inner EMTV iterations and $\alpha = 0.004$.
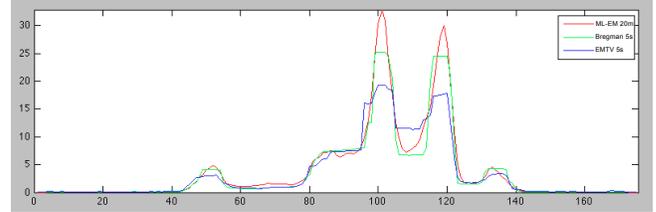

Fig. 2. Line profile through images from Fig. 1 (a), (c), (d) indicated by the red line in Fig. 1 (a).

This method can be seen as an inverse scale space method, with a stepwise refinement of the iterates f^l. We refer to this algorithm as BREGMAN EMTV algorithm (cf. [7], [4] , [11]) .

C. Implementation

Since for both EMTV and BREGMAN EMTV the TV step solves a slightly modified ROF model, this part can be efficiently computed via a primal dual quasi Newton method which in addition is also parallelizable [12]. The ML-EM reconstructions as well as the EM step in the proposed methods are performed with EMRECON [13].

In the BREGMAN EMTV algorithm a fixed number of inner iterations is performed (e.g. 15) and the outer iteration is stopped before to small scales reappear in the reconstruction (for more details see [14]). The number of outer iterations depends heavily on the regularization parameter α. For a large α the refinement steps are much smaller and hence many outer

iterations have to be performed until the reappearance of the small scales. For a small α one has coarser refinement steps and hence needs less outer iterations. It seems, that choosing α such that the algorithm stops after 5-10 BREGMAN iterations is a good trade-off between computation time and the quality of the results.

III. RESULTS

The proposed methods are tested on F-FDG[18] measurements acquired by a Siemens Biograph Sensation 16 PET/CT scanner which is located at the University Hospital of Münster.

As a first example we used a ML-EM reconstruction of a 20 minutes PET acquisition of the thorax as reference image (Fig. 1 (a)). To simulate data from a short time scan, as it may arise due to gating in motion correction, we use only data from the first five seconds of the aquisition. These are reconstructed with the standard ML-EM algorithm, leading to a noisy image, although it was smoothened with a Gaussian kernel at each 10th iteration step (Fig. 1 (b)).

The images in Fig. 1 (c) and (d) show the results of the EMTV and the BREGMAN EMTV algorithm, respectively. One observes that the EMTV approach can effectively reduce the noise, but still introduces oversmoothing at the myocardium. This oversmoothing and the resulting loss of contrast is eliminated by the BREGMAN EMTV method (see the line profile in Fig. 2), obtaining a reconstruction of comparable quality to the 20 minutes scan.

As a second example a reconstruction of a 7 minutes PET aquisition of the thorax was used as reference image. In the slice shown in Fig. 3 (a), a hot lesion is well visible, which is nearly undistinguishable from the noise in the ML-EM reconstruction of the 30 seconds data aquisition (Fig. 3 (b)). Although the EMTV algorithm suppresses the noise very well, the lesion is still hardly recognizable due to the loss of contrast (Fig. 3 (c)). However, with the proposed BREGMAN EMTV method the lesion becomes clearly visible (Fig. 3 (d)). The compensation for the loss of contrast is also very well visible in a line profile through the lesion (Fig. 4).

(a) 7 min - ML-EM   (b) 30 sec - ML-EM

(c) 30 sec - EMTV   (d) 30 sec - BREGMAN EMTV

Fig. 3. 2D slices of F-FDG[18] reconstructions. (a) 7 minutes of data reconstructed with 20 ML-EM iterations (reference image) (b) as (a) but only 30 seconds of data (c) reconstructed with the EMTV algorithm, 20 iterations, $\alpha = 0.25$ (d) reconstructed with the BREGMAN EMTV algorithm, 5 Bregman iterations, each with 15 inner EMTV iterations and $\alpha = 0.02$.

Fig. 4. Line profile through images from Fig. 3 (a), (c), (d) indicated by the red line in Fig. 3 (a).

REFERENCES

[1] F. Büther et al, "List mode-driven cardiac and respiratory gating in PET," *Journal of Nuclear Medicine*, vol. 50, pp. 674–681, 2009.

[2] A. Sawatzky, C. Brune, J. Müller, and M. Burger, "Total variation processing of images with Poisson statistics," in *Proc. 13th Int. CAIP Conference*, ser. CS. Springer, 2009, pp. 533–540.

[3] A. Sawatzky, C. Brune, F. Wübbeling, T. Kösters, K. Schäfers, and M. Burger, "Accurate EM-TV algorithm in PET with low SNR," in *IEEE NSS/MIC Conference Record*, 2008, pp. 5133–5137.

[4] A. Sawatzky, "(Nonlocal) total variation in medical imaging," Ph.D. dissertation, Institute for Computational and Applied Mathematics, University of Münster, 2011.

[5] L. I. Rudin, S. Osher, and E. Fatemi, "Nonlinear total variation based noise removal algorithms," *Phys. D*, vol. 60, pp. 259–268, 1992.

[6] S. Osher, M. Burger, D. Goldfarb, J. Xu, and W. Yin, "An iterative regularization method for total variation-based image restoration," *Multiscale Model. Simul.*, vol. 4, no. 2, pp. 460–489, 2005.

[7] C. Brune, A. Sawatzky, and M. Burger, "Primal and dual Bregman methods with application to optical nanoscopy," *Int. J. Comput. Vis.*, vol. 92, pp. 211–229, 2011.

[8] L. A. Shepp and Y. Vardi, "Maximum likelihood reconstruction for emission tomography," *IEEE Trans. Med. Imaging*, vol. 1, no. 2, pp. 113–122, 1982.
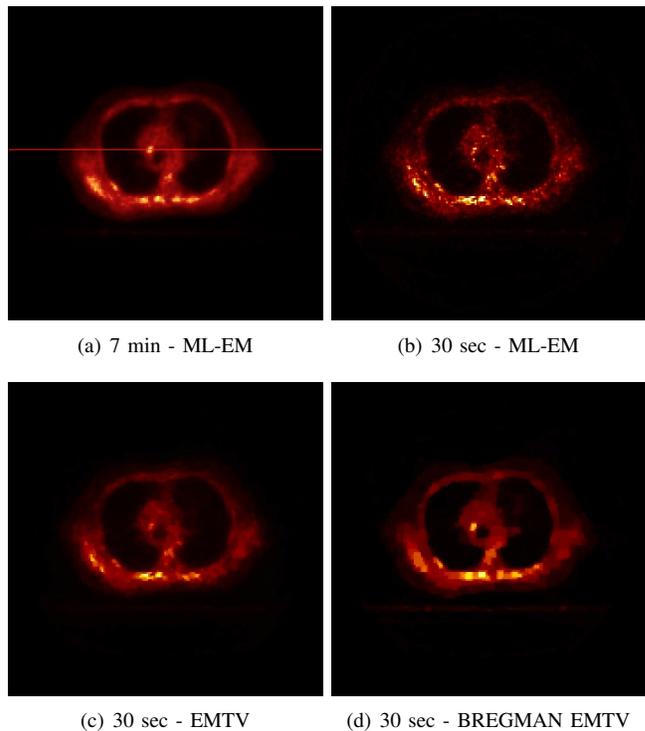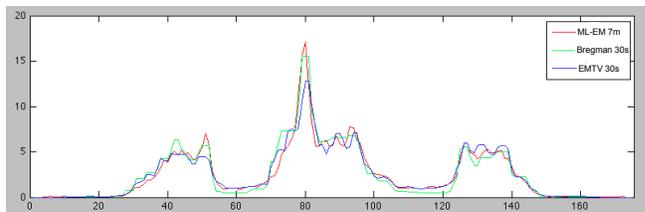
[9] V. Y. Panin, G. L. Zeng, and G. T. Gullberg, "Total variation regulated EM algorithm [SPECT reconstruction]," *IEEE Trans. Nucl. Sci.*, vol. 46, no. 6, pp. 2202–2210, 1999.

[10] E. Jonsson, S. C. Huang, and T. Chan, "Total variation regularization in positron emission tomography," UCLA, CAM Report 98-48, 1998.

[11] C. Brune, A. Sawatzky, and M. Burger, "Bregman-EM-TV methods with application to optical nanoscopy," in *Proceedings of the 2nd International Conference on Scale Space and Variational Methods in Computer Vision*, ser. LNCS, vol. 5567. Springer, 2009, pp. 235–246.

[12] J. Müller, "Parallel total variation minimization," Master's thesis, Institute for Computational and Applied Mathematics, University of Münster, 2008.

[13] T. Kösters, K. Schäfers, and F. Wübbeling, "EMRECON: An expectation maximization based image reconstruction framework for emission tomography data," in *IEEE NSS/MIC Conference Record*, 2011.

[14] M. Burger, G. Gilboa, S. Osher, and J. Xu, "Nonlinear inverse scale space methods," *Comm. Math. Sci.*, vol. 4, no. 1, pp. 179–212, 2006.