

# **Real-Time PET Tomographic Image Reconstruction Based on the Pseudo-Inverse of System Matrices**

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# INTRODUCTION

- Real-time Positron Emission Tomography (PET) has been proposed in recent years [1], but it requires very fast data processing and reconstruction methods.
- The process can be speeded-up by rebinning the acquired data in the axial dimension into a stack of 2D datasets before the image reconstruction.
- 2D datasets can be reconstructed with standard analytical methods
- **Single Slice ReBinning (SSRB)** [2] is the most straightforward method to perform axial rebinning. It can be used for real time PET, but it is only accurate for centered sources.
- FOurier Rebinning (FORE) Is an accurate alternative to SSRB but it is not fast enough.
  - We propose using the **Pseudoinverse (PINV)** [2-5] of the axial part of the System Response Matrix (SRM) to obtain fast but accurate images. 2D datasets can be reconstructed also with PINV methods or with standard Filtered Backprojection (FBP)

# METHODS

# **SYSTEM RESPONSE MATRIX**

- PET data (Y) and reconstructed images (X) are related by the SRM A:  $Y = A \cdot X$
- The SRM contains the probability that a emission from a voxel of the image creates a coincidence in a pair of crystals.
- In this work, we used a model of the preclinical PET-CT scanner SUPERARGUS [9] and the clinical PET-CT scanner Biograph mCT[10].



#### **AXIAL SRM**

- The whole 3D SRM for a PET scanner is too large to be handled directly in current computers.
- We dvide the reconstruction into axial rebinning and

### **PSEUDOINVERSE**

- If the reconstruction problem is considered a linear least squares method (LLSM), the solution can be obtained with the Pseudoinverse A<sup>+</sup> of the SRM [7]  $X=Y \cdot A^+$
- ThePseudoinverse of a matrix can be obtained using its Singular Value Decomposition (SVD):

 $A = U \cdot S \cdot V^T \to A^+ = V \cdot S^+ \cdot U^T$ 

- U and V are orthonormal matrices and S is a diagonal matrix which elements (s) are known as singular values of A. S<sup>+</sup> contains the reciprocal elements of S (1/s) or 0 if s is 0 as well.
- PET data is noisy and without a proper regularization of the reconstruction problem, that noise leads to reconstructed images far away from the original.
- **Tikhonov regularization** can be described in terms of SVD, changing the reciprocal singular values to  $s^+ = 1$ •  $\frac{s}{s^2+k}$  with k a small regularization parameter.
- There is a connection between the results obtained using the pseudoinverse of a matrix and linear iterative methods such as the SART [8]. SART with n<sub>iter</sub> iterations provide similar results to Tikhonov with k=1/n<sub>iter</sub>.

## **RECONSTRUCTION WITH THE PINV**

 $2DA^+(x,y;\rho,\theta) \times Sinogram(\rho,\theta,z_1,z_2) \times AxialA^+(z_1,z_2;z) = Reconstructed Image(x,y,z)$ 

reconstruction of the resulting transverse slices. We focus this work in the axial rebinning of the problem using the PINV of the axial part of the SRM.



# RESULTS













Table 1. Approximated computing times for the different rebinning methods studied in this work. These times were computed using FORTRAN in a CPU E5-2640 v4 @ 2.40 GHz processor.

| Reconstruction<br>Method | Time (s) |
|--------------------------|----------|
| FBP                      | 4        |
| PINV                     | 1        |

Table 2. Approximated computing times for the different 2D reconstruction methods studied in this work. These times were computed using FORTRAN in a CPU E5-2640 v4 @ 2.40 GHz processor.



Fig 2. Noise vs resolution recovery for different rebinning methods, including SSRB, FORE and PINV studied over point sources simulated in a scanner with the geometry of Biograph mCT scanner. The curves for PINV represent the axial resolution vs recovery for a different number of equivalent iterations. Far from the transaxial center of the scanner SSRB is not accurate while FORE is still good enough. PINV keep its resolution recovery with no great changes in the whole FOV.



Fig 1. Transverse (up) and Saggital (down) view different reconstructed image of a real acquisition of a rat with FDG using SUPERARGUS scanner. Comparative between SSRB+FBP (left) with PINV+FBP (middle) and PINV+2DPINV (right).

#### **SUMMARY AND CONCLUSIONS**

- Pseudoinverse-based rebinning methods outperform SSRB in terms of resolution for non-centered sources.
- Pseudoinverse methods provide an accurate data rebinning and they can be implemented for real time applications, while other methods such as FORE are not fast enough.
- Pseudoinverse 2D image reconstruction is an accurate alternative to FBP and can provide similar results even in less computational time.

#### REFERENCES

[1] J.M. Arco, J.M.Udias, J.L.Herraiz, M.Desco, J.L.Longas, R.Matesanz, J.J.Vaquero. Real Time PET on a Preclinnical Scanner. WMIC 2015 [2] S.R.Cherry. Physics in Nuclear Medicine (Elsevier).

[3] J.Sánchez-González, S. España, M.Abella, J.J. Vaquero, E.Lage, J.Pascau, M.Desco. Quasi pseudo-inverse reconstruction for rotating PET scanners IEEE NSS/MIC 2005.

[4] J.L.Herraiz, J.J.Vaquero, J.M. Udias. FBP reconstruction of sinograms with gaps based on the inversion of a perturbed matrix. IEEE 2011. [5] V.V. Selivanov, R.Lecomte Fast PET image reconstruction based on SVD decomposition of the system matrix. [6] S. España, J L Herraiz, E Vicente, J J Vaquero, M Desco and J M Udias. PeneloPET, a Monte Carlo PET simulation tool based on PENELOPE: features and validation, *Phys. Med. Biol.*54 1723-1742

[7] Gene H. Golub et al Matrix Computations.

[8] A.H. Andersen, A.C. Kak.Simultaneous algebraic reconstruction technique (SART): a superior implementation of the art algorithm. [9]http://www.sedecal.com

[10] https://www.healthcare.siemens.es/molecular-imaging/pet-ct/biograph-mct

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