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A modified likelihood distribution for bias reduction in low-statistics PET

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Overview

- Introduction
  - Reconstruction in PET
  - Bias in MLEM
- Bias reduction
  - NEGML
  - AML
- Experiments
  - Simulation
  - Reconstruction
  - Evaluation
- Results
- Conclusion

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Reconstruction in PET

Filtered back projection **FBP**	**Maximum likelihood expectation maximization MLEM**
+ Fast + Bias-free	– Slow – Positive bias (cold regions and noisy data)
– Only basic 'ideal' model (no resolution model) – No priors	+ More complex model (with e.g. resolution effect) + Based on Poisson model (reduced noise) + Priors

MLEM often superior image quality + less partial volume effects

FBP often used for dynamic studies

Bias in MLEM

1. ***Cold regions:*** activity dependent convergence

$$\Delta\lambda_j = \frac{\lambda_j}{\sum_i c_{ij}} \sum_i c_{ij} \frac{y_i - \hat{y}_i}{\hat{y}_i}$$

$$\hat{y}_i = \sum_i c_{ij}\lambda_j + r_i$$

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Bias in MLEM

2. ***Cold regions + noisy data***: non-negativity constraint in image

TRUE

1	1	1	1	1	1
1	0	0	0	0	1
1	0	0	0	0	1
1	0	0	0	0	1
1	0	0	0	0	1
1	1	1	1	1	1

Mean cold region = 0.00

FBP

Negative values allowed

1	1	1	1	1	1
1	0.32	-0.16	-0.31	0.33	1
1	-0.29	-0.12	0.43	-0.23	1
1	0.09	0.10	-0.05	-0.17	1
1	-0.47	0.23	0.01	0.29	1
1	1	1	1	1	1

Mean cold region = 0.00
Std cold region = 0.27

MLEM

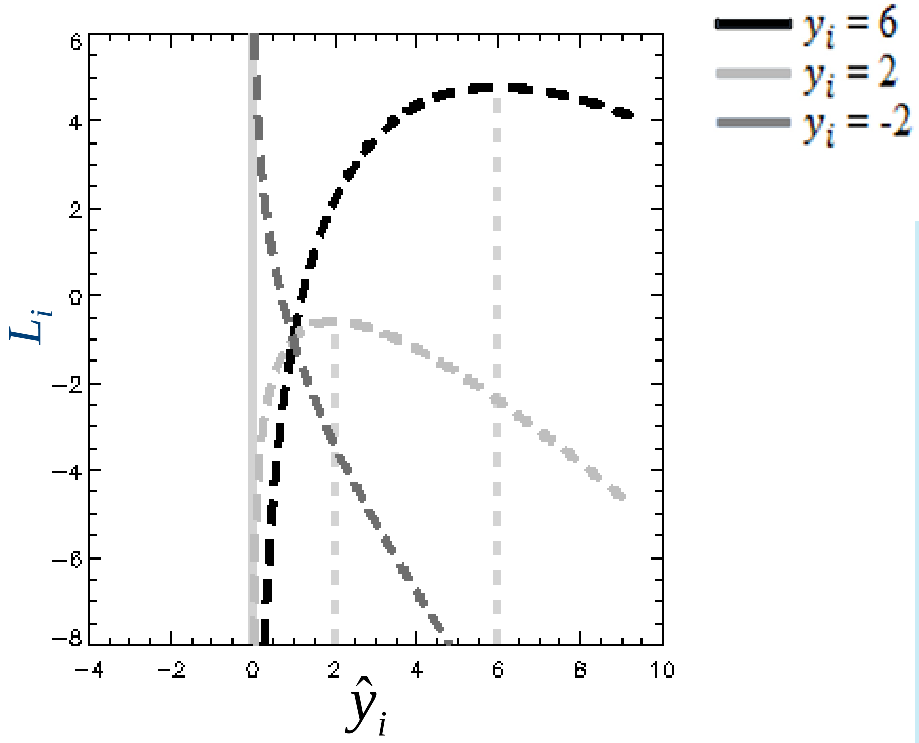
No negative values allowed

1	1	1	1	1	1
1	0.07	0.03	0.05	0.06	1
1	0.04	0.02	0.12	0.03	1
1	0.05	0.07	0.01	0.09	1
1	0.01	0.10	0.02	0.03	1
1	1	1	1	1	1

Mean cold region = 0.05
Std cold region = 0.03

Bias in MLEM

3. *Noisy data*: asymmetry of the Poisson likelihood



$$L = \sum_i L_i = y_i \ln \hat{y}_i - \hat{y}_i$$

Possible explanation:

The likelihood = gamma distribution

$$Gamma(\hat{y}_i | \alpha, \beta)$$

with $\alpha = \hat{y}_i + 1$ and $\beta = 1$

The maximum of this function is y_i
The mean is $y_i + 1$

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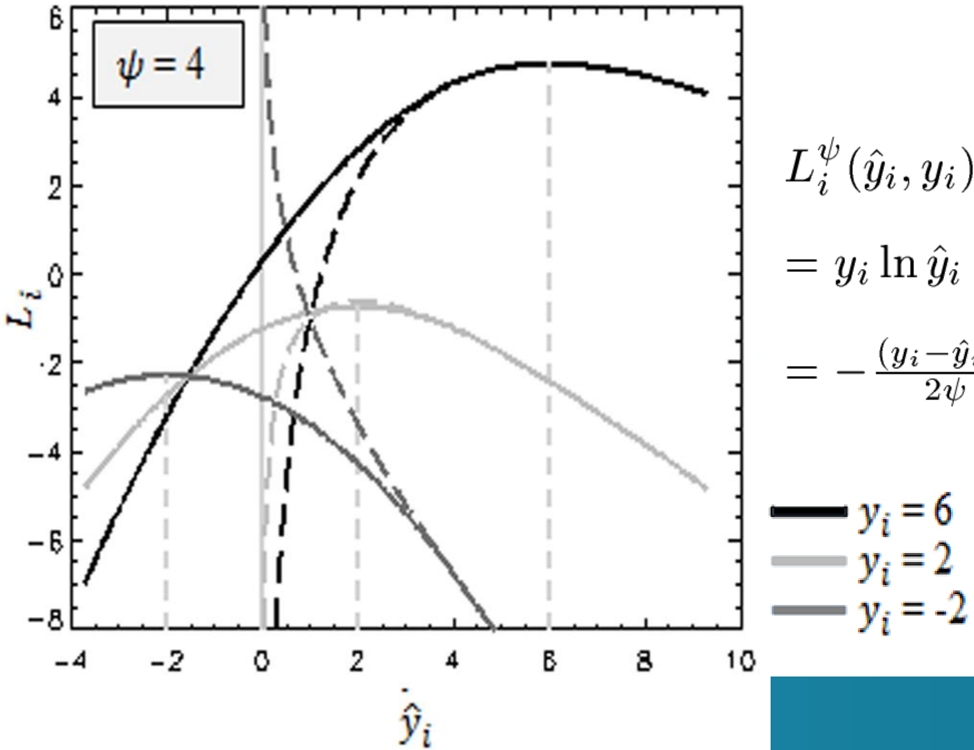
NEGML algorithm

- Modified likelihood
  - Poisson for large values
  - Gaussian for low values (symmetric + defined for negative sinogram values)



$$L_i^{\psi}(\hat{y}_i, y_i)$$

$$= y_i \ln \hat{y}_i - \hat{y}_i \qquad \text{when} \quad \hat{y}_i \geq \psi$$

$$= -\frac{(y_i - \hat{y}_i)^2}{2\psi} + y_i \ln \psi - \psi + \frac{(y_i - \psi)^2}{2\psi} \qquad \text{when} \quad \hat{y}_i < \psi$$

NEGML algorithm

- Modified likelihood
  - Poisson for large values
  - Gaussian for low values (symmetric + defined for negative sinogram values)
- Negative image voxel values are allowed
- Update not activity dependent (due to gradient ascent likelihood optimization)

$$\Delta\lambda_j = \frac{\sum_i c_{ij} \frac{y_i - \hat{y}_i}{\max(\psi, \hat{y}_i)}}{\sum_i c_{ij} \frac{\sum_k c_{ik}}{\max(\psi, \hat{y}_i)}}$$

<u>Note</u>: extension of existing NEGML algorithm[(1)], created to obtain more quantitative data without attenuation correction

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(1) J. Nuyts et al. "Reducing loss of image quality due to the attenuation artifact in uncorrected PET whole body images." Journal of Nuclear Medicine, 43, pp. 1054-1062, 2002.

AML algorithm

ABML[2] :

- A_j lower bound for voxel j + bound $\sum_j c_{ij} A_j$ in sinogram
- B_j upper bound for voxel j + bound $\sum_j c_{ij} B_j$ in sinogram

Modified version: AML

- Single lower bound A
- Upper bound $B \longrightarrow \infty$

$$\Delta\lambda_j = \frac{\lambda_j - A}{\sum_i c_{ij}} \left(\sum_i c_{ij} \frac{y_i - \hat{y}_i}{\hat{y}_i - A \sum_k c_{ik}} \right)$$

<u>Intuitive interpretation</u>: sinogram and image are shifted towards higher values

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(2) C. Byrne. *"Iterative algorithms for deblurring and deconvolution with constraints.", Inverse Problems 14, pp. 1455-1467, 1998.*

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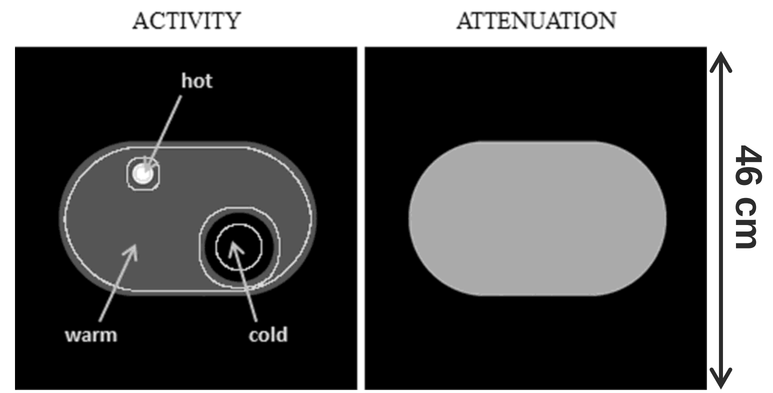
Simulations

Phantom 1

- 920 x 920
- 200 angles
- 2 phantom settings



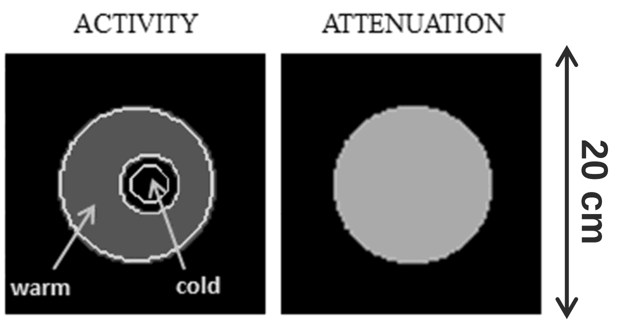
Setting 1
cold = 0
warm = 1
hot = 4

Setting 2
cold = 0
warm = 3
hot = 12

Phantom 2

- 400 x 400
- 3 projection settings

cold = 0
warm = 1



Setting 1: 100 projection angles
Setting 2: 500 projection angles
Setting 3: 1000 projection angles

- Two dimensional
- Parallel beam
- Attenuation
- Randoms
- Different frame durations (0.05 – 1000 counts)
- Multiple noise realisations
- Rebinned by 4 after simulation

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Reconstruction

Reconstruction methods:

- FBP
- MLEM
- NEGML (ψ = 1, 4, 9, 16, 25)
- AML (A = -1, -5, -10, -50, -100)

Random handling

- Precorrection = subtraction of the randoms:

  $y_i \rightarrow y_i - {s_i}^S$ or $y_i \rightarrow y_i - s_i$

- Ordinary Poisson

  y_i *with randoms estimate* $r_i = s_i$ or $r_i = {s_i}^S$

- Shifted Poisson

  $y_i + s_i$ *with randoms estimate* $r_i = 2s_i$

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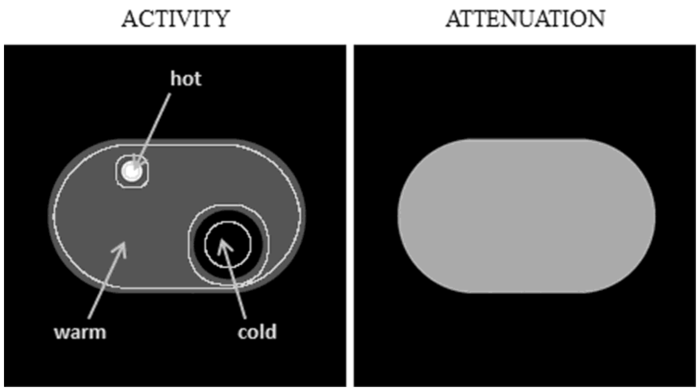
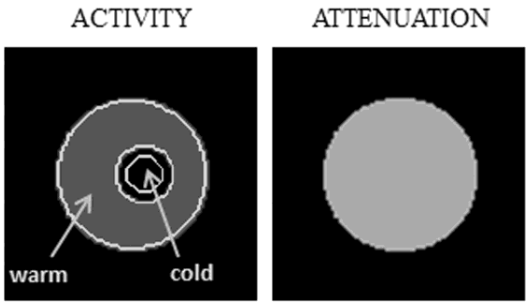
Evaluation

- Mean in each region
- Variance in each region

$$\text{ROI Mean} = \frac{1}{N J_{\text{ROI}}} \sum_{n}^{N} \sum_{j \in \text{ROI}} \lambda_{j,n}$$

$$\text{ROI Var} = \frac{1}{N} \sum_{n} (\text{ROImean} - \sum_{j \in \text{ROI}} \lambda_{j,n})^2$$





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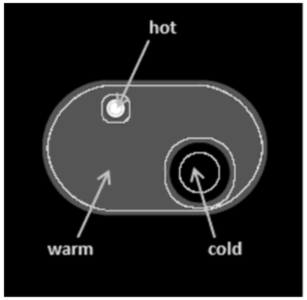
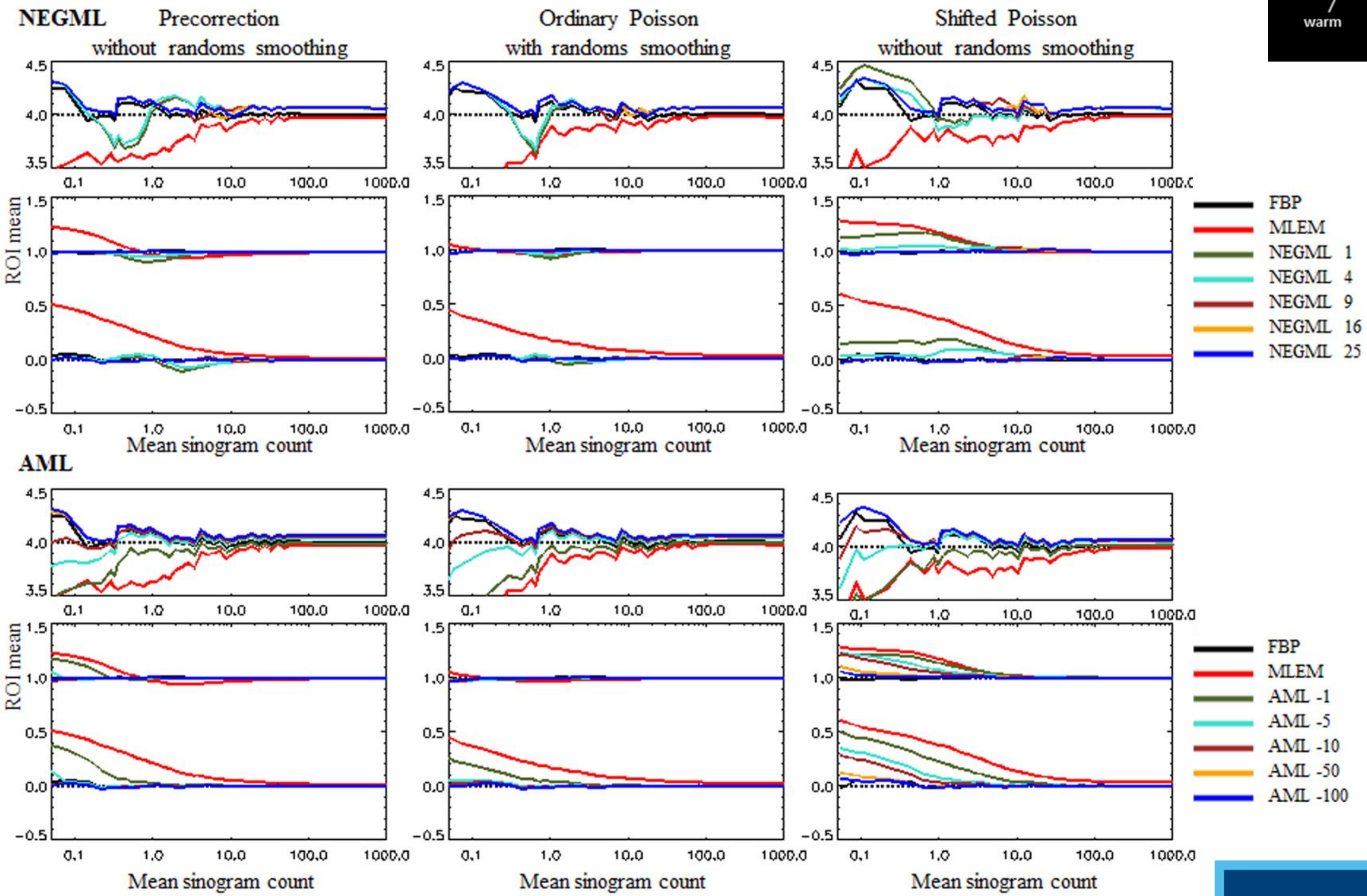
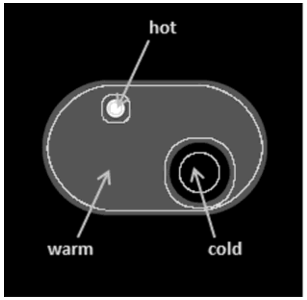
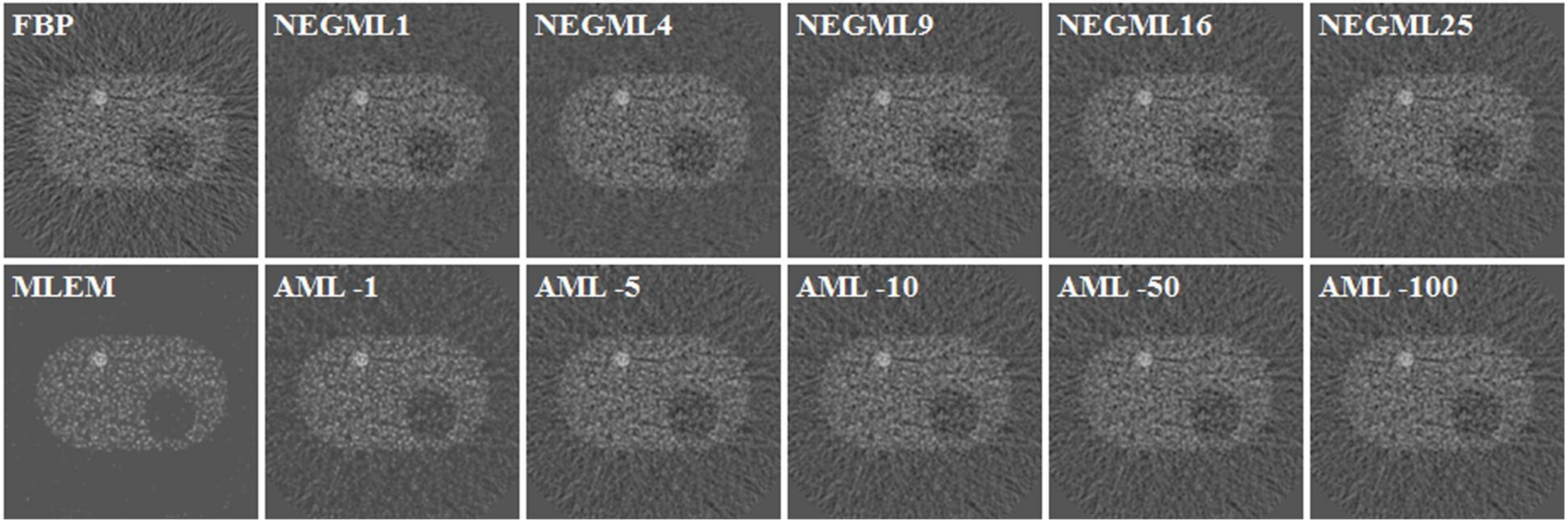
Results: bias vs sinogram count



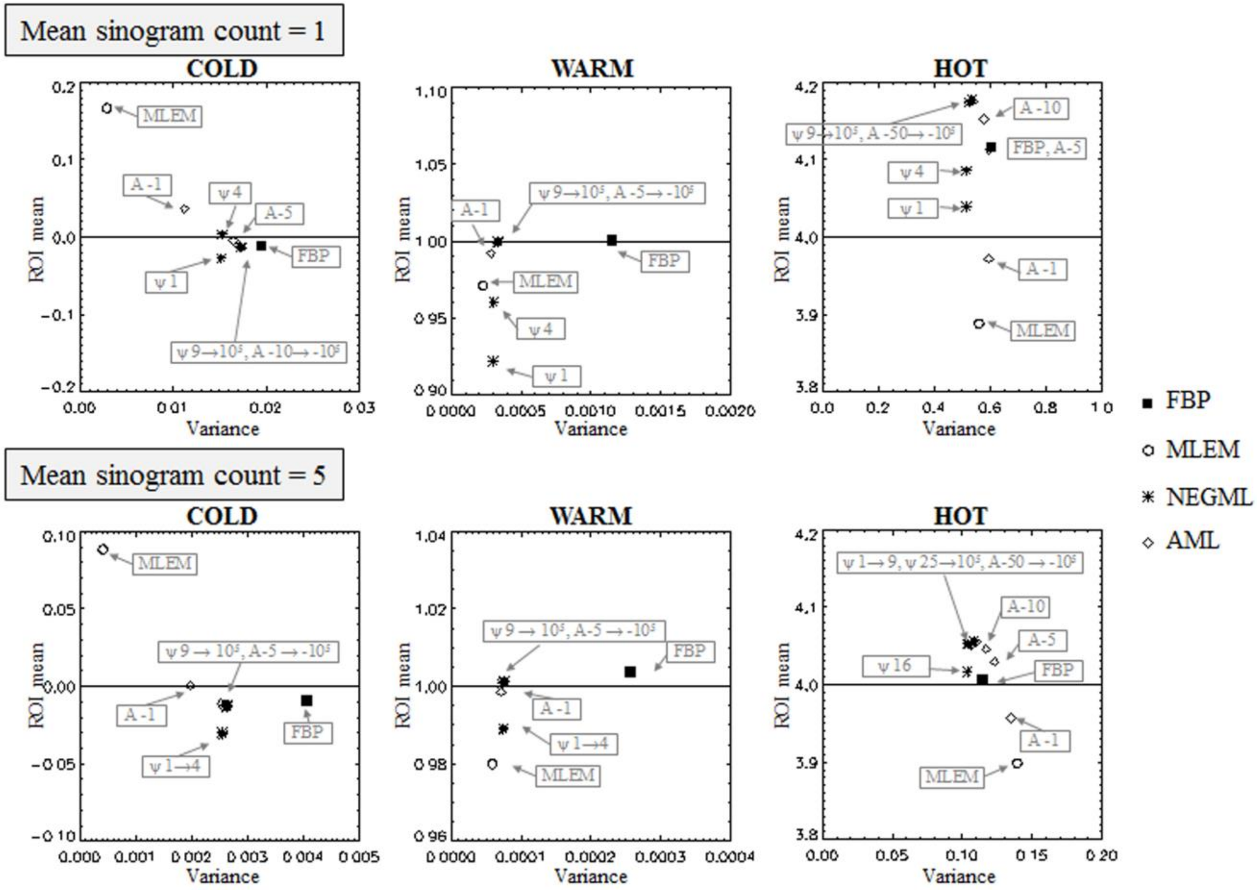


Results: reconstructions





Results: bias vs variance



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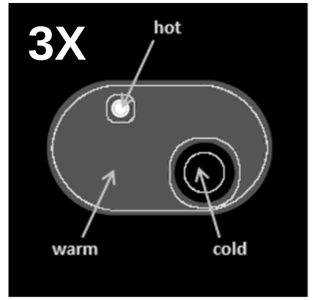
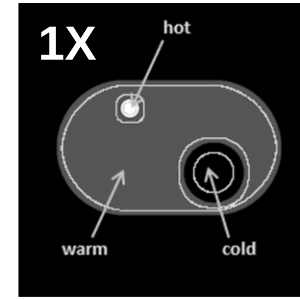
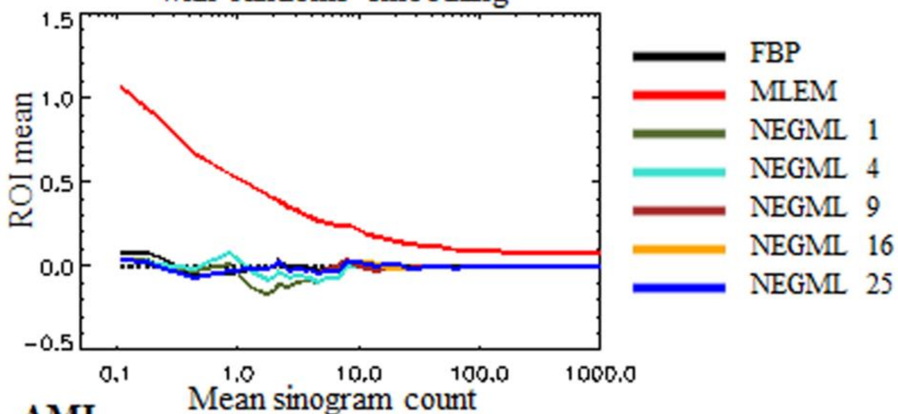
Results

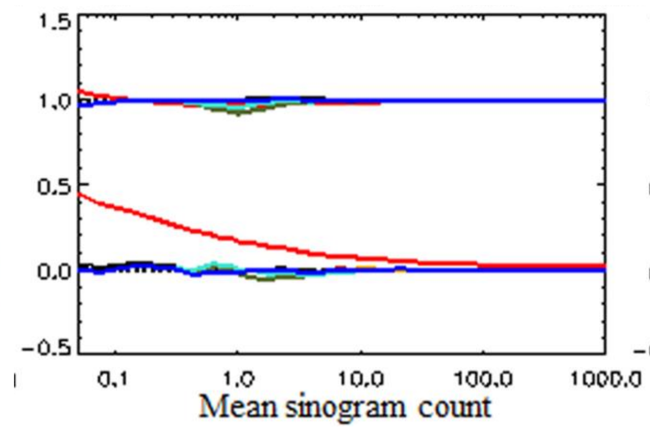




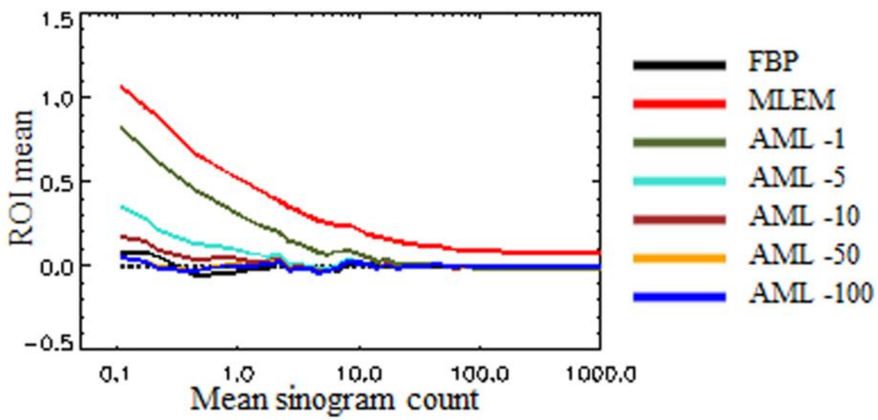
NEGML

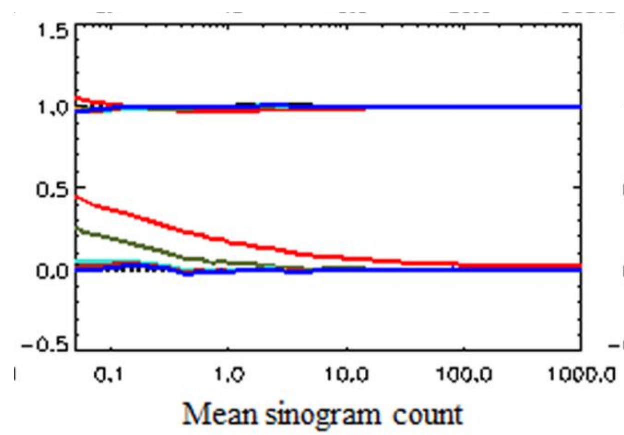
Ordinary Poisson with randoms smoothing



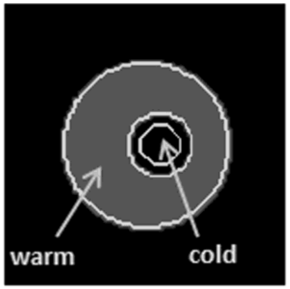


AML

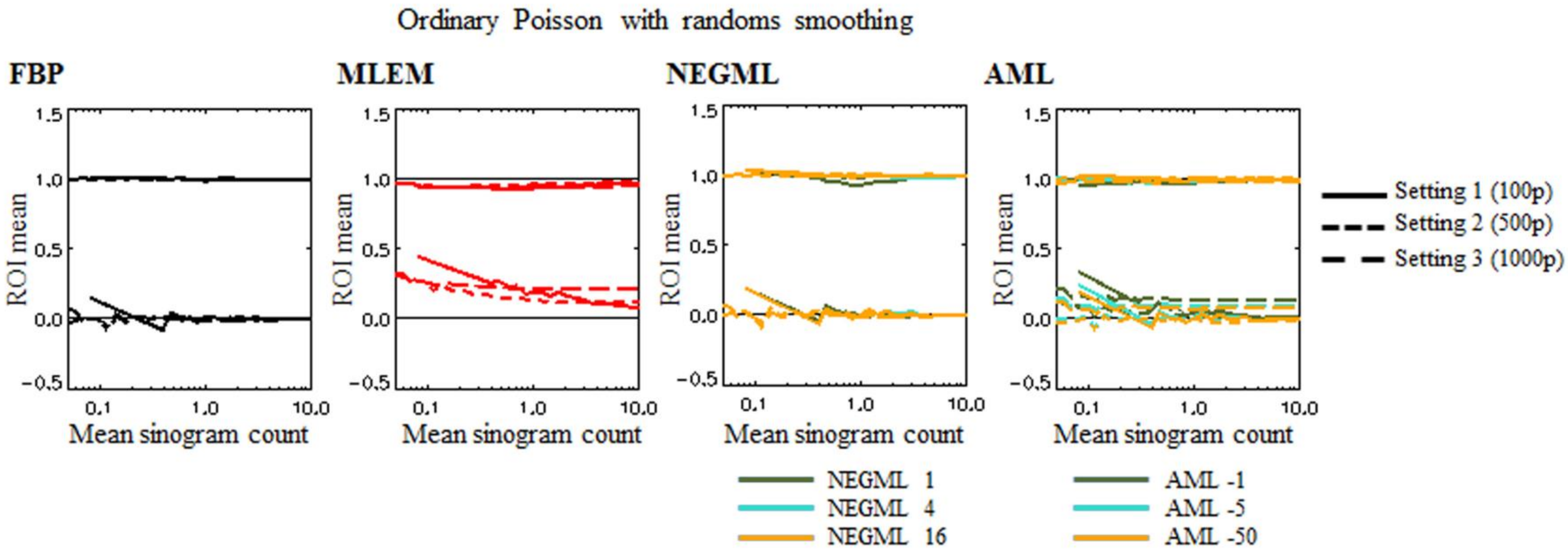




Results



warm
cold



Ordinary Poisson with randoms smoothing
FBP
MLEM
NEGML
AML
ROI mean
1.5
1.0
0.5
0.0
−0.5
0.1
1.0
10.0
Mean sinogram count
Setting 1 (100p)
Setting 2 (500p)
Setting 3 (1000p)
NEGML 1
NEGML 4
NEGML 16
AML -1
AML -5
AML -50

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Conclusion

Filtered back projection FBP	Maximum likelihood expectation maximization MLEM	Poisson + Gauss Gradient ascent NEGML
+ Fast + Bias-free	– Slow – Positive bias (cold regions and noisy data)	– Slow **+ Bias free (for $\psi \geq 16$)**
– Only basic ‘ideal’ model (no resolution model) – No priors	+ More complex model (with e.g. resolution effect) + Based on Poisson model (reduced noise) + Priors	+ More complex model (with e.g. resolution effect) **+ Poisson model is used when possible** **– Increased noise in Gaussian mode** + Priors

Conclusion

NEGML	AML
Sinogram based parameter ▪ Independent of application ▪ Poisson is still used for high counts ▪ Single parameter in dynamic studies	Image based parameter ▪ Defined in image, effect in sinogram ▪ Application dependent ▪ Parameter tuning needed in dynamic studies to keep Poisson for higher counts ▪ Optimal value that combines low bias and MLEM-look might exist

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Thank you!

Questions?