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Structured Regularization for Material Decomposition of Photon Counting CT Data using Collaborative Total Variation

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Model for Material Decomposition:

$$\mathbf{y}_i = \mathbf{A}_0\mathbf{x}_i$$

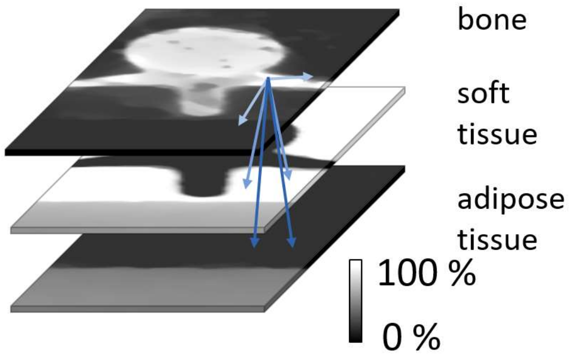
with $\mathbf{y}_i$ denoting the MECT data for pixel i, attenuation coefficients given by matrix $\mathbf{A}_0$.

$$\hat{\boldsymbol{x}} = \operatorname{argmin}_{\boldsymbol{x}}\{\bar{L}(\boldsymbol{x}) + R(\boldsymbol{x})\}$$

$$\bar{L}(\boldsymbol{x}) = \frac{1}{\nu}||\boldsymbol{y} - \mathbf{A}\boldsymbol{x}||^2_{2,\mathbf{\Sigma}^{-1}}$$

$$R(\boldsymbol{x}) = \underline{\beta_{\text{noi}}\, R_{\text{noi}}(\boldsymbol{x})} + \underline{\beta_{\text{spa}}\, R_{\text{spa}}(\boldsymbol{x})} + \underline{\beta_{\text{mas}}\, R_{\text{mas}}(\boldsymbol{x})}$$

$$\mathbf{Dx} \in \mathbb{R}^{N_p \times N_d \times L_0}$$



Noise Reduction

- Either based on $l^{p,q,r}$ norm

$$||\mathbf{Dx}||_{p,q,r} := \left(\sum_{i=1}^{N_p}\left(\sum_{j=1}^{N_d}\left(\sum_{k=1}^{L_0}|(\mathbf{Dx})_{i,j,k}|^p\right)^{\frac{q}{p}}\right)^{\frac{r}{q}}\right)^{\frac{1}{r}}$$

- Or $\|\cdot\|_{(S^p,l^q)}$

$$\|\mathbf{Dx}\|_{(S^p,l^q)} := \left(\sum_{i=1}^{N_p}\left\|\begin{pmatrix}(\mathbf{Dx})_{i,1,1} & \dots & (\mathbf{Dx})_{i,1,L_0}\\ \vdots & \ddots & \vdots\\ (\mathbf{Dx})_{i,N_d,1} & \dots & (\mathbf{Dx})_{i,N_d,L_0}\end{pmatrix}\right\|^q_{S^p}\right)^{\frac{1}{q}}$$

Sparsity enforcing term

$$R_{\text{spa}}(\boldsymbol{x}) = \sum_{j=1}^{N_p}\|\boldsymbol{X}(:,j)\|_0 =: \|\boldsymbol{x}\|_0$$

counting non-zero entries of $\boldsymbol{x}$ (nonconvex)

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dkfz. Forschen für ein Leben ohne Krebs

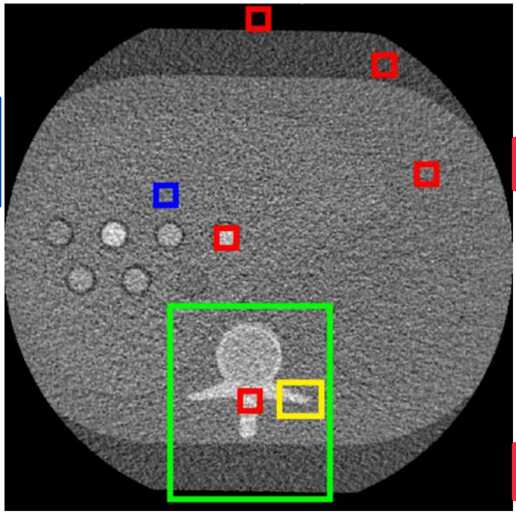
$$R(\boldsymbol{x}) = \beta_{\text{noi}}\, R_{\text{noi}}(\boldsymbol{x}) + \beta_{\text{spa}}\, R_{\text{spa}}(\boldsymbol{x}) + \beta_{\text{mas}}\, R_{\text{mas}}(\boldsymbol{x})$$

- Non-negativity and conservation of mass:

$$R_{\text{mas}}(\boldsymbol{x}) = \chi_S(\boldsymbol{x}) = \begin{cases} 0, & \boldsymbol{X} \in S \\ \infty, & \boldsymbol{X} \notin S \end{cases}$$

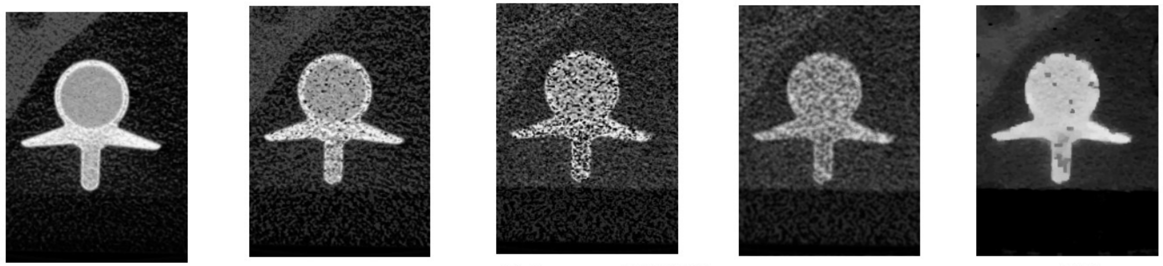
Solve $\hat{\boldsymbol{x}} = \operatorname{argmin}_{\boldsymbol{x}} \{\bar{L}(\boldsymbol{x}) + R(\boldsymbol{x})\}$ using ADMM

Antropomorphic abdomen phantom



Results: Bone material image:

$$\text{RMSE} = \frac{\|\boldsymbol{x} - \boldsymbol{x}_{\text{ref}}\|_2}{\sqrt{N_p}}$$



(a) reference RMSE =0 — ~ 30x dose

(b) mean 7 measur. RMSE = 0.0923

(c) 1 measur. (MMD [2]) RMSE =0.1774 — MMD (Mendonca)

(d) FS [9] RMSE =0.1300 — Frequ. Split

(e) $l^{1,1,1}$ RMSE = 0.0890 — Total Variation

(f) $l^{\infty,1,1}$ RMSE =**0.0875** — Strong channel coupling

(g) $S^1 l^1$ [4] RMSE =0.0915 — Total Nuclear Variation

(h) $S^\infty l^1$ RMSE =0.0902 — Strong channel coupling

- ➢ Images tend to profit from strong channel coupling
- ➢ (S^p, l^q)-based CTV did not outperform $l^{p,q,r}$-based CTV

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Thank you!