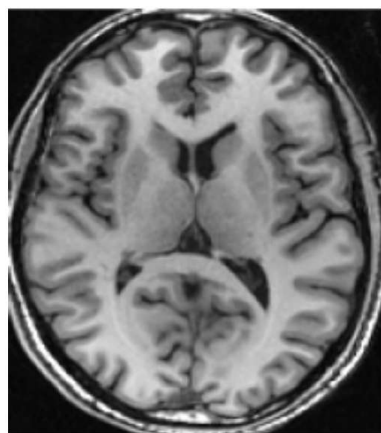
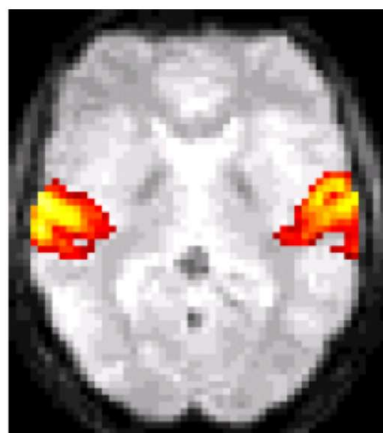


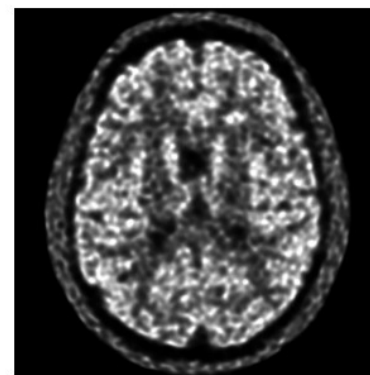
Multimodality Imaging



T1 weighted anatomical
MR image



T2* weighted fMR image



PET-MR



Edge alignment

Basic idea for regularizations: edges are aligned, i.e. mainly at the same locations and normal vectors are parallel

Normal vectors to level sets can be written in terms of image gradients as $n = \frac{\nabla u}{|\nabla u|}$

Incorporate edge alignment into regularization terms

Given prior image v construct gradient based priors for unknown u

Paradigm: only use gradient information, no explicit segmentation of the image v (costly, difficult to reproduce, not possible on the fly if joint reconstruction in u and v is desired)

Joint total variation (Haber 2013)

$$R(u|v) = \int_{\Omega} \sqrt{|\nabla u|^2 + |\nabla v|^2} \, dx$$

Advantage: convex in u and v , well-understood properties of total variation

Disadvantage: : favours equal magnitude of gradients

Weighted total variation

$$R(u|v) = \int_{\Omega} W(|\nabla v|) |\nabla u| \, dx$$

Advantage: easy to compute, no correlation of magnitude, convex in u

Disadvantage: no correlation of gradient direction, difficult to define rigorously
(Relaxation Holler et al 2017)

Directional total variation

$$R(u|v) = \int_{\Omega} \left| \left(I - \frac{\nabla v}{|\nabla v|} \otimes \frac{\nabla v}{|\nabla v|} \right) \nabla u \right| dx$$

Advantage: convex in u , reasonably easy to compute (Holler et al 2017, Klages 2018), no correlation of magnitude

Disadvantage: difficult to analyze, needs some smoothing, no definition for u, v of bounded variation (Holler et al 2017)

Parallel level sets (Ehrhardt-Arridge et al 2014-2018)

$$R(u|v) = \int_{\Omega} \varphi(\psi(|\nabla u| |\nabla v|) - \psi(|\nabla u \cdot \nabla v|)) dx$$

Advantage: convex in u at least in the linear case, no correlation of magnitude

Disadvantage: difficult to analyze, nonconvexity for joint reconstruction

Total variation Bregman distances (Moeller et al 2014)

$$R(u|v) = \int_{\Omega} |\nabla u| - \frac{\nabla v}{|\nabla v|} \cdot \nabla u \, dx$$

Advantage: convex in u , easy to, no correlation of magnitude, rigorous definition with subgradients

Disadvantage: depends on size of the jump, penalizes opposite directions

Formally

$$D_{TV}^q(u, v) = \|\nabla u\|_1 - \langle q, u \rangle = \int |\nabla u| \left(1 - \frac{\nabla u}{|\nabla u|} \cdot \frac{\nabla v}{|\nabla v|} \right) dx$$

Subgradient interpretation opens rigorous definition and generalization to other systems based on absolutely homogeneous convex regularizers (e.g. shearlets)

$$D_J^q(u, v) = J(u) - \langle q, u \rangle, \quad q \in \partial J(v)$$

Known techniques (Bregman iterations / ADMM) open the way to unbiased methods and joint reconstruction

Bregman iteration with data fidelity H

$$u^{k+1} \in \arg \min H(u, f) + \alpha D_J^{p^k}(u, u^k), \quad p^k \in \partial J(u^k)$$

Coupled Bregman iteration for joint reconstruction (Moeller et al 2014)

$$u_i^{k+1} \in \arg \min H_i(u_i, f_i) + \alpha \sum_j w_{ij} D_J^{p_j^k}(u_i, u_j^k), \quad p_j^k \in \partial J(u_j^k)$$

Efficient computation, appropriate choice of weights

Convergence analysis: converges to solutions with joint subgradients in the noise-free case, iterative regularization

Bregman Iteration

$$\frac{\lambda}{2} \|Au - f\|_2^2 + D_J^{p^k}(u, u^k)$$

$$p^{k+1} = p^k + \lambda A^*(f - Au^{k+1})$$

$$\tilde{p} = \tilde{p} + \lambda A^*(f - A\tilde{u})$$

$A^*(f - A\tilde{u}) = 0$ means that u is a minimizer of $\|Au - f\|_2^2$; Since $\tilde{p} \in \text{range}(A^*)$, $\tilde{u}$ is J -minimizing

Color Bregman Iteration

$$\frac{\lambda}{2} \|A_i u_i - f_i\|_2^2 + \sum_j w_{i,j} D_J^{p_j^k}(u_i, u_j^k)$$

$$p^{k+1} = Wp^k + \lambda A^*(f - Au^{k+1})$$

$$0 = (W - I)\tilde{p} + \lambda A^*(f - A\tilde{u})$$

$A_i^*(f_i - A_i \tilde{u}_i) = 0$ only if $\tilde{p}$ is an eigenvector of W with eigenvalue 1.

Coupled Bregman Iterations

Bregman Iteration

$$\text{Residual } r^k = \lambda(f - Au^k)$$

$\|r^k\|$ monotonically decreasing

$$(u^k, q^k) \xrightarrow{(w^*, w)} (\tilde{u}, \tilde{q}),$$

$$p^k = A^* q^k$$

$$\|r^k\| \leq C/\sqrt{k}$$

$WA^* = A^* W$, W symmetric, non-negative, rows sum to one, W has a single maximal positive eigenvalue.

Color Bregman Iteration

$$r^k = (W - I)q^k + \lambda(f - Au^k)$$

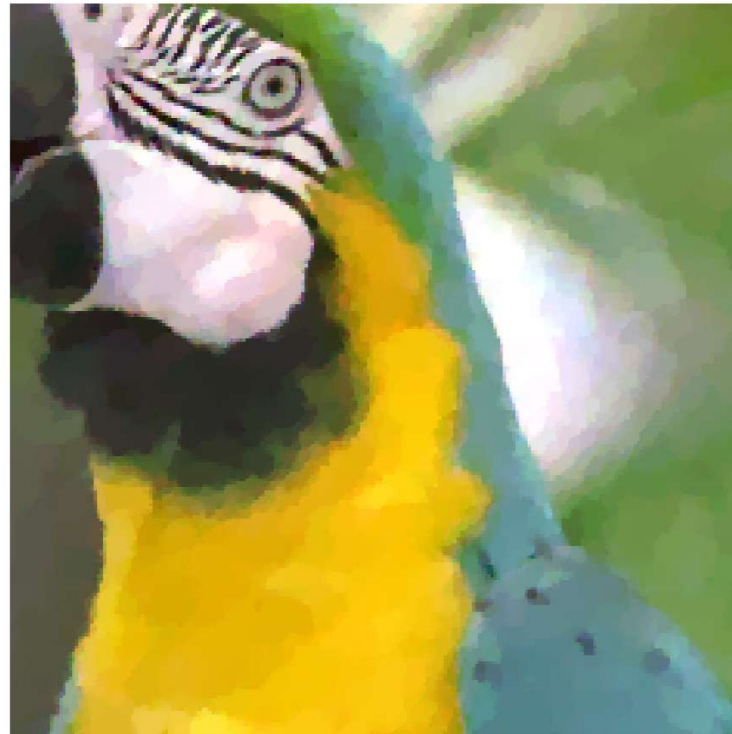
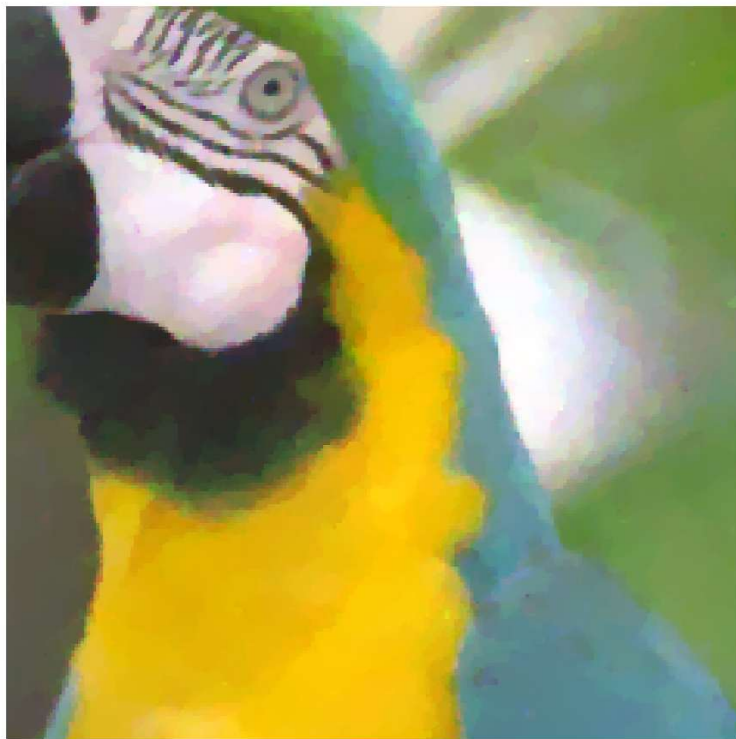
$\|r^k\|$ monotonically decreasing

$$(u^k, q^k) \xrightarrow{(w^*, w)} (\tilde{u}, \tilde{q}),$$

$$p^k = A^* q^k$$

$$\|r^k\| \leq C/\sqrt{k}$$

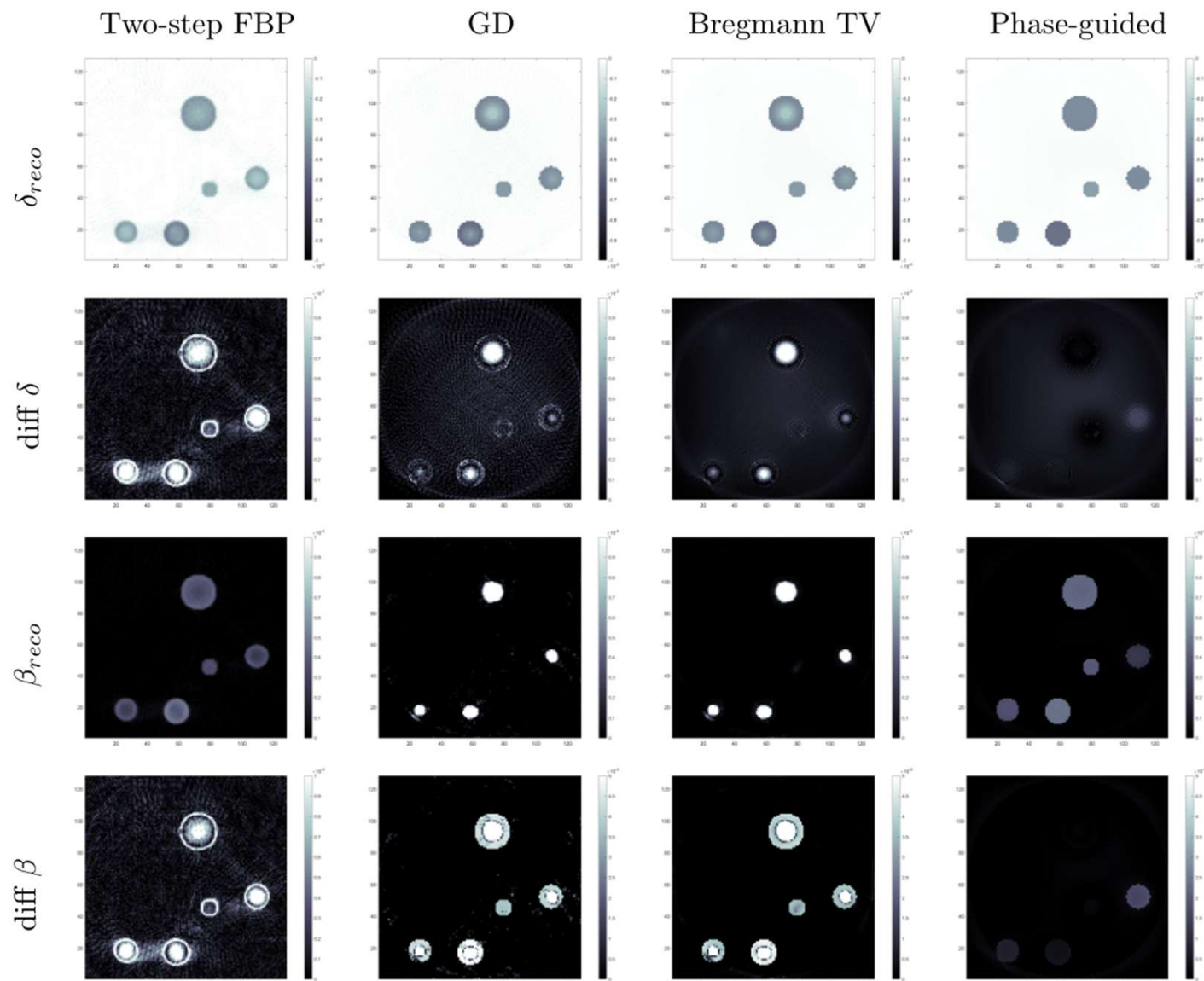
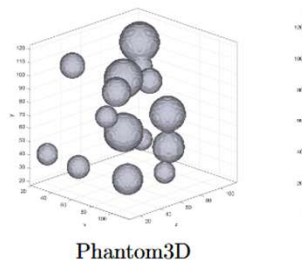
Coupled Bregman Iterations



Holotomography

Phase-Guided Regularization

Fresnel Nr = 0.04



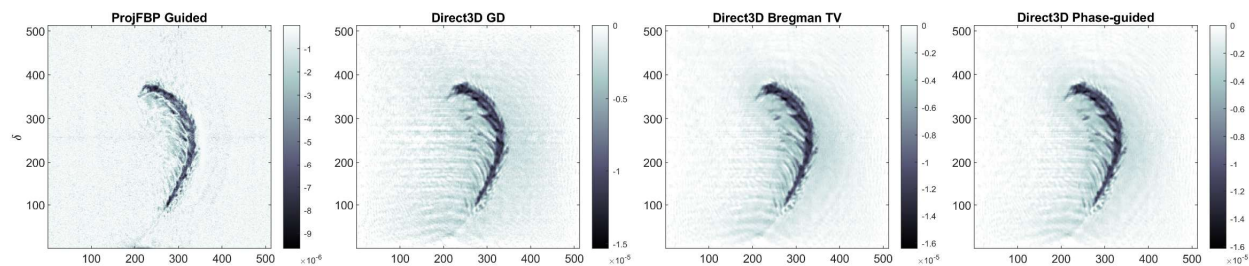
Holotomography

Spider Hair

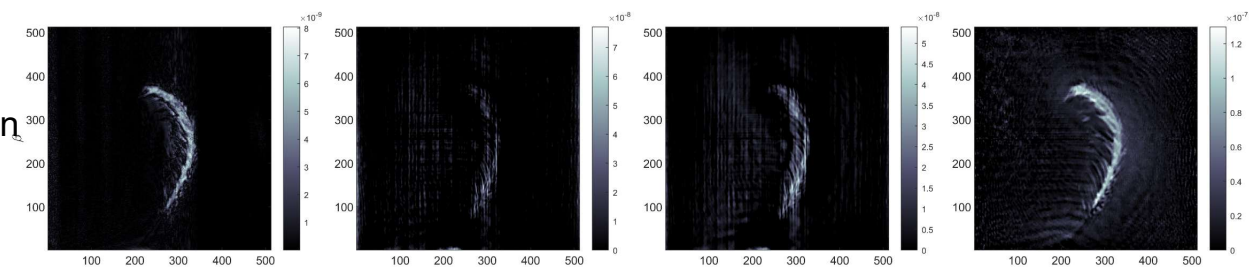
Liu-Hagemann-mb

2026 (almost finished)

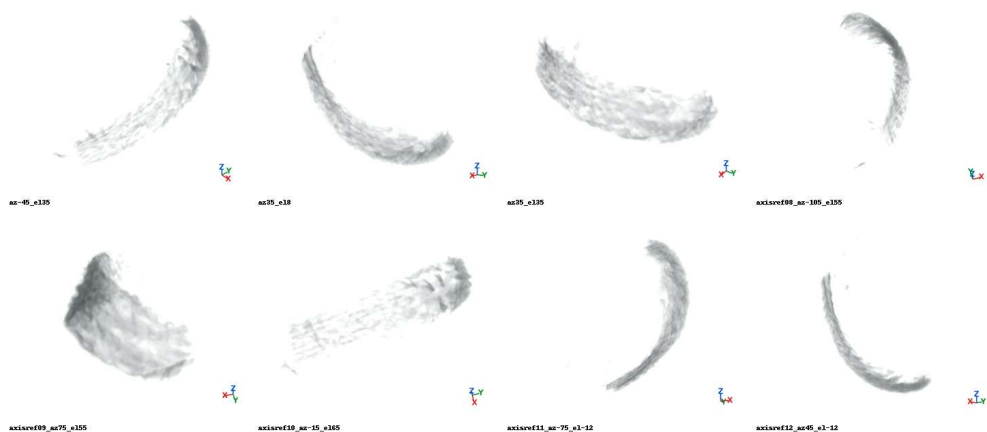
Phase



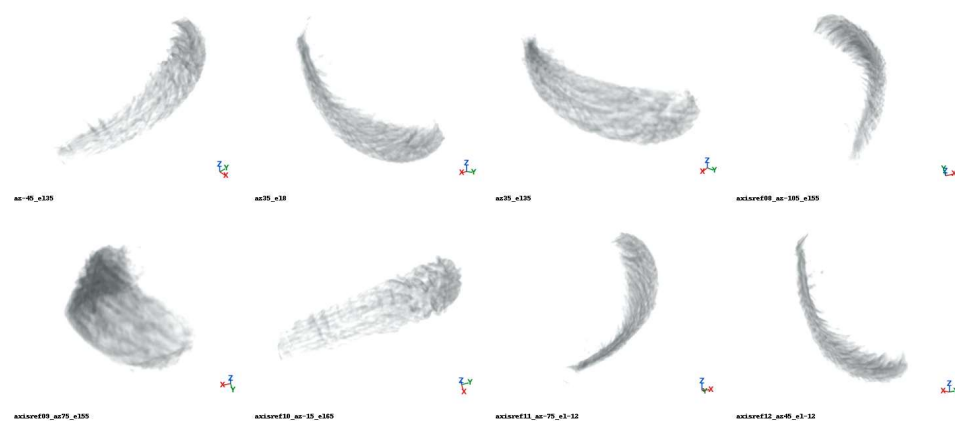
Absorption



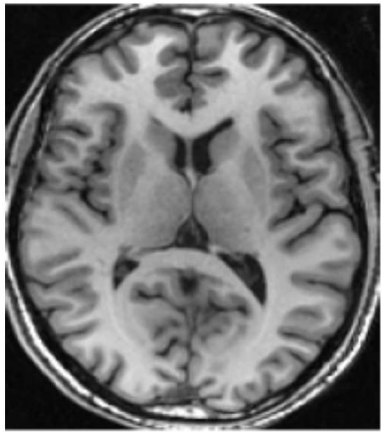
Phase, rendered



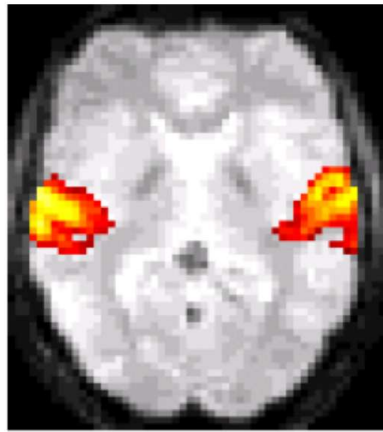
Absorption, rendered



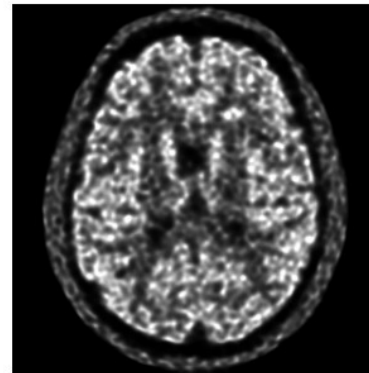
Opposite edges



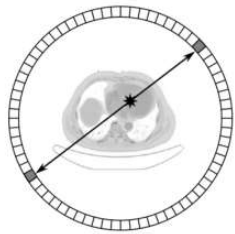
T1 weighted anatomical
MR image



T2* weighted fMR image

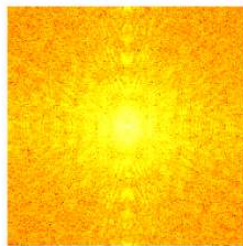


PET: Metabolic information $\rightsquigarrow$ Functional imaging.



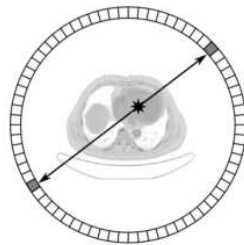
- Estimate tracer distribution from photon emissions.
- Low resolution, high amount of noise in the data, blurry reconstructions.

MRI: Anatomical information $\rightsquigarrow$ Structural imaging.



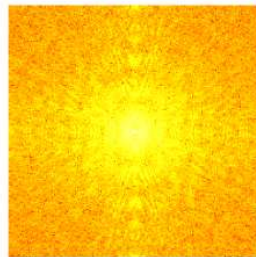
- Estimate proton density from their resonant frequencies $\rightarrow$ Fourier data.
- High resolution, detailed and sharp reconstructions, no metabolic information.

PET: Metabolic information $\rightsquigarrow$ Functional imaging.



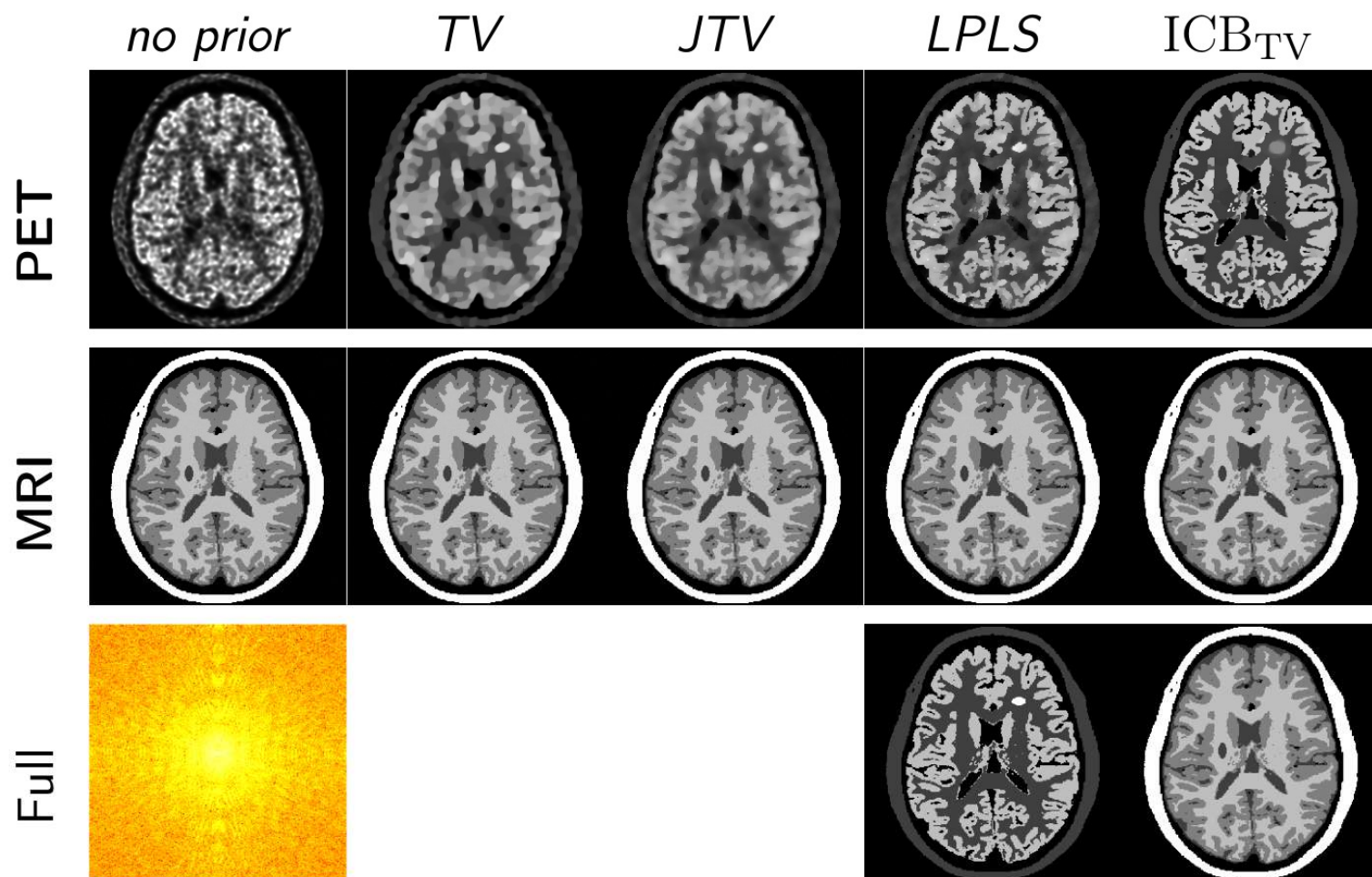
- Poisson data.
- $Au = f$
- $\int Au - f \log(Au) \, dx \rightarrow \min_{u \geq 0}$

MRI: Anatomical information $\rightsquigarrow$ Structural imaging.

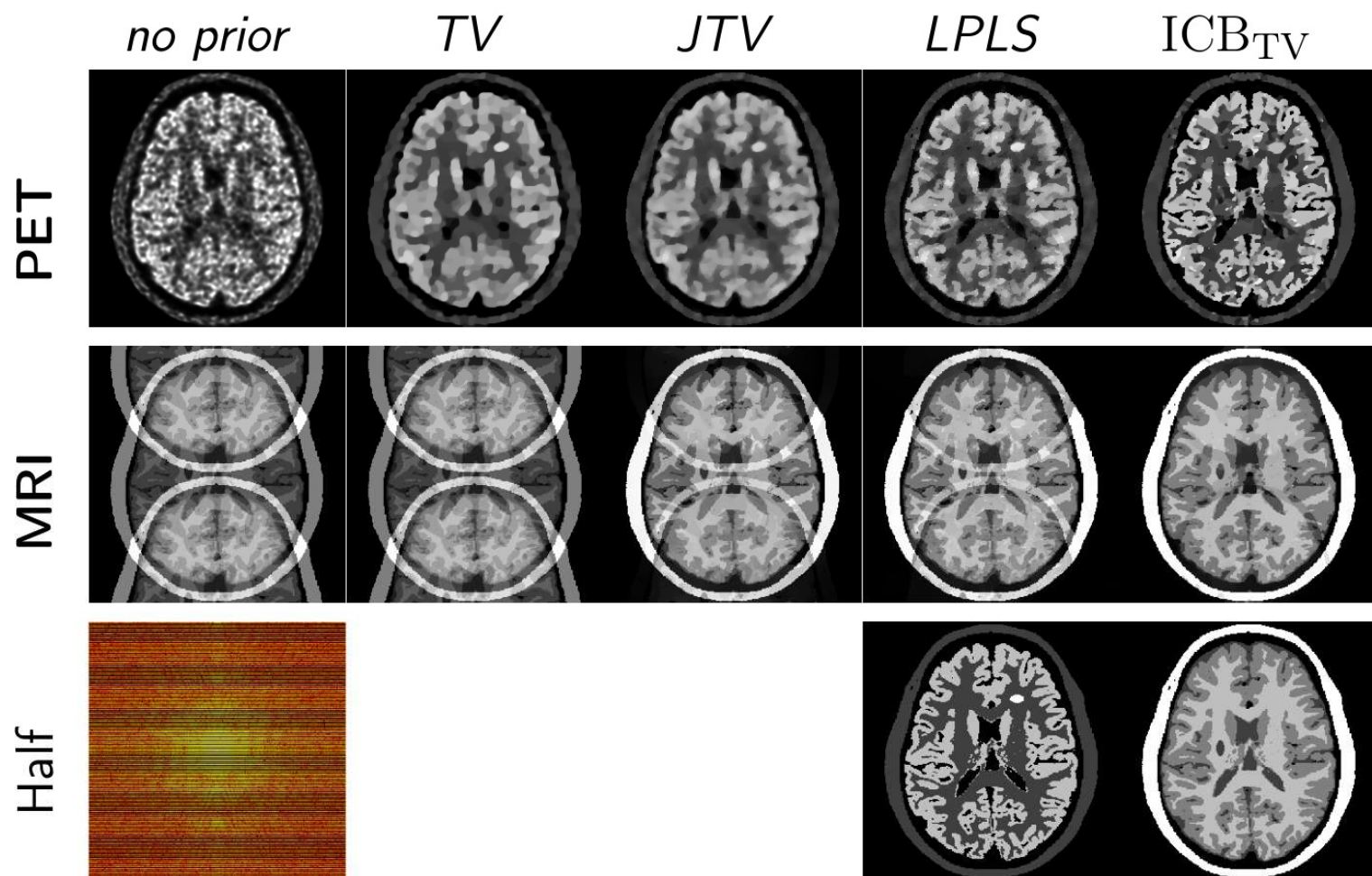


- Gaussian data.
- $Bv = g$
- $\frac{1}{2} \int (Bv - g)^2 \, dx \rightarrow \min_v$

PET-MR



PET-MR

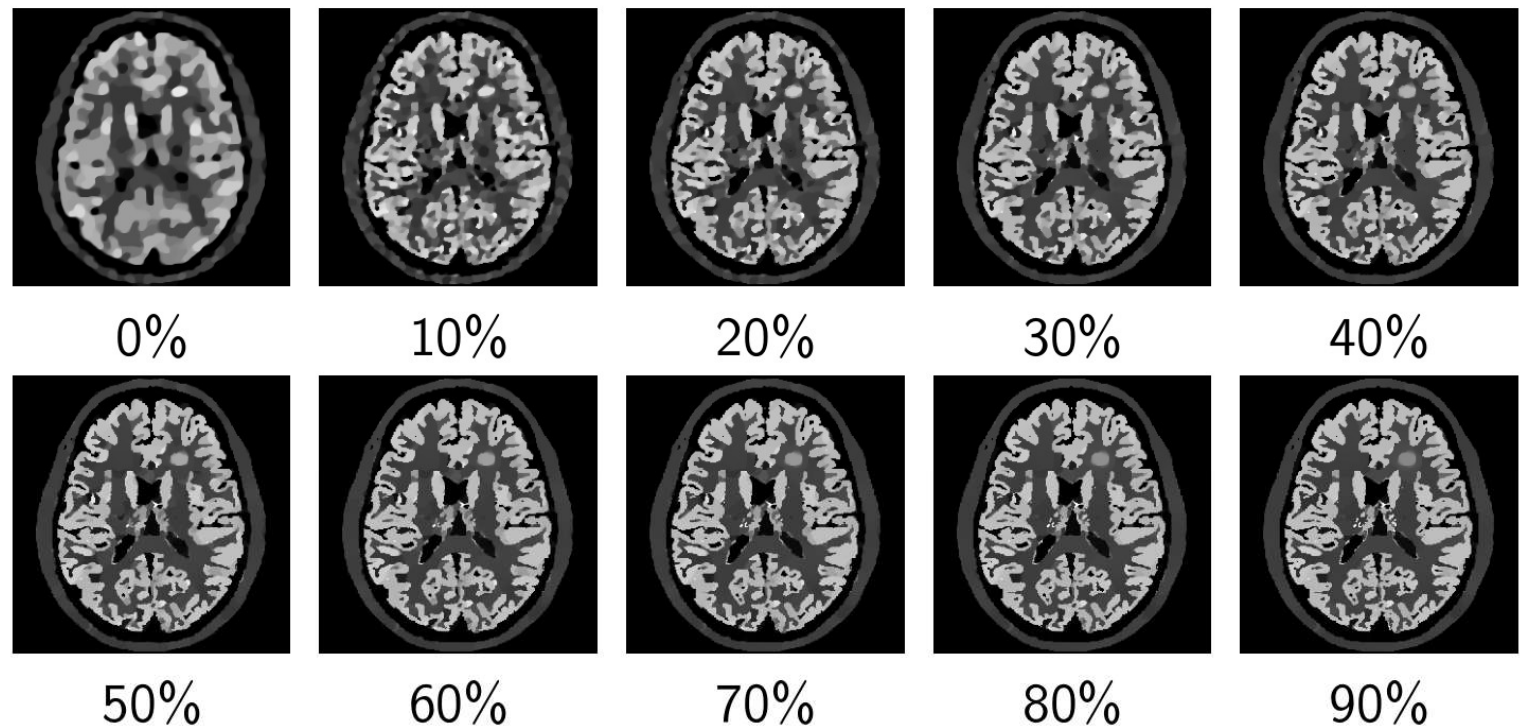


PET-MR Measures: SSIM

	Full		Half		Spokes		Spiral	
	PET	MRI	PET	MRI	PET	MRI	PET	MRI
no prior	0.5366	0.9940	0.5366	0.6722	0.5366	0.7804	0.5366	0.5283
TV	0.5657	0.9942	0.5657	0.6718	0.5657	0.9415	0.5657	0.7807
BTV	0.5760	0.9999	0.5760	0.6695	0.5760	0.9453	0.5760	0.8086
ICB	0.9218	0.9999	0.8025	0.8969	0.7695	0.9453	0.7017	0.8240

PET-MR

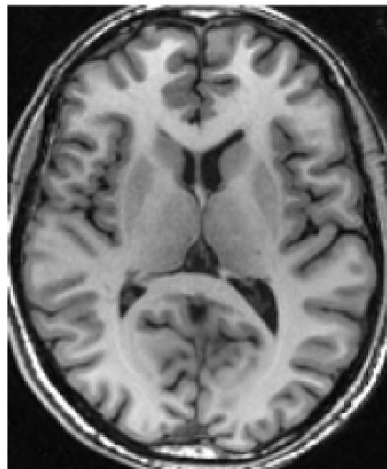
Weights



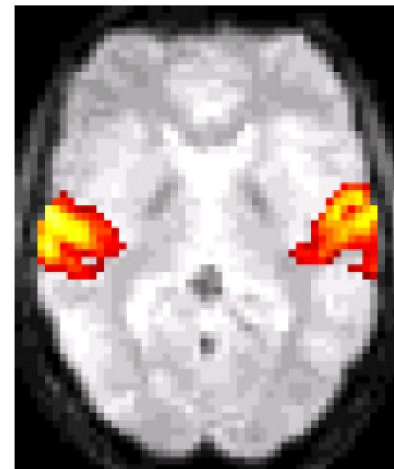
- ~> Possibility to identify artifacts caused by the reconstruction.
- ~> Control the amount of influence of the other channels.

Dynamic MR / fMRI

Anatomical high-resolution T₁ weighted MRI scan
Actual fMRI scan: fast (subsampling) T₂* weighted MRI scan over time



T₁ weighted anatomical MR image

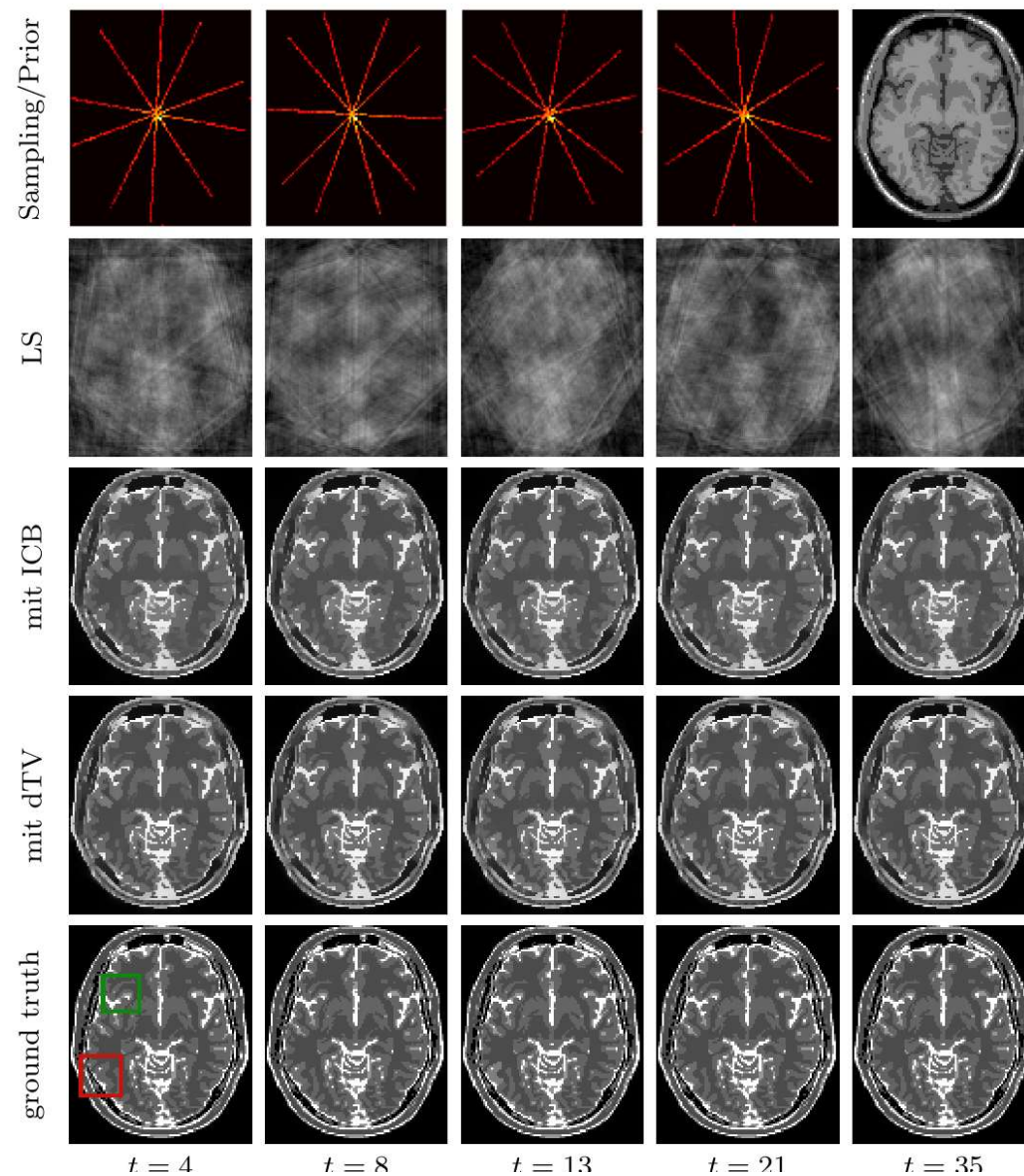


T₂* weighted fMRI image

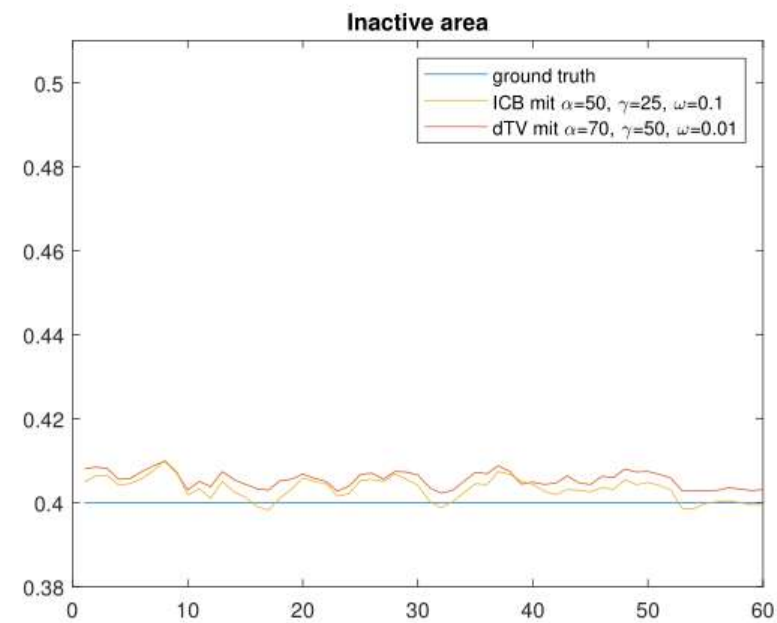
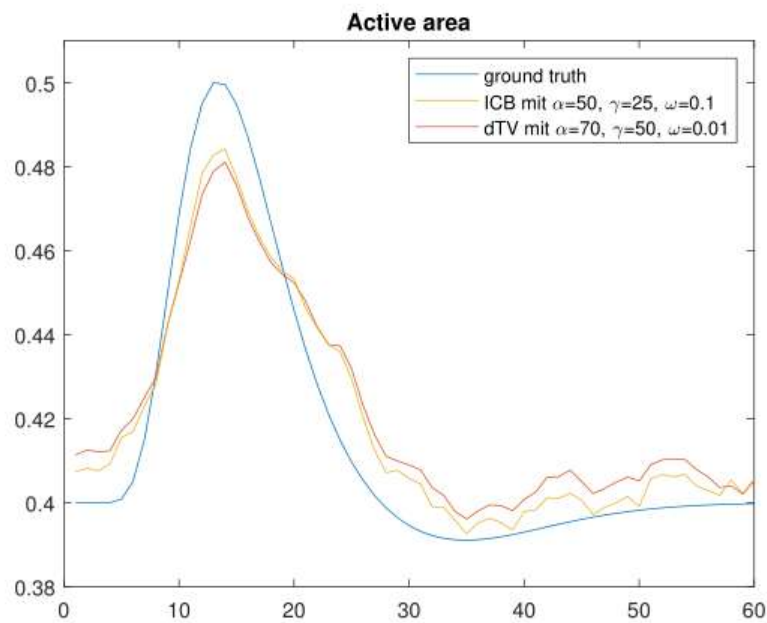
Anatomical scan is a prior for other images

$$\begin{aligned} \arg \min_{\mathbf{u}=(u_t)_t} & \sum_{t=1}^T \frac{\alpha_t}{2} \|B_t u_t - g_t\|_{\mathbb{C}}^2 && \text{(data fidelity)} \\ & + w_t \text{TV}(u_t) && \text{(piecewise constant)} \\ & + (1 - w_t) \text{ICB}_{\text{TV}}^p(u_t, \mathbf{v}) && \text{(structural prior)} \\ & + \sum_{t=1}^{T-1} \frac{\gamma_t}{2} \|u_{t+1} - u_t\|^2. && \text{(temporal smoothing)} \end{aligned}$$

Dynamic MR / fMRI

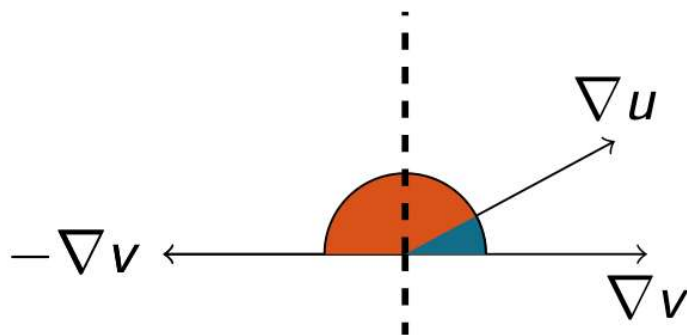


Pixelwise activation curves over time



Bregman distances

$$D_{TV}^q(u, v) = \int |\nabla u| \underbrace{\left(1 - \frac{\nabla u}{|\nabla u|} \cdot \frac{\nabla v}{|\nabla v|}\right)}_{\in [-1, 1]} dx.$$



- Opposing edges are highly penalized.

Infimal convolution

$$q \in \partial \text{TV}(v) \Leftrightarrow -q \in \partial \text{TV}(-v)$$

Couple two Bregman distances with the infimal convolution

$$\text{ICB}_{\text{TV}}^q(u, v) = \inf_{\phi + \psi = u} \left\{ D_{\text{TV}}^q(\phi, v) + D_{\text{TV}}^{-q}(\psi, -v) \right\}.$$

Theorem (Moeller et al 2014)

Let u and v be piecewise constant with C^1 discontinuity sets

$$D(u) = \Gamma \cup \Sigma \quad (4)$$

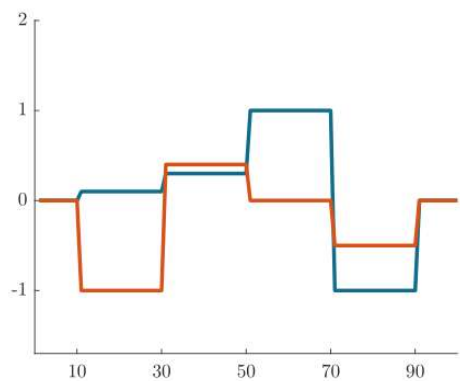
$$D(v) = \Gamma \cup \Upsilon, \quad (5)$$

such that Γ , Σ , and Υ have pairwise positive distance. Then there exists $p \in \partial J(u)$ such that

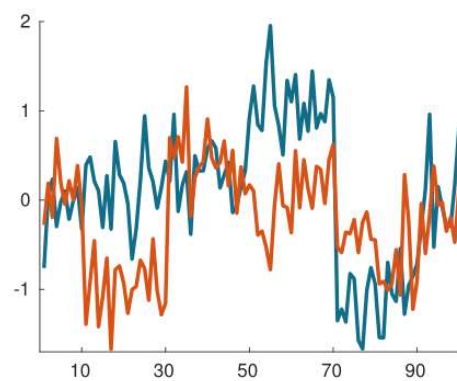
$$D_J^p(v, u) \square D_J^{-p}(v, -u) = 0.$$

Joint reconstruction model for two images

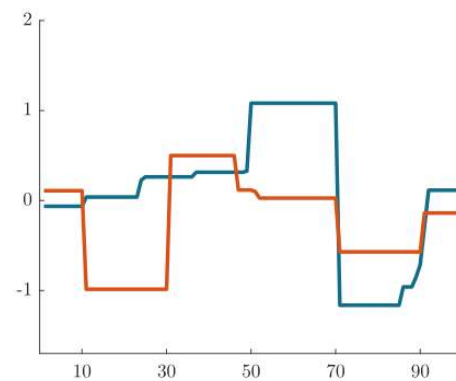
$$u^{k+1} \in \arg \min_u \left\{ \alpha H_1(u, f) + \lambda D_{\text{TV}}^{p^k}(u, u^k) + (1 - \lambda) \text{ICB}_{\text{TV}}^{q^k}(u, v^k) \right\}$$
$$v^{k+1} \in \arg \min_v \left\{ \beta H_2(v, g) + \mu D_{\text{TV}}^{q^k}(v, v^k) + (1 - \mu) \text{ICB}_{\text{TV}}^{p^k}(v, u^k) \right\}$$



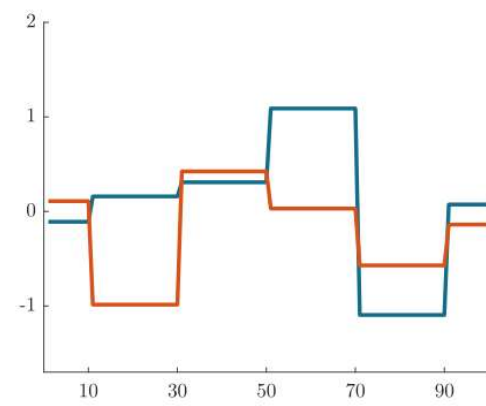
(a) clean



(b) noisy



(c) Bregman TV



(d) ICB_{TV}