UCL INM biweekly meeting

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Part of **PET++ project** with Matthias Ehrhardt (Bath), Carola-Bibiane Schönlieb and Jonas Latz (Cambridge).
Goal: improve (fast) PET image reconstruction in order to benefit clinical diagnosis.

Background of PET++ project

PET reconstruction.
Statistical model:

$$d \sim \text{Poisson}(Ax + b)$$
$$A : \text{attenuation} + \text{ray-transform}$$
$$b : \text{randoms} + \text{scatters}$$

Inverse problem:

$$\min_{x \in X} \underbrace{\text{KL}(d, Ax + b)}_{\text{data fit}} + \underbrace{R(x)}_{\text{prior}}$$

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TV regularization: $R(x) = \alpha \|\nabla x\|_1$
Guided TV regularization: $R(x) = \alpha \|M \nabla x\|_1$. where M incorporates information from MR or CT image.

Influence of non-smooth priors

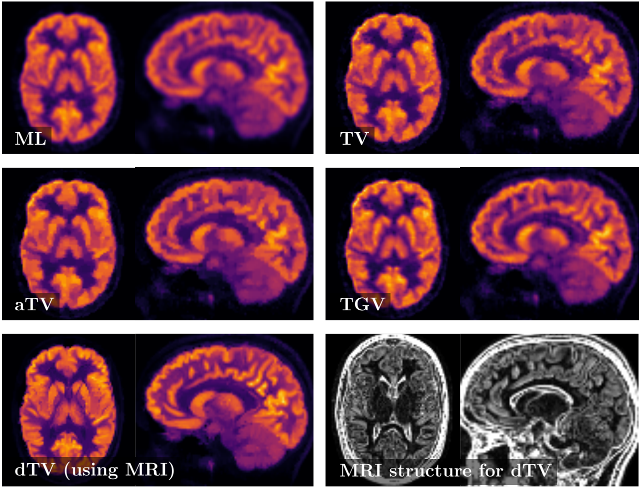

Figure: From *Faster PET Reconstruction with Non-Smooth Priors by Randomization and Preconditioning*, M. J. Ehrhardt, P. Markiewicz and C.-B. Schönlieb, Physics in Medicine and Biology, 2019

Algorithms

$$\min_{x \in X} \mathrm{KL}(d, Ax + b) + \alpha \|M \nabla x\|_{1,2}$$

Forward projection A and back-projection A^* have high computational cost.

OSEM

- Ordered **Subsets** Expecation Minimization: $A = (A_1, \ldots, A_n)$
- No prior
- No convergence guarantee

PDHG

- No subsets
- Prior
- Convergence guarantee

SPDHG: Best of two worlds

General formulation

$$\min_{x \in X} F(Ax) + G(x)$$

with F, G convex and A linear.

Introduce the **convex conjugate** and **proximal operator** of a convex function F:

$$F^*(y) = \sup_{z \in \mathcal{Y}} \langle z, y \rangle - F(z)$$

$$\mathrm{prox}_F^{\tau}(y) = \arg\min_{z \in Y} \frac{1}{2\tau} \|z - y\|^2 + F(z).$$

PDHG

$$\min_{x\in X} F(Ax) + G(x) = \min_{x\in X} \sup_{y\in Y} \langle Ax, y\rangle - F^*(y) + G(x).$$

Primal-Dual Hybrid Gradient (PDHG) or Chambolle-Pock algorithm:
Input: initialization point $x \in \mathcal{X}, y \in \mathcal{Y}$; step parameters σ, τ.

Initialize $z = \bar{z} = P^T y$.

Iterate

- $x = \mathrm{prox}_G^\tau(x - \tau\bar{z})$
- $y^+ = \mathrm{prox}_{F^*}^\sigma(y + \sigma Ax)$
- $\Delta z = A^T(y^+ - y)$
- $z = z + \Delta z$, $y = y^+$
- $\bar{z} = z + \Delta z$.

Convergence condition: $\|\sigma^{1/2} A \tau^{1/2}\| < 1$.

Separability

Assume we have a **separability** property:

$$F(Ax) = \sum_{i=1}^{n} F_i(A_i x).$$

For example,

$$\mathrm{KL}(d, Ax + b) = \sum_{i=1}^{n} \mathrm{KL}(d_i, A_i x + b_i),$$

where the forward projection is divided into subsets $A = (A_1, \ldots, A_n)$.

Stochastic PDHG

Input: initialization point $x \in \mathcal{X}, y \in \mathcal{Y}$; step parameters σ_i, $1 \leq i \leq n$, τ.

Initialize $z = \bar{z} = P^T y$.

Iterate

- $x = \text{prox}_G^{\tau}(x - \tau \bar{z})$
- Select a subset i with probability p_i
- $y_i^+ = \text{prox}_{F_i^*}^{\sigma_i}(y_i + \sigma_i A_i x)$
- $\Delta z = A_i^T (y_i^+ - y_i)$
- $z = z + \Delta z$, $y_i = y_i^+$
- $\bar{z} = z + \frac{1}{p_i} \Delta z$.

Recent developments: improving SPDHG step-size

Joint work with J. Latz, P. J. Markiewicz, C.-B. Schönlieb, M. J. Ehrhardt.

Convergence condition $(*)$ form *Stochastic primal-dual hybrid gradient algorithm with arbitrary sampling and imaging applications*, by A. Chambolle, M. J. Ehrhardt, P. Richtárik and C.-B. Schönlieb, SIAM J. Optim, 2018:
There exists (v_i) such that for all $y \in Y$,

$$\mathbb{E}\left\|\sum_{i\in\mathbb{S}}(\sigma_i^{1/2}A_i\tau^{1/2})^* y_i\right\|^2 \leq \sum_{i=1}^{n} p_i v_i \|z_i\|^2,$$

and for all i, $v_i < p_i$.

Alternative convergence condition $(**)$: $\|\sigma^{1/2}A\tau^{1/2}\| < 1$
and $(**) \Leftarrow (*)$.

For pre-conditioned step-sizes, the same kind of formulas exist.

Comparing step-sizes

Dataset: real data corresponding to the last 10 minutes of a brain amyloid scan with florbetapir tracer with Siemens Biograph mMR scanner.
Numerical experiments: open-source packages NiftyPET and ODL.

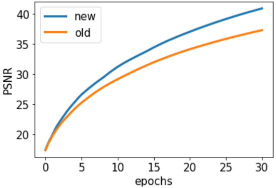

Figure: PSNR evolution for old and new step-sizes. New step-size speeds up reconstruction.

SPDHG step-sizes: second advance

Admissible step-sizes read as, for a positive γ:

$$\sigma_i = \frac{1}{\gamma \|A_i\|}, \quad \tau = \frac{\gamma}{\sum_i \|A_i\|}.$$

How to calibrate γ, which is commonly fixed to 1?

SPDHG step-sizes: second advance

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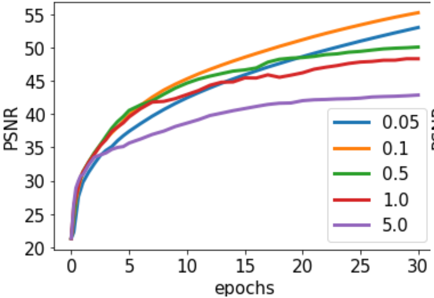
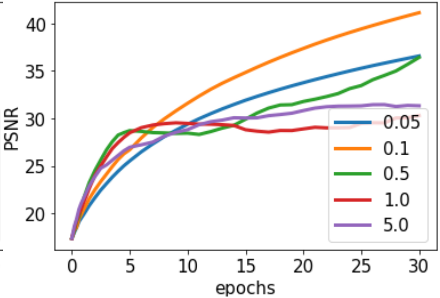


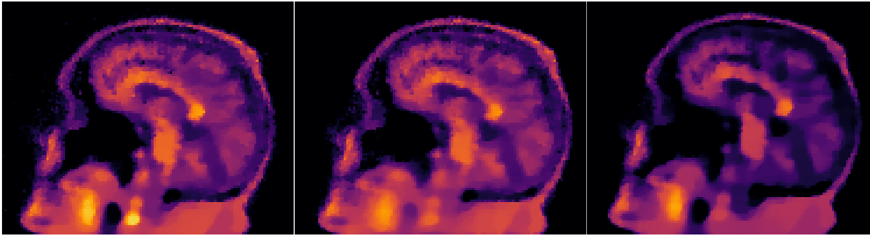
(a) synthetic data



(b) real data

Figure: PSNR evolution for different values of γ. Fastest reconstruction is obtained with same value $\gamma = 0.1$ for both datasets.

Calibrating the trade-off between primal and dual convergence



(a) Reference
PSNR$= +\infty$

(b) $\gamma = 0.1$
PSNR $= 37$

(c) $\gamma = 1.0$
PSNR $= 29$

Figure: PET reconstruction. SPDHG result with calibrated $\gamma = 0.1$ looks closer to reference than with $\gamma = 1$ after 20 epochs.

Implementations

ODL: https://github.com/odlgroup/odl/tree/master/odl/contrib/solvers/spdhg

CIL: https://github.com/vais-ral/CCPi-Framework/blob/master/Wrappers/Python/ccpi/optimisation/algorithms/SPDHG.py

https://github.com/vais-ral/CIL-Demos/blob/master/Tomography/Simulated/SingleChannel/PDHG_vs_SPDHG.py

Outlook

- Test on PET-CT data from pituitary gland study: collaboration of PET++ group with Addenbrookes' hospital

- Motion reconstruction: subsetting on gates, not only on subsets. Joint work with Kris Thielemans, Richard Brown, Evangelos Papoutsellis, Edoardo Pascoa, Christoph Kolbitsch...