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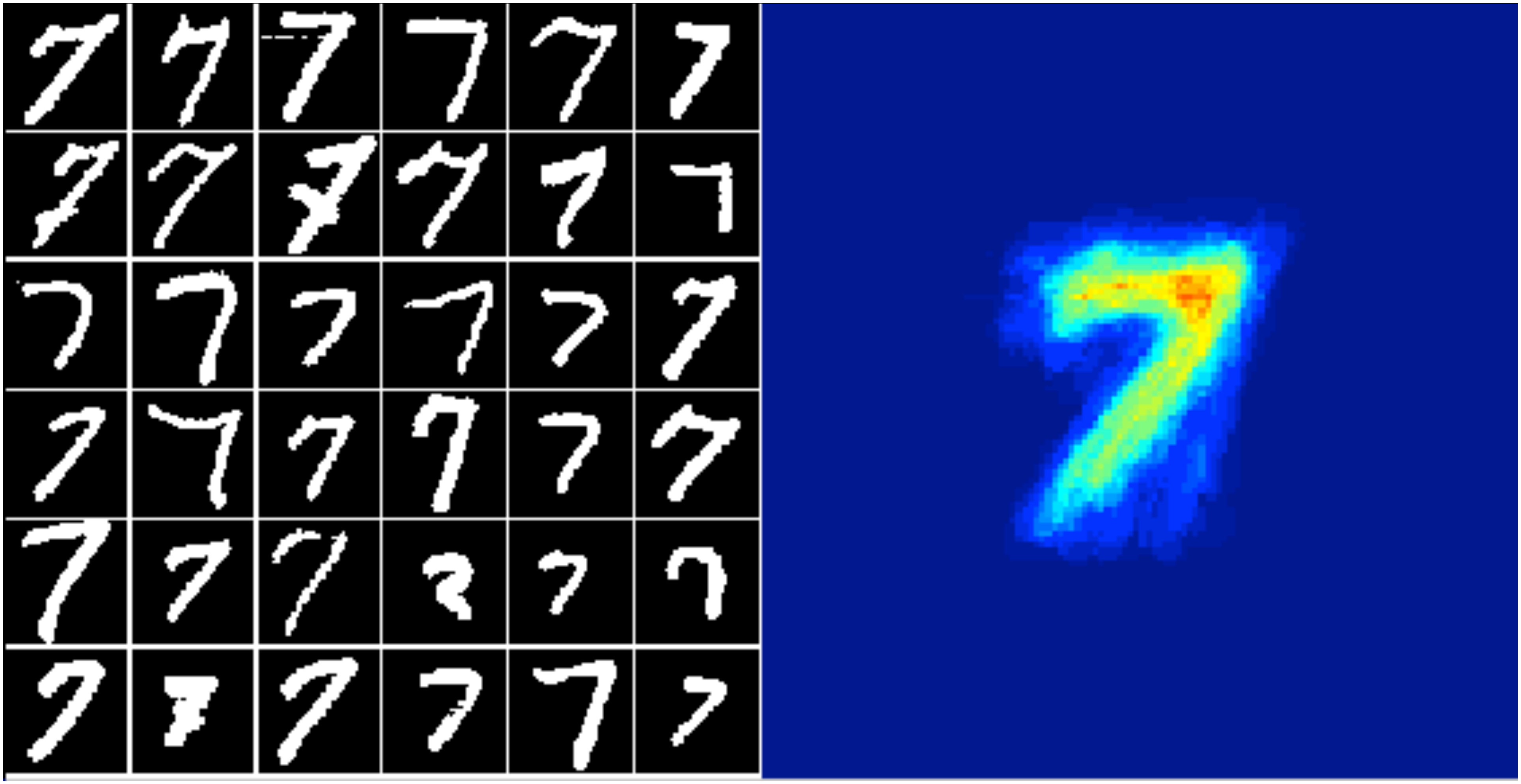
Computer Vision 691A: Joint Alignment

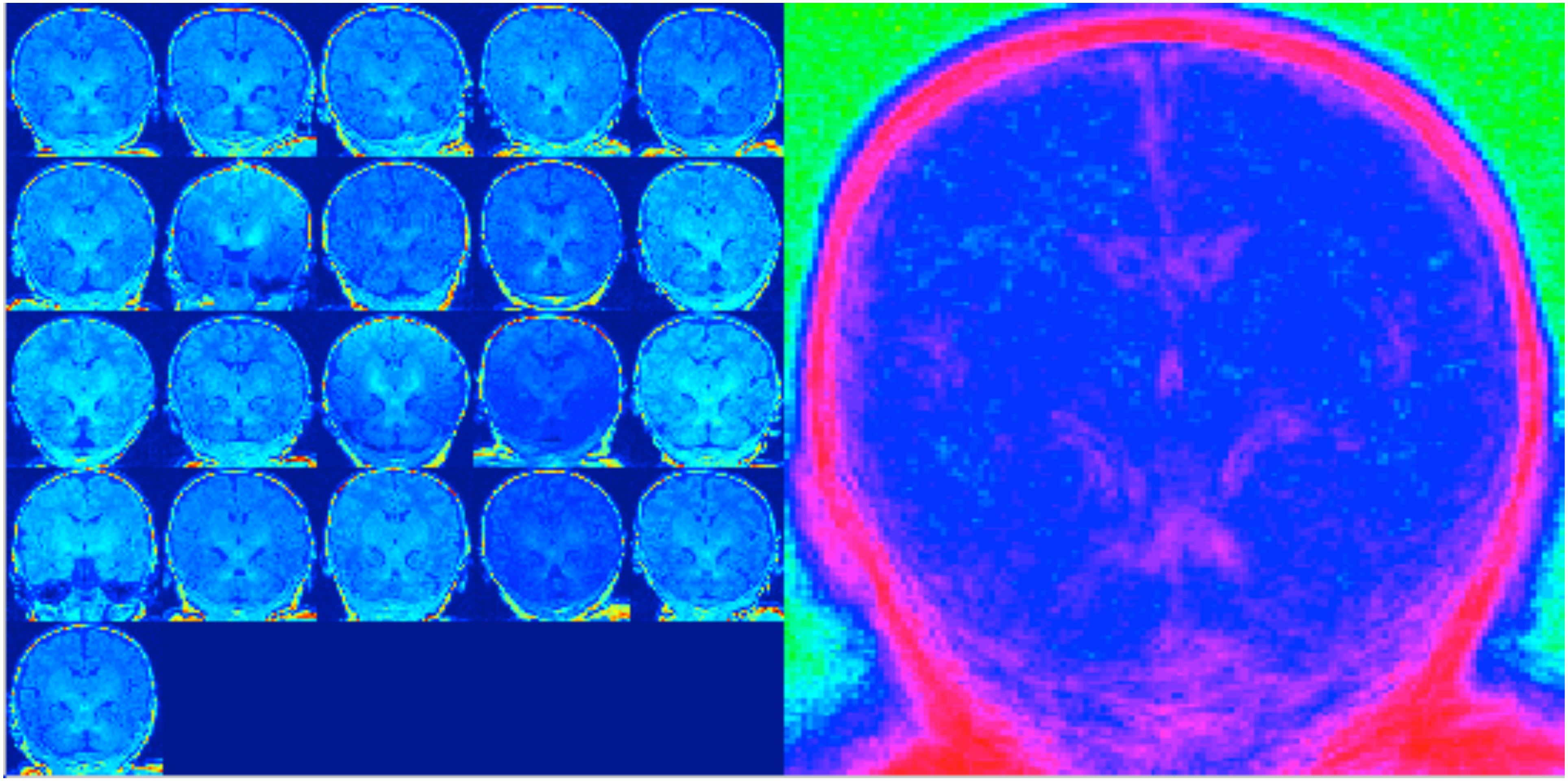
Erik Learned-Miller, with

Vidit Jain, Andras Ferencz, Gary Huang, Lilla Zollei, Sandy Wells, ….

Congealing *(CVPR 2000, PAMI 2006)*



MRI Bias Removal *(NIPS 2005, MICCAI 2005, PAMI 2006)*



Five Applications

- Image factorizations
  - For transfer learning, learning from one example
- Alignment for Data Pooling
  - 3D MR registration
  - EEG registration
- Artifact removal
  - Magnetic resonance bias removal
- Improvements to recognition algorithms
  - Alignment before recognition
- Defining anchor points for registration
  - Find highly repeatable regions for future registrations

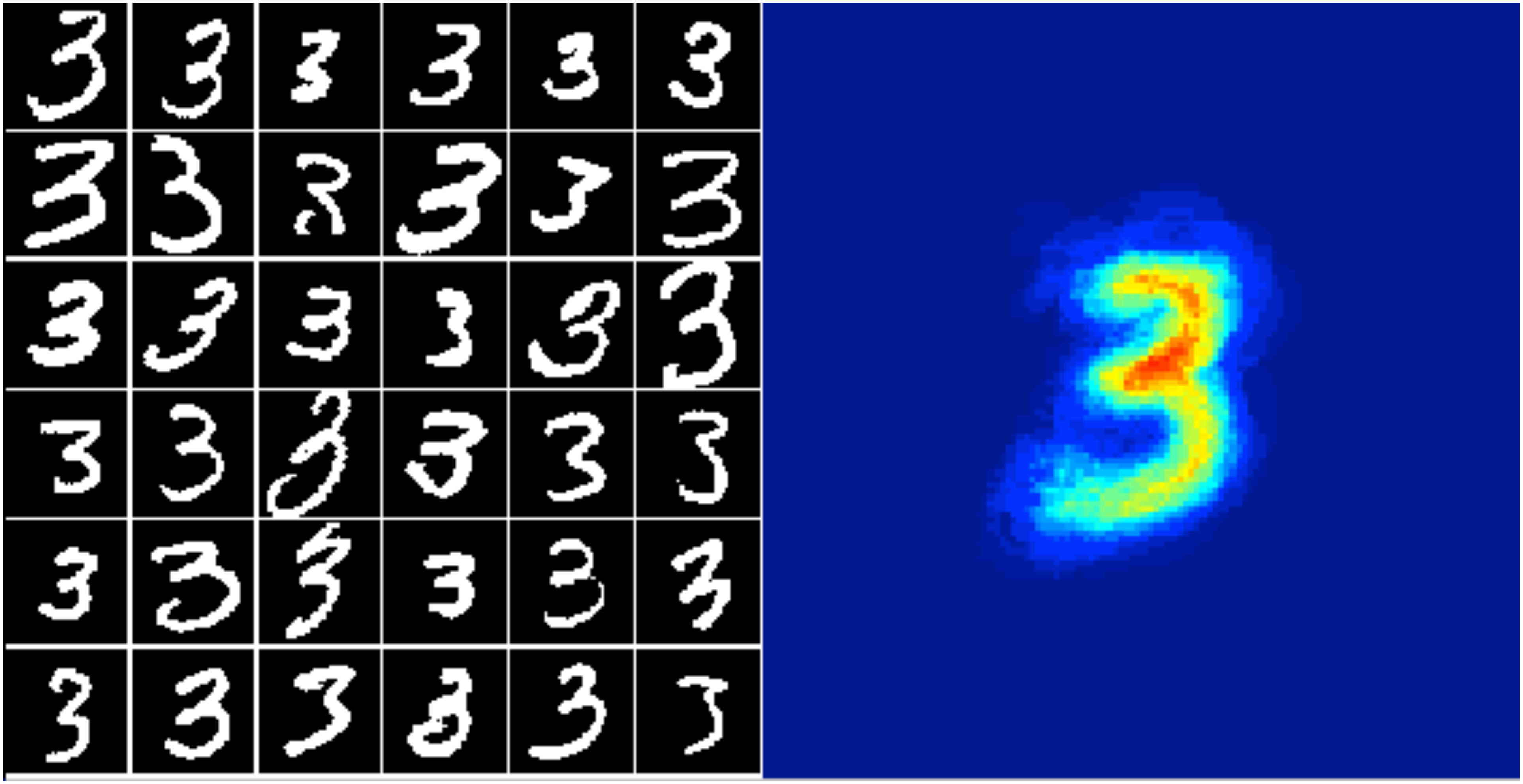
Congealing

- Process of joint “alignment” of sets of arrays (samples of continuous fields).
- 3 ingredients
  - A set of arrays in some class
  - A parameterized family of *continuous* transformations
  - A criterion of joint alignment

Congealing Binary Digits

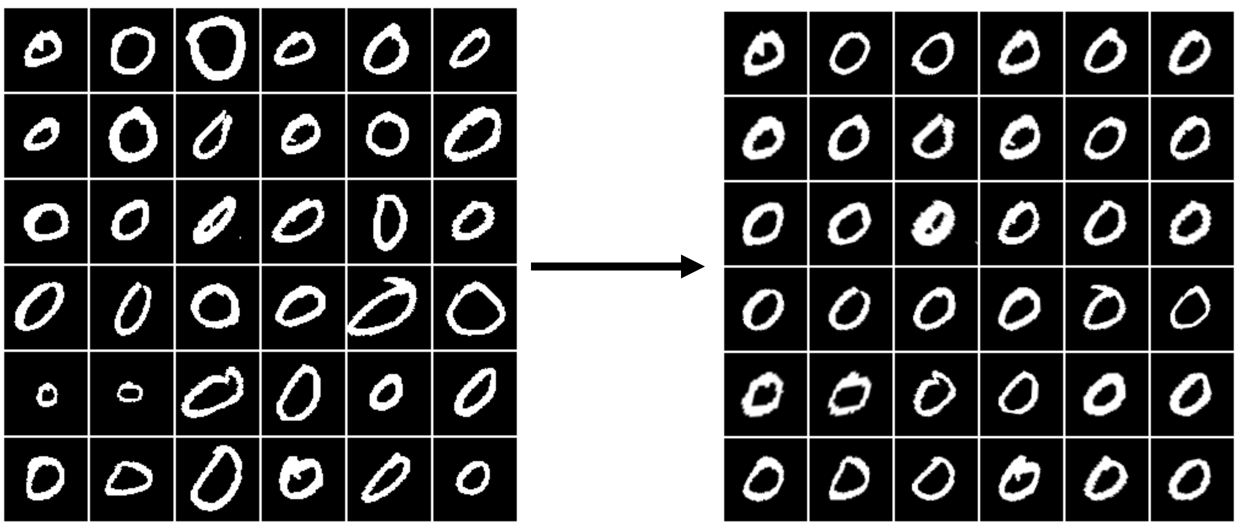
- 3 ingredients
  - A set of arrays in some class:
    - Binary images
  - A parameterized family of *continuous* transformations:
    - Affine transforms
  - A criterion of joint alignment:
    - Entropy minimization

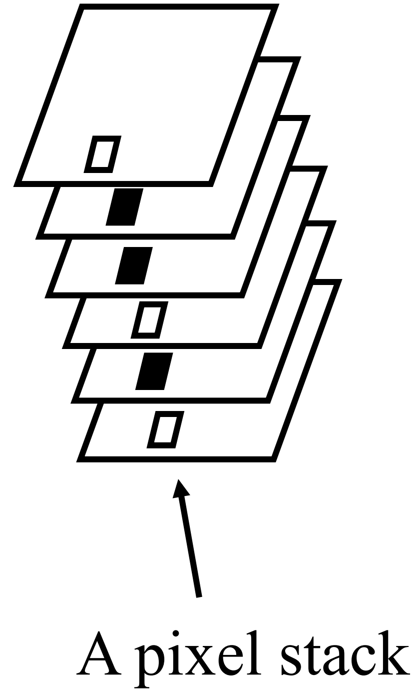
Congealing



Criterion of Joint Alignment

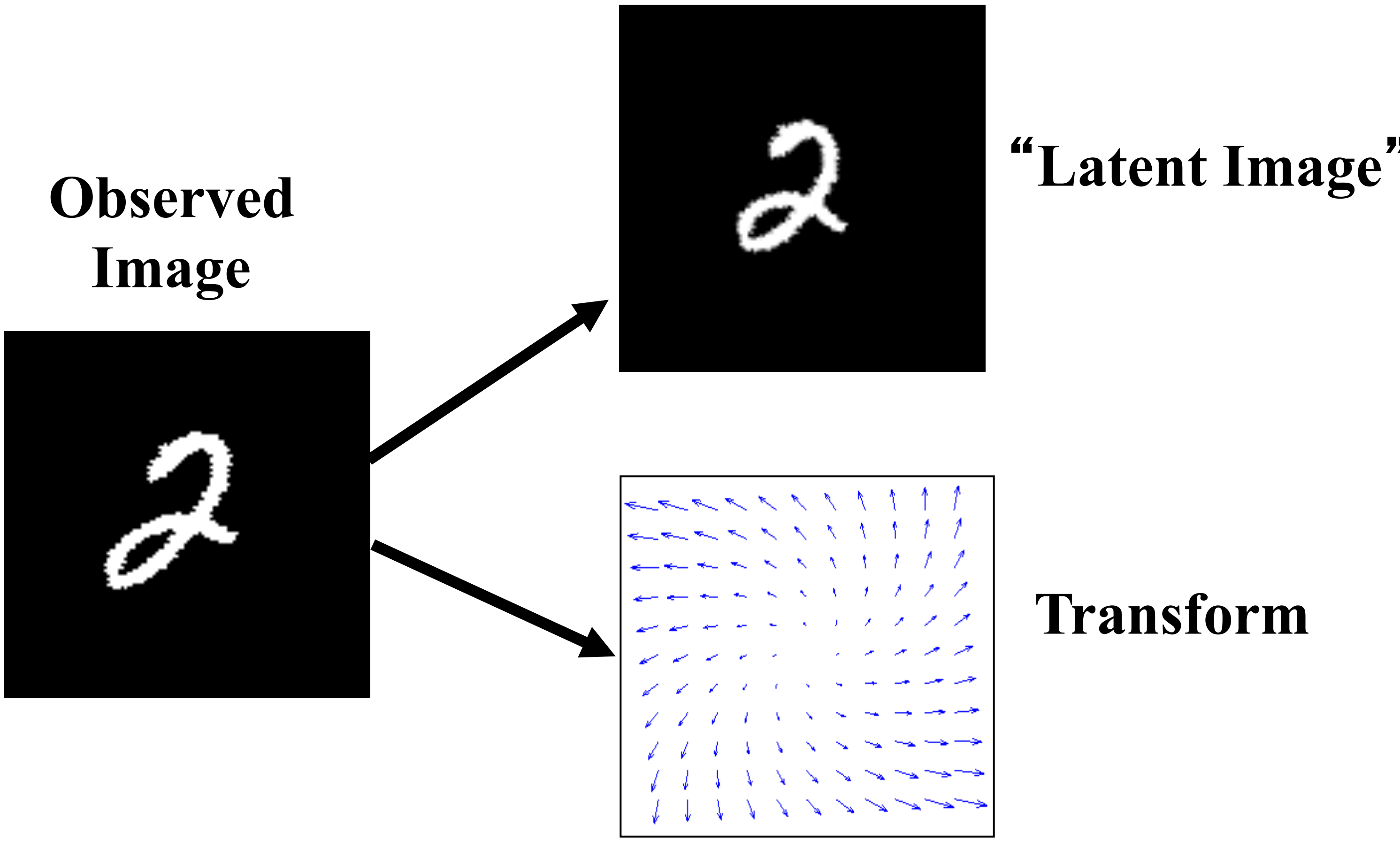
- Minimize sum of pixel stack entropies by transforming each image.





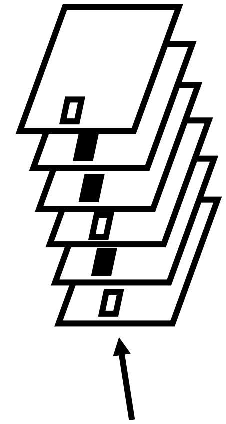
Note: Mutual Information doesn't make sense here.

An Image Factorization



 (Previous work by Grenander,, Frey and Jojic.)

$$
\begin{aligned}
\arg\max_{\mathbf{T}\in\mathcal{T}} P(\mathbf{T}|\mathbf{I}) &\overset{(a)}{=} \arg\max_{\mathbf{T}\in\mathcal{T}} P(\mathbf{I}|\mathbf{T})P(\mathbf{T}) \\
&\overset{(b)}{=} \arg\max_{\mathbf{T}\in\mathcal{T}} P(\mathbf{I}|\mathbf{T}) \\
&\overset{(c)}{=} \arg\max_{\mathbf{T}\in\mathcal{T}} P(\mathbf{L}(\mathbf{I},\mathbf{T})) \\
&= \arg\max_{\mathbf{T}\in\mathcal{T}} \prod_{x,y}\prod_{i=1}^{N} p_{x,y}(L_i(x,y)) \\
&= \arg\max_{\mathbf{T}\in\mathcal{T}} \sum_{x,y}\sum_{i=1}^{N} \log p_{x,y}(L_i(x,y)) \\
&\overset{(d)}{\approx} \arg\min_{\mathbf{T}\in\mathcal{T}} \sum_{x,y} H(p_{x,y}) \\
&\overset{(e)}{\approx} \arg\min_{\mathbf{T}\in\mathcal{T}} \sum_{x,y} \hat{H}_{\text{Vasicek}}(L_1(x,y),\ldots,L_N(x,y))
\end{aligned}
$$



A pixel stack

Why Minimize Entropy?

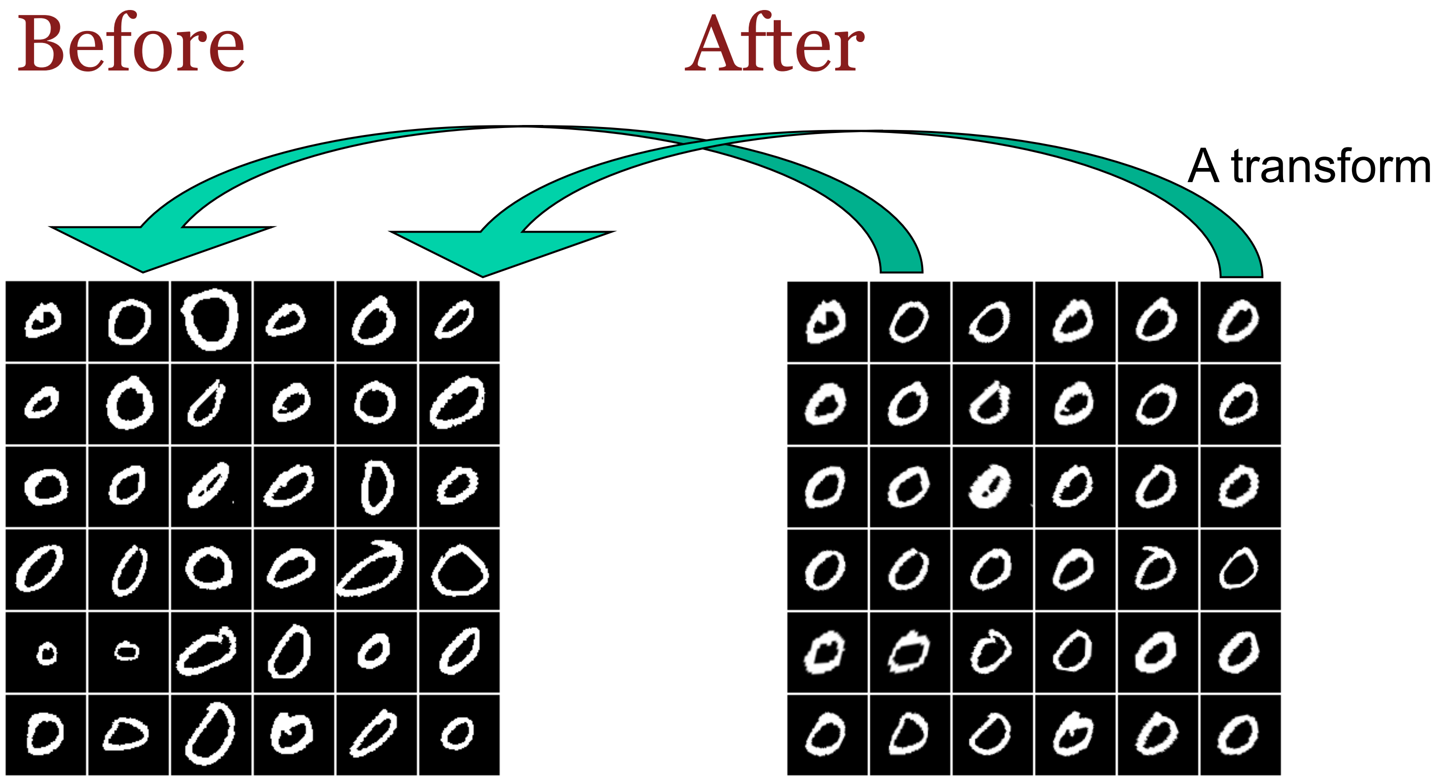
- Negative entropy is just the average log likelihood of points under their own distribution.

Min entropy =
maximum non-parametric likelihood

The Independent Pixel Assumption

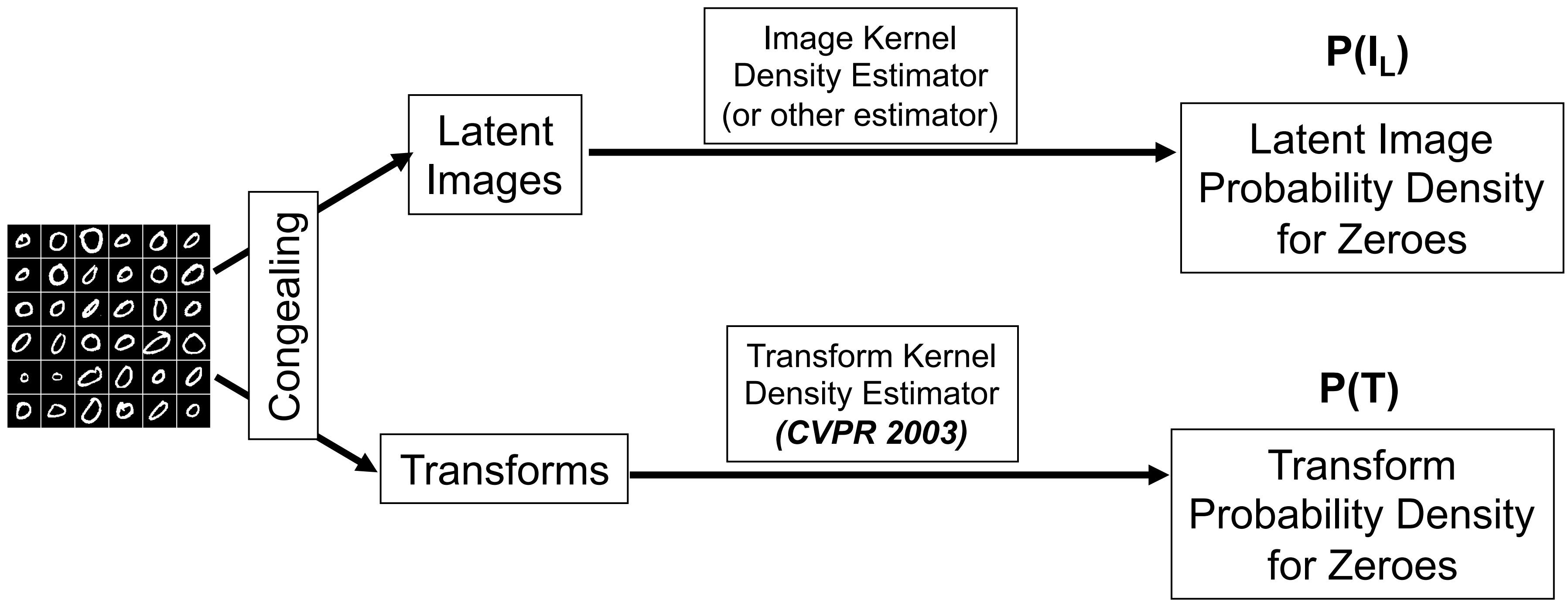
- Model assumes independent pixels
- A poor generative model:
  - True image probabilities don't match model probabilities.
  - Reason: heavy dependence of neighboring pixels.
- However! This model is great for alignment and separation of causes!
  - Why?
  - Relative probabilities of "better aligned" and "worse aligned" are usually correct.
- Once components are separated, a more accurate (and computationally expensive) model can be used to model each component.

Congealing



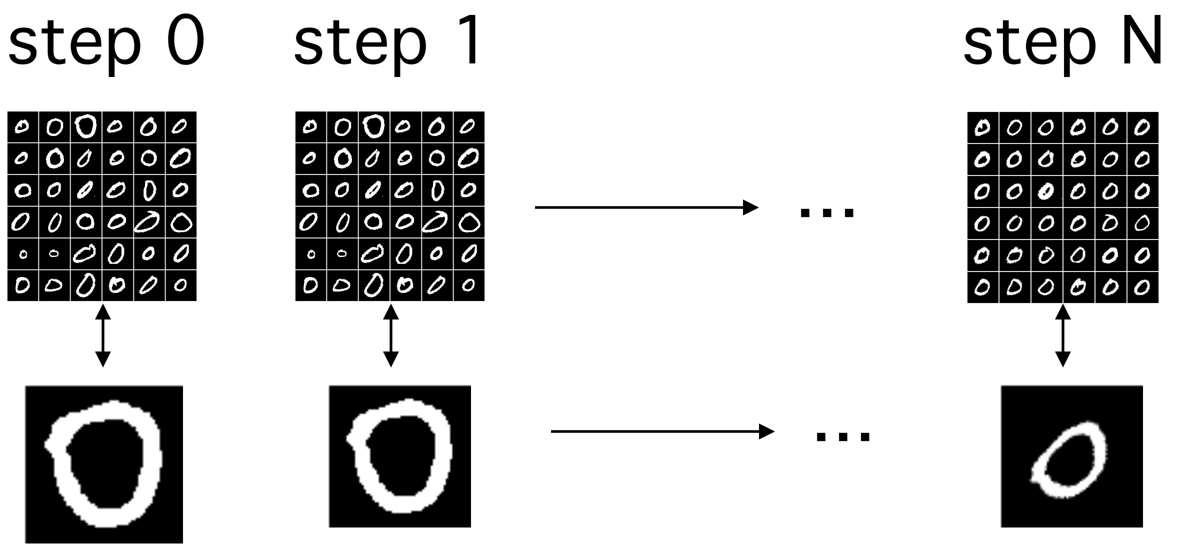
Each pair implicitly creates a sample of the transform T.

Character Models



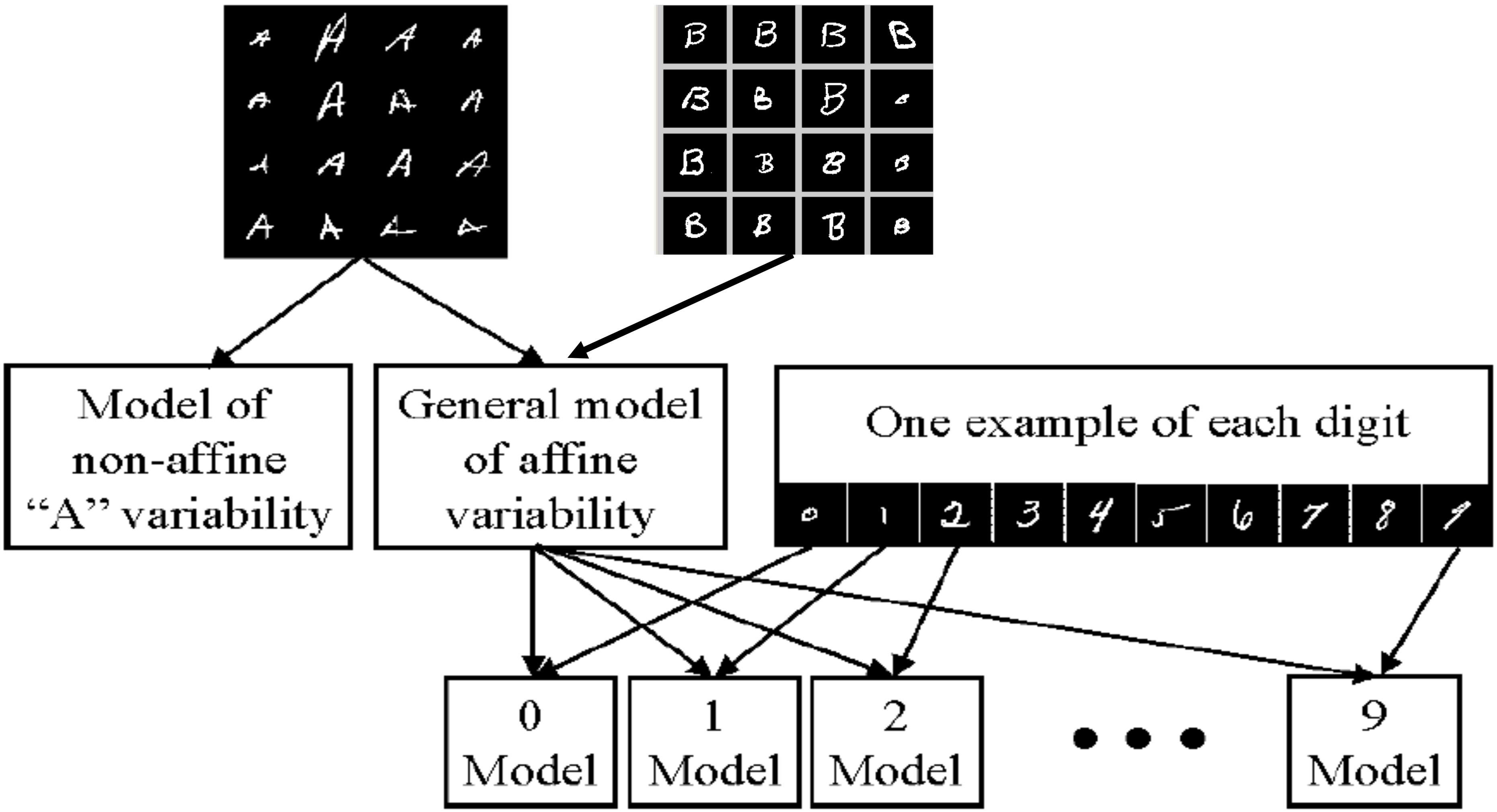
How do we line up a new image?

Sequence of successively “sharper” models



Take one gradient step with respect to each model.

Digit Models from One Example



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Next Application:
Alignment of 3D Magnetic Resonance Volumes

Lilla Zollei, Sandy Wells, Eric Grimson

Congealing MR Volumes: Joint Registration

- 3 ingredients
  - A set of arrays in some class:
    - Gray-scale MR volumes
  - A parameterized family of *continuous* transformations:
    - 3-D affine transforms
  - A criterion of joint alignment:
    - Grayscale entropy minimization

- Purposes:
  - Pooling data for fMRI studies
  - Building general purpose statistical anatomical atlases

Why Entropy?

- Drives volumes to having mass concentrated in a small number of tissues.
- Comparison to Transformed Mixture of Gaussians (Frey and Jojic).
- Convexity of entropy in distribution.

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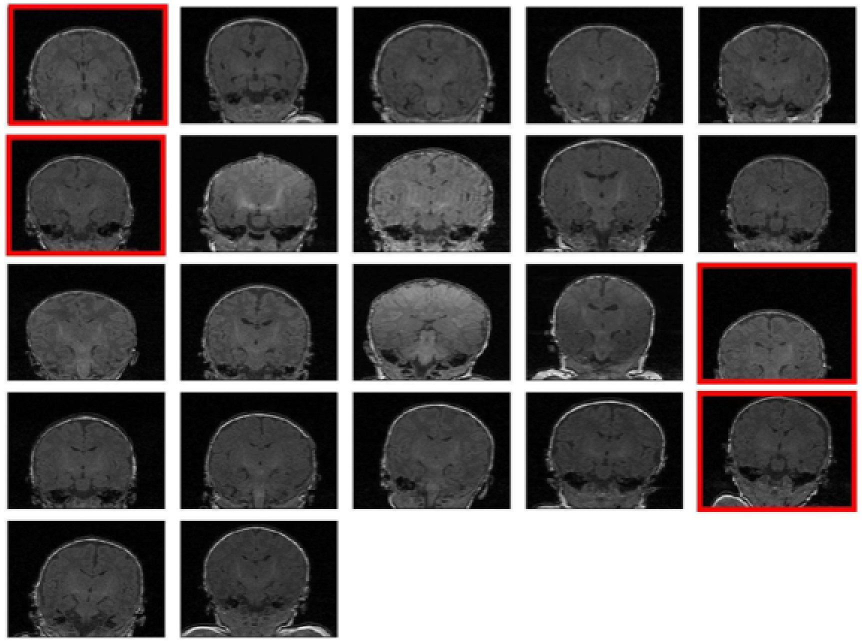
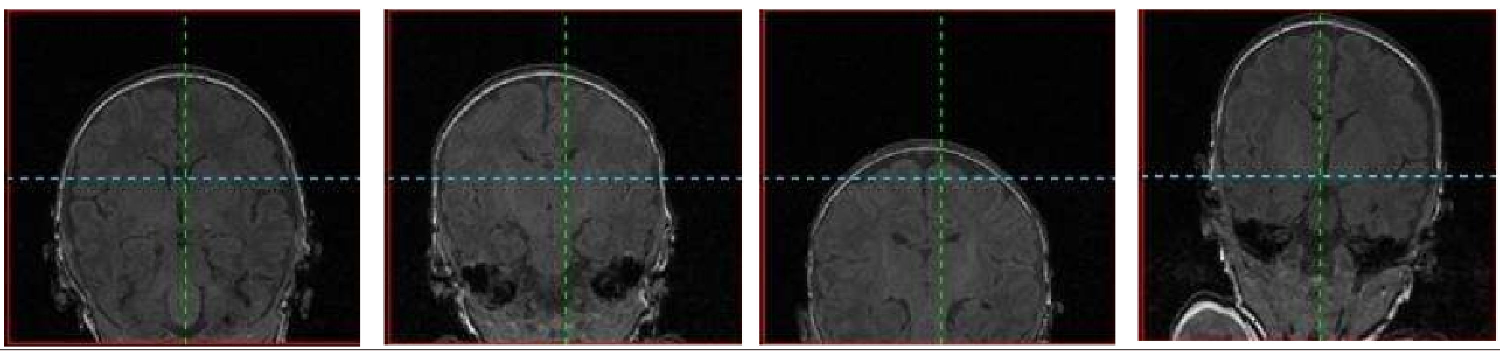
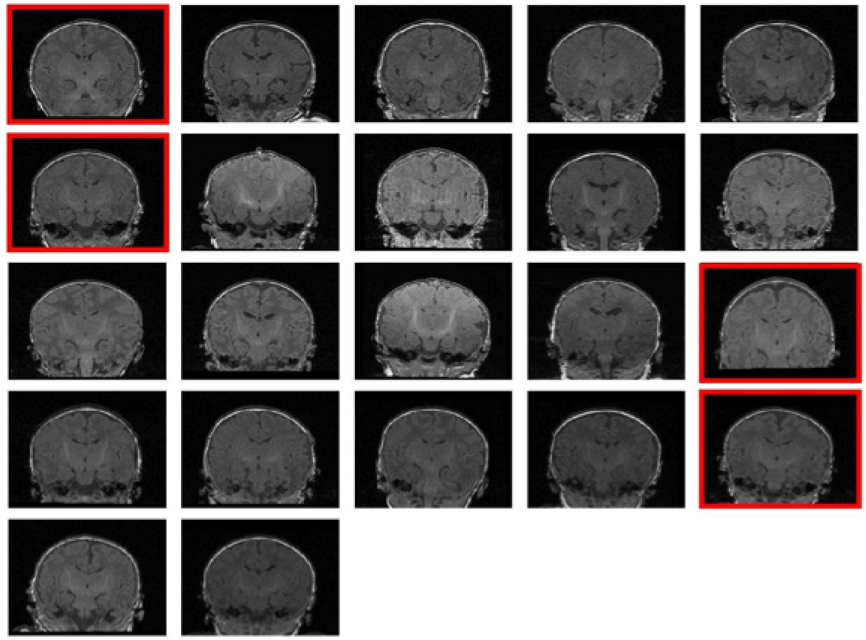
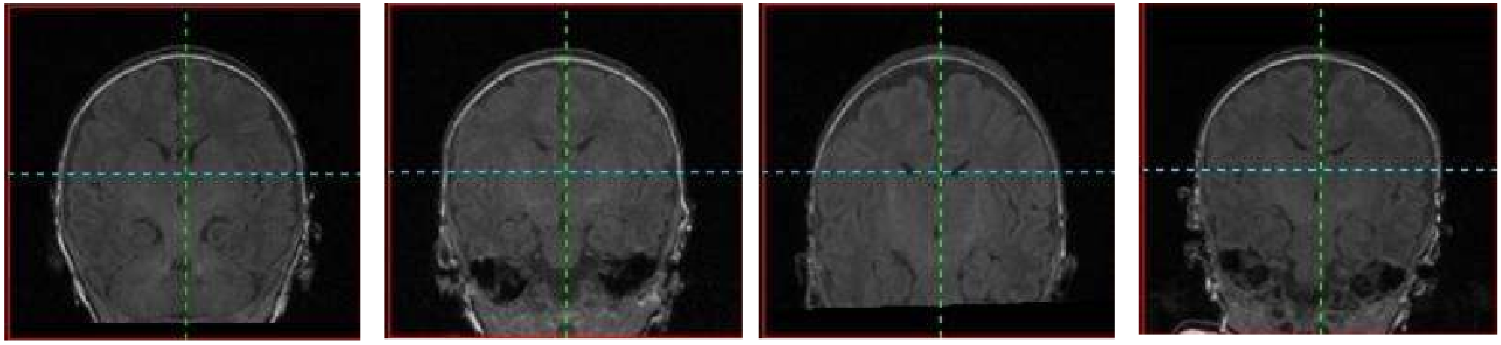
Congealing Gray Brain Volumes *(ICCV 2005 Workshop)*



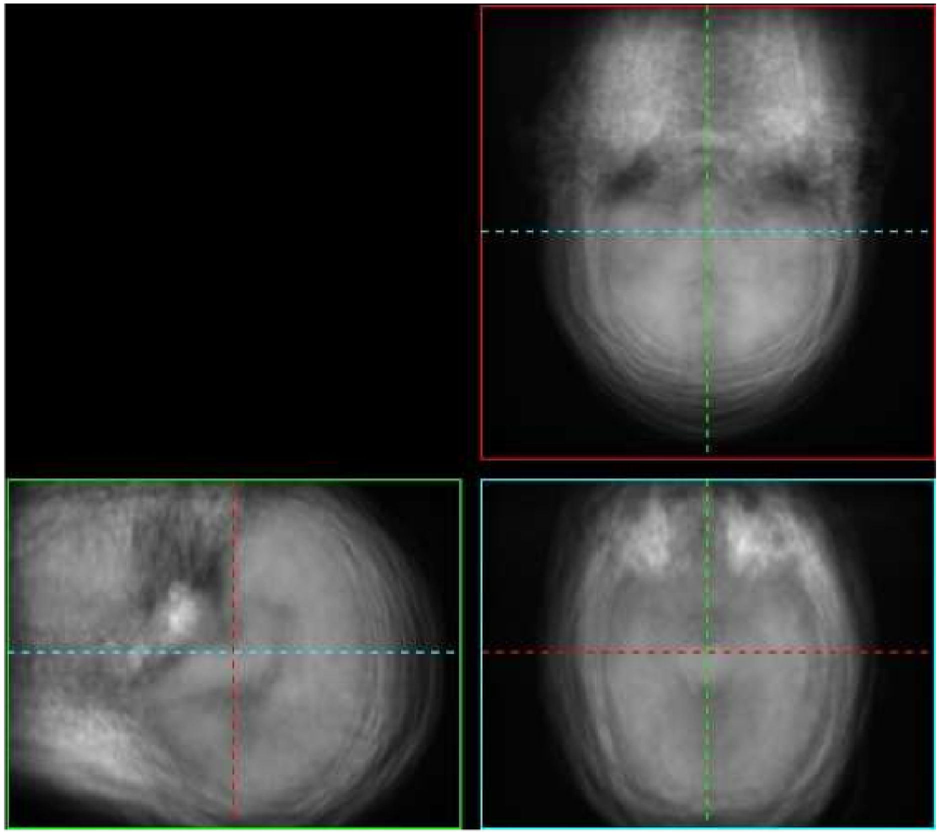


Aligned Volumes

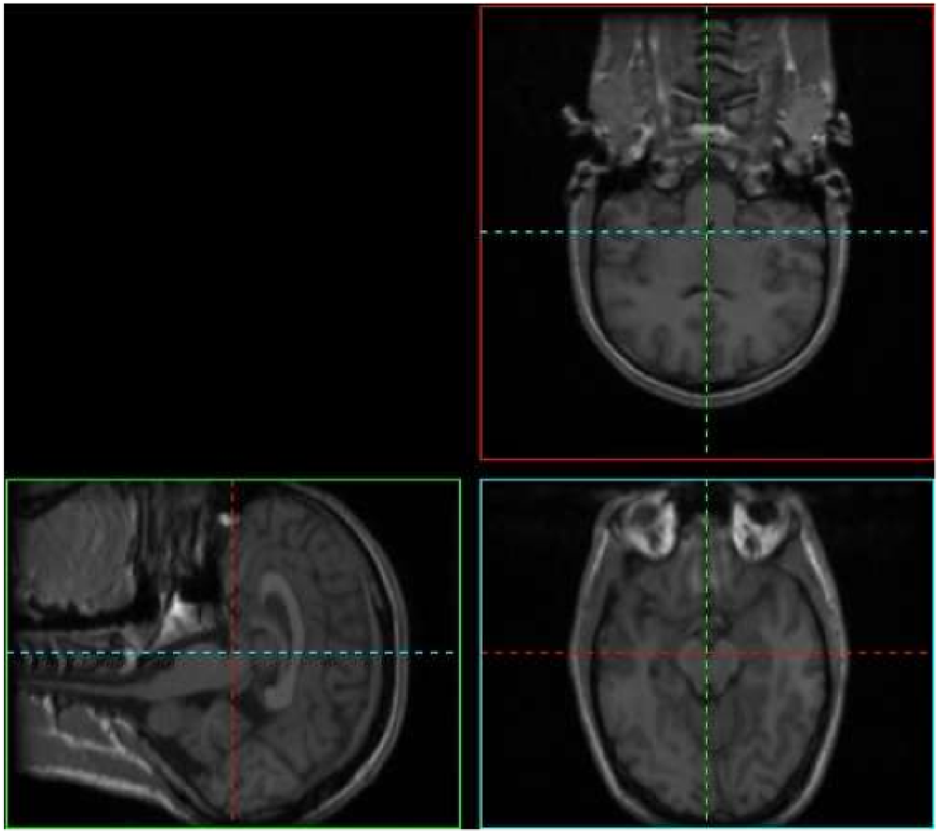




Validation: Synthetic Data



Unaligned input data sets



Aligned input data sets

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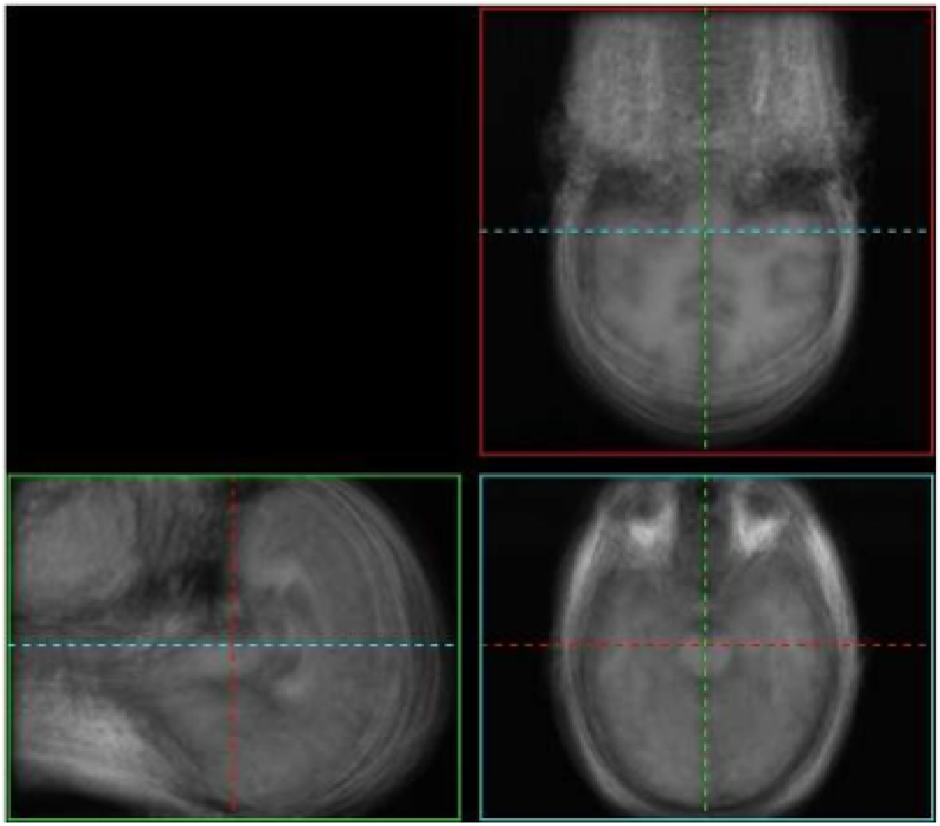
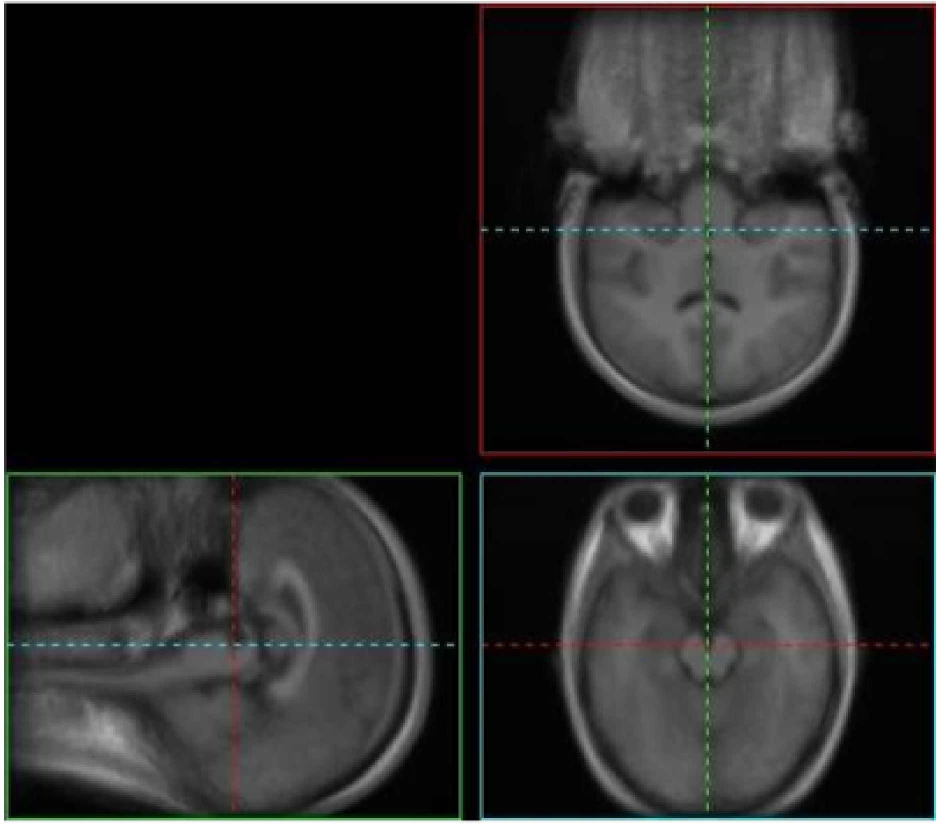
Real Data



Unaligned input data sets

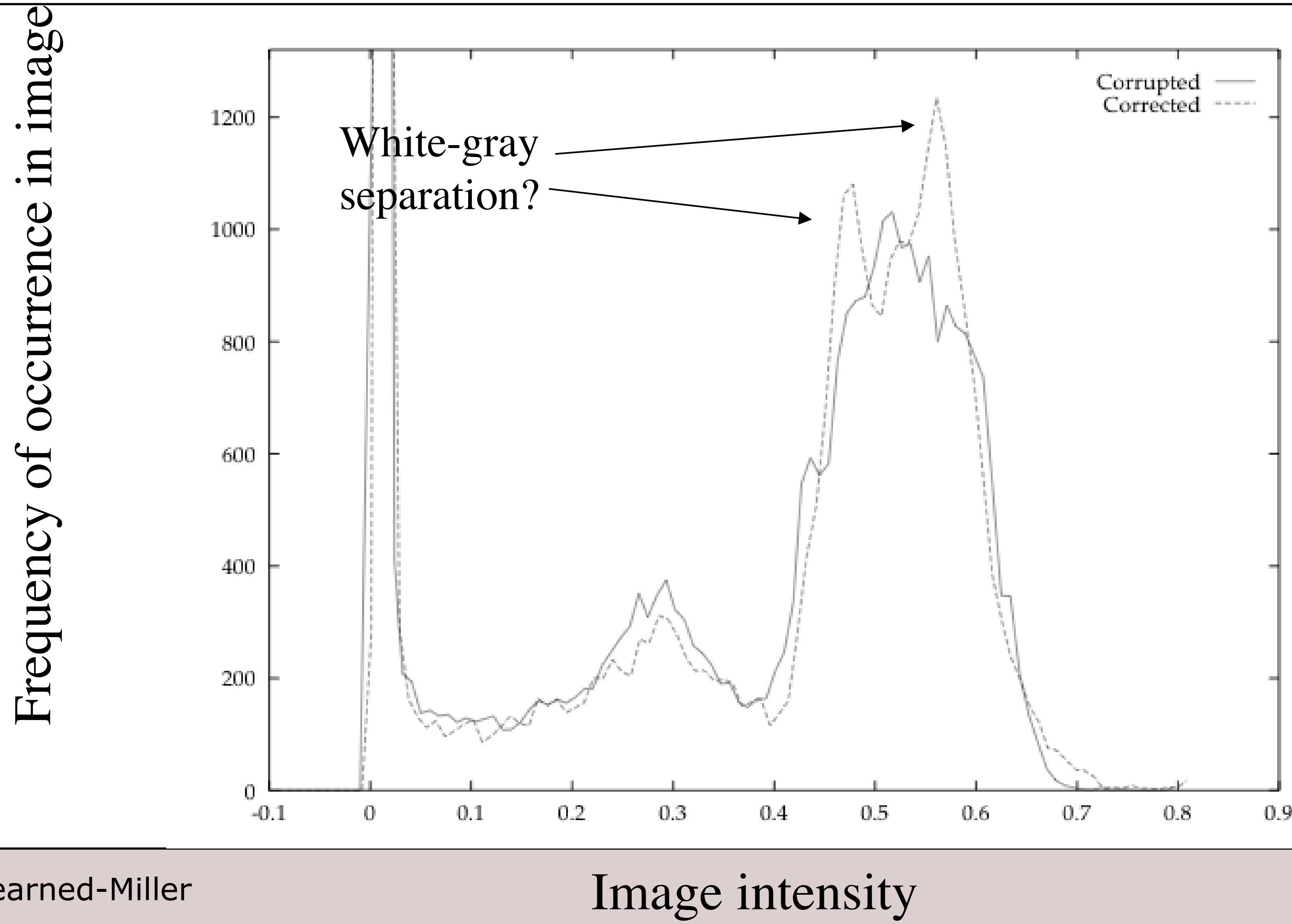


Aligned input data sets

Data set: 28 T1-weighted MRI; [256x256x124] with (.9375, .9375, 1.5) mm^3 voxels

Experiment: 2 levels; 12-param. affine; N = 2500; iter = 150; time = **1209 sec!!**

Grayscale Entropy Minimization

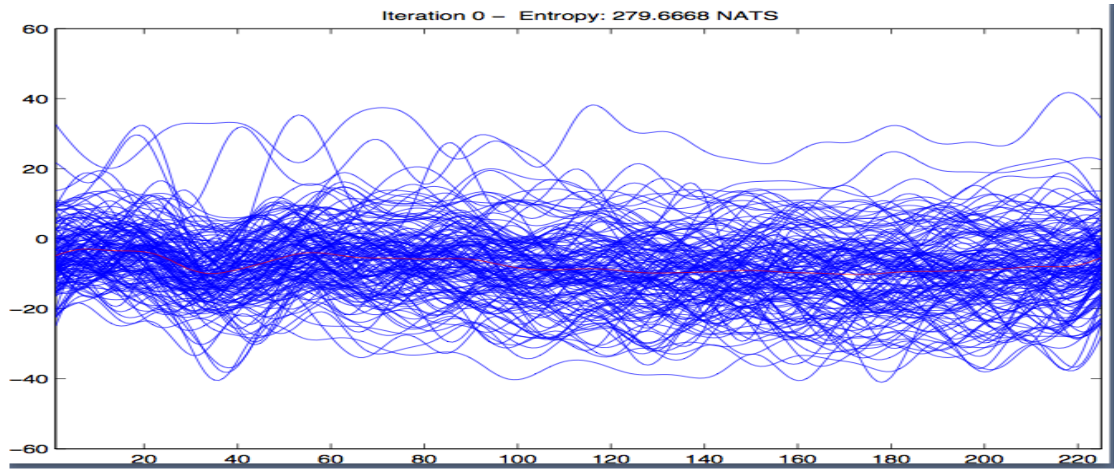


MR Congealing Challenges

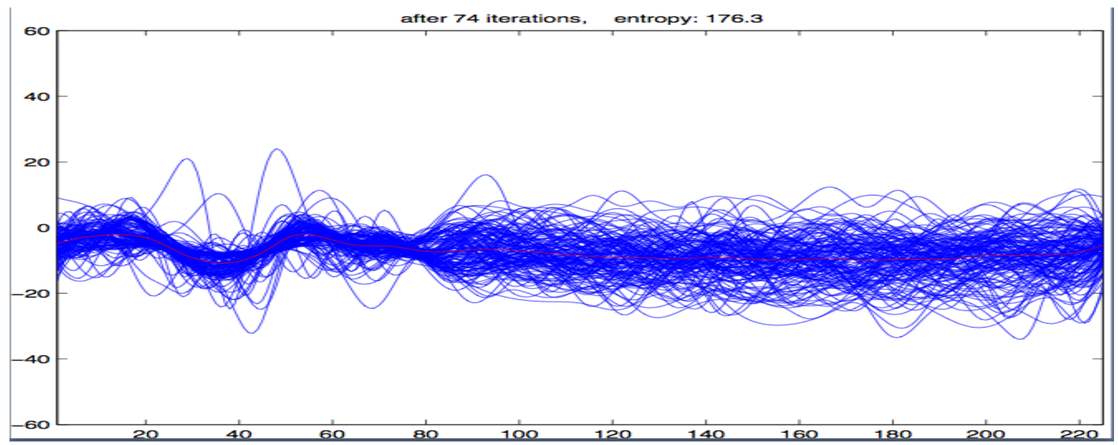
- Big data
  - 8 million voxels per patient
  - 100 patients
  - 12 transform *parameters*
  - 20 iterations
- Techniques:
  - Stochastic sampling
  - Multi-resolution techniques
  - Don't use visual basic

Signal to Noise in Event Related Potentials

Before congealing



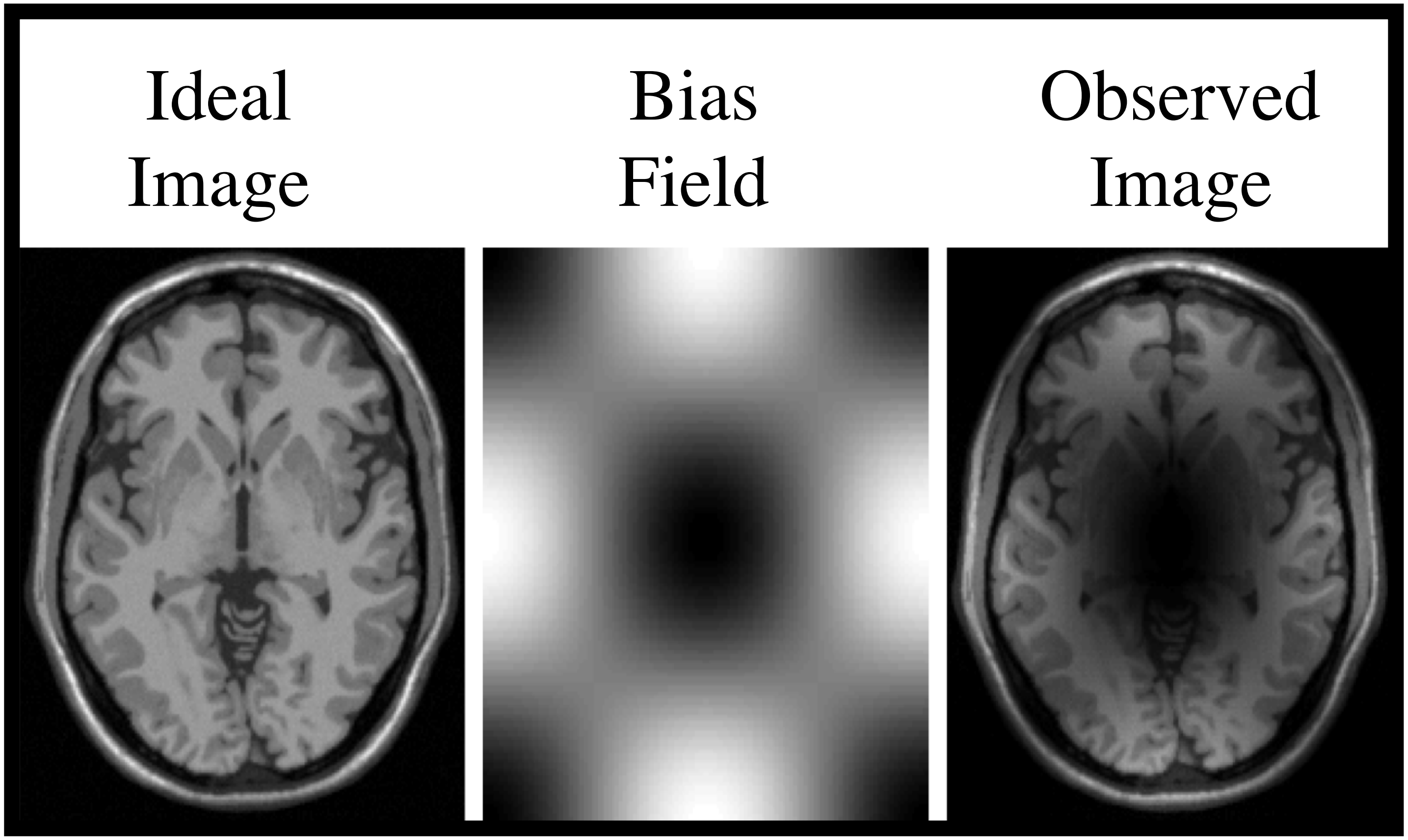
After congealing



Next Application:
Bias Removal in Magnetic Resonance Images

Parvez Ahammad, Vidit Jain

The Problem

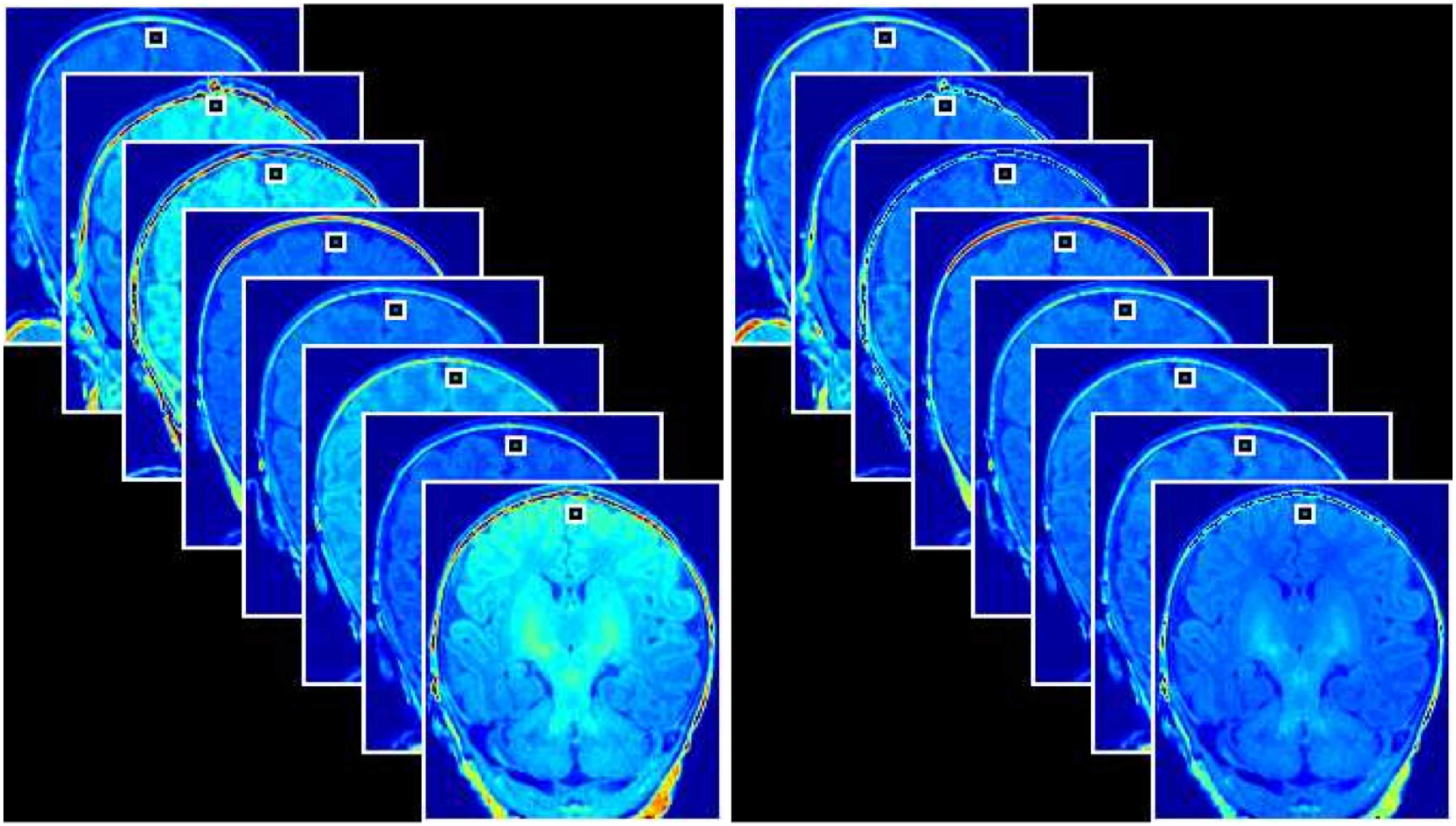


Bias fields have low spatial frequency content

Bias Removal in MR as a Congealing Problem

- 3 ingredients
  - A set of arrays in some class:
    - MR Scans of Similar Anatomy (2D or 3D)
  - A parameterized family of *continuous* transformations:
    - Smooth brightness transformations
  - A criterion of joint alignment:
    - Entropy minimization

Congealing with brightness transforms



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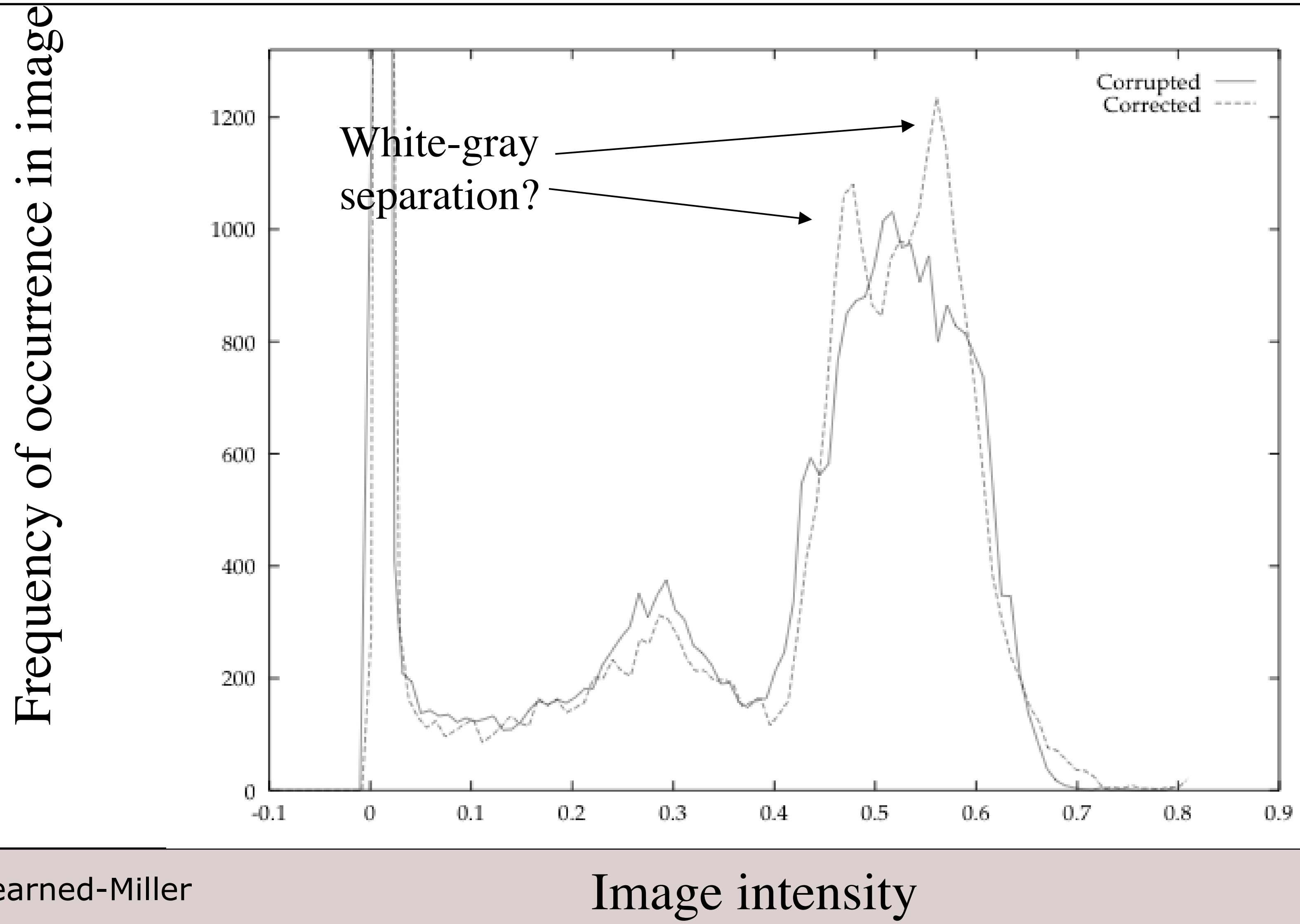
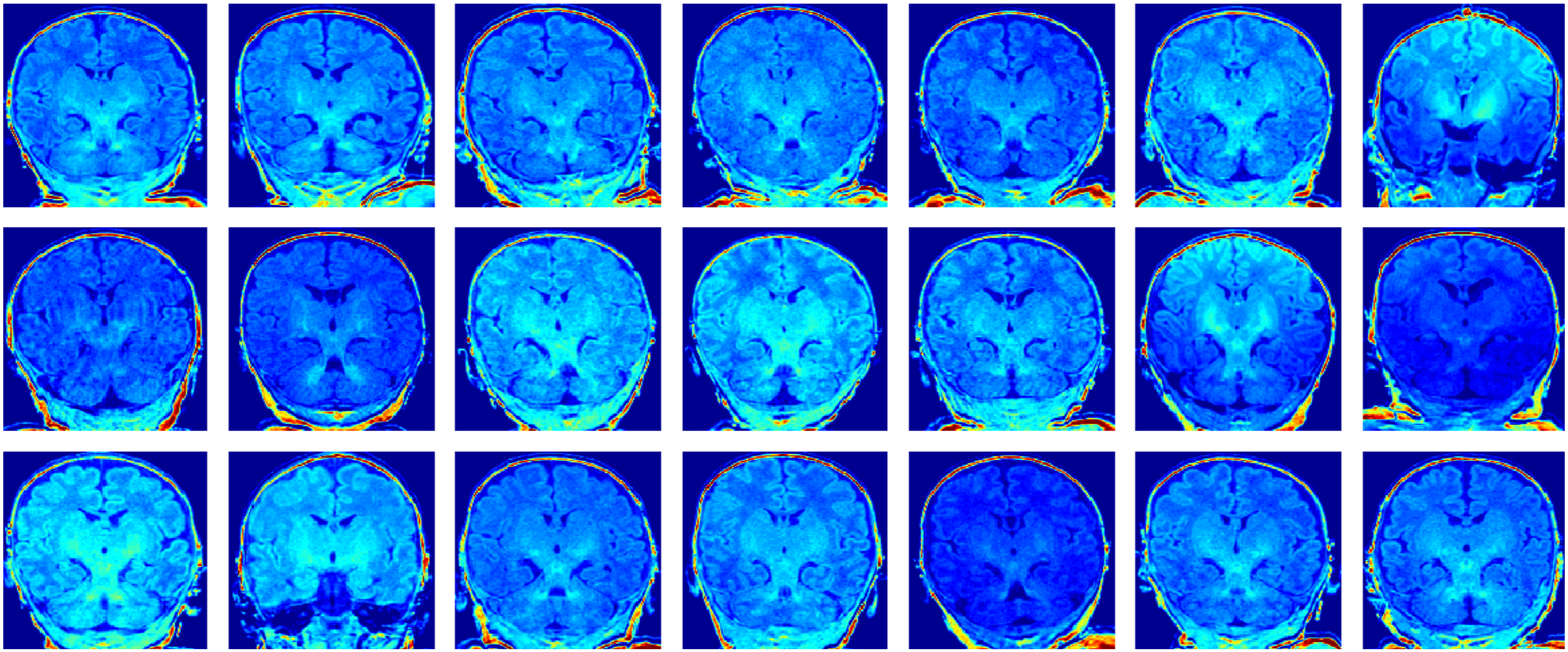
Grayscale Entropy Minimization



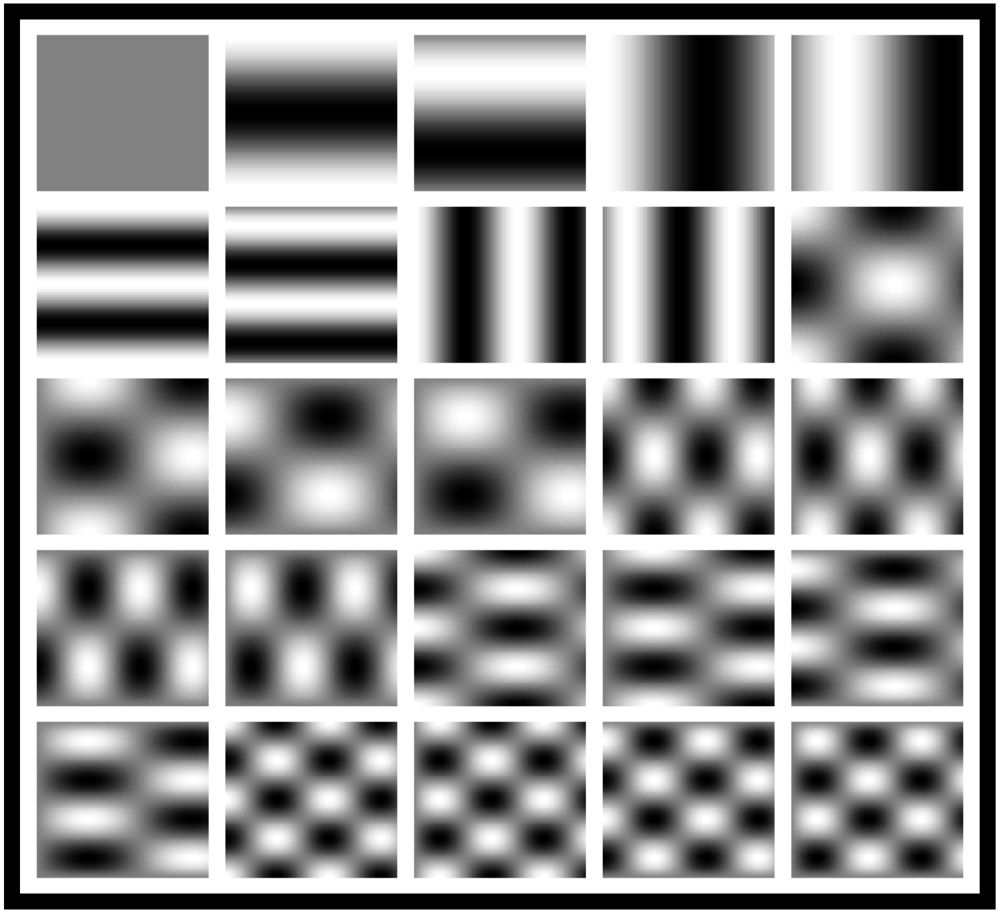
Some Infant Brains

(thanks to Inder, Warfield, Weisenfeld)



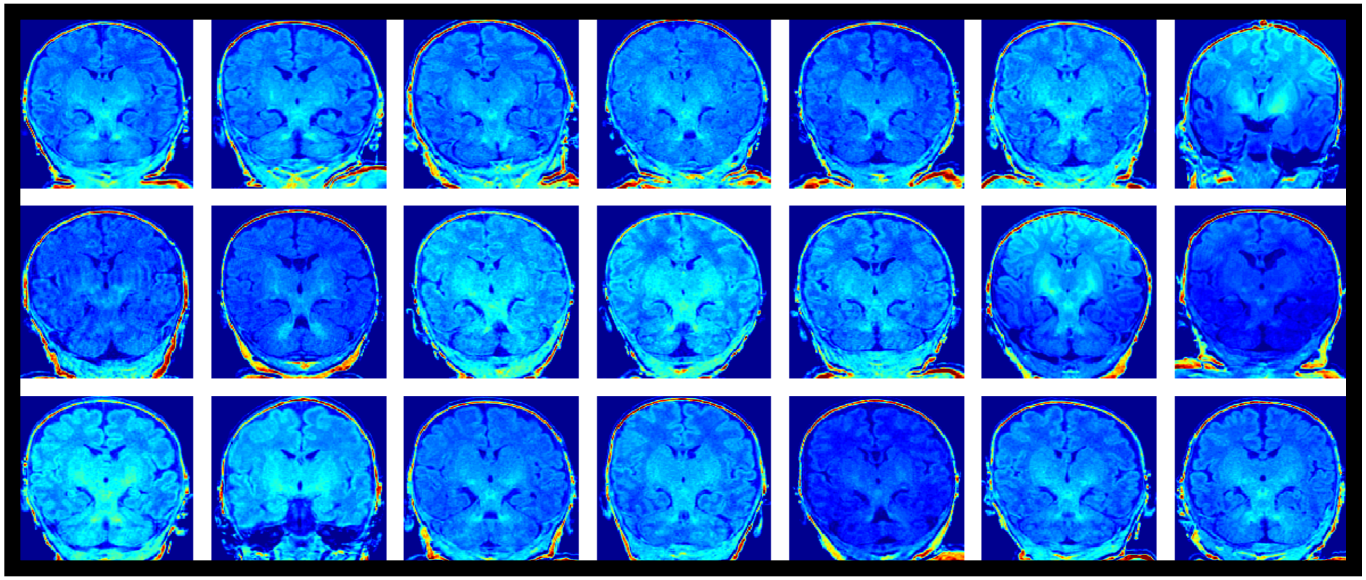
- Pretty well registered (not perfect)
- Pretty bad bias fields

Fourier Basis for Smooth Bias Fields

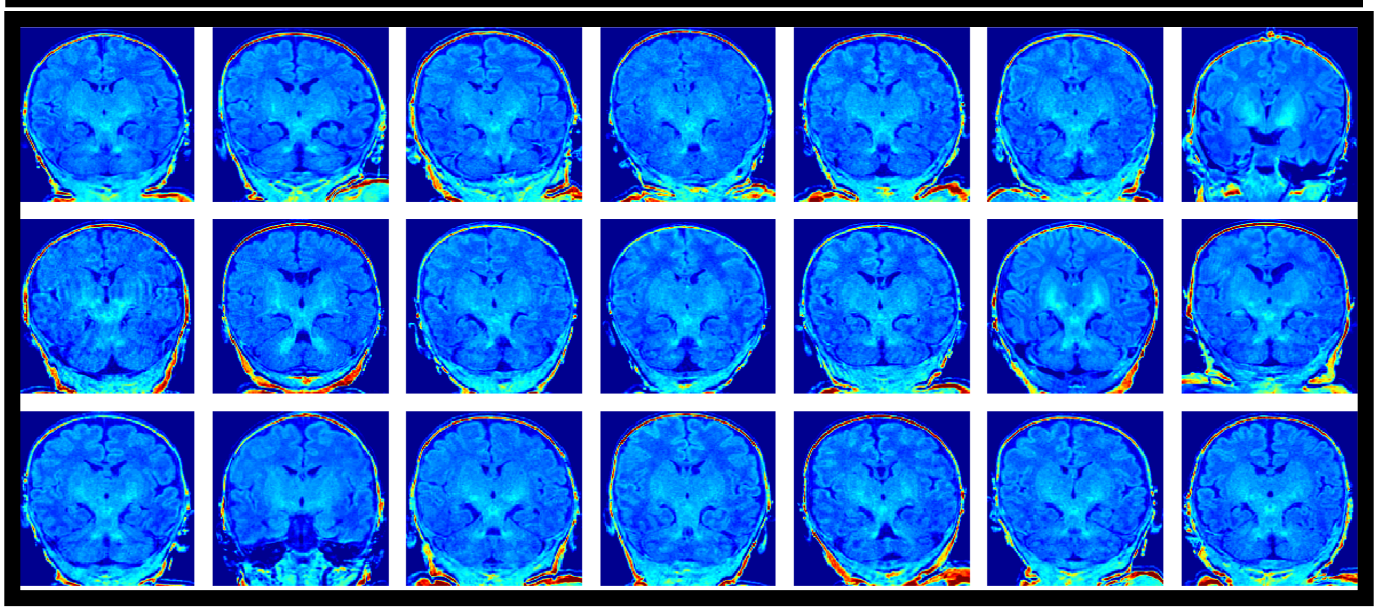


Results

Original Images



Bias Corrected Images



Assumptions

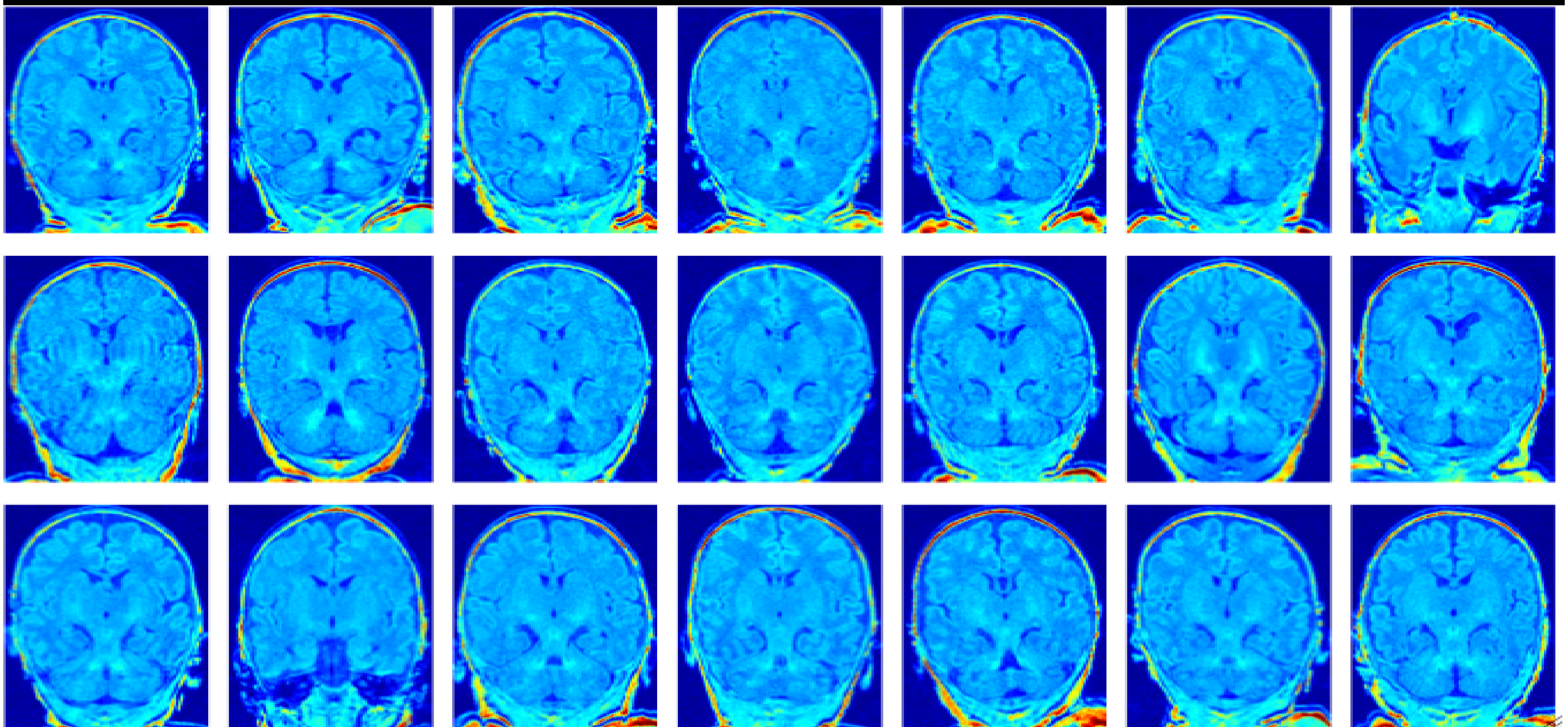
- Pixels in same location, across images, are independent.
  - When is this not true?
    - Systematic bias fields.
- Pixels in same image are independent, given their location.
  - Clearly not true, but again, doesn't seem to matter.
- Bias fields are truly bandlimited.

Some Other Recent Approaches

- Minimize entropy of intensity distribution in single image
  - Viola (95)
  - Warfield and Weisenfeld extensions (current)
- Wells (95)
  - Use tissue models and maximize likelihood
  - Use Expectation Maximization with unknown tissue type
- Fan (02)
  - Incorporate multiple images from different coils, but same patient.

Potential difficulties with single image method

- If there is a component of the brain that looks like basis set, it will get eliminated.
- Does this occur in practice?
  - Yes!



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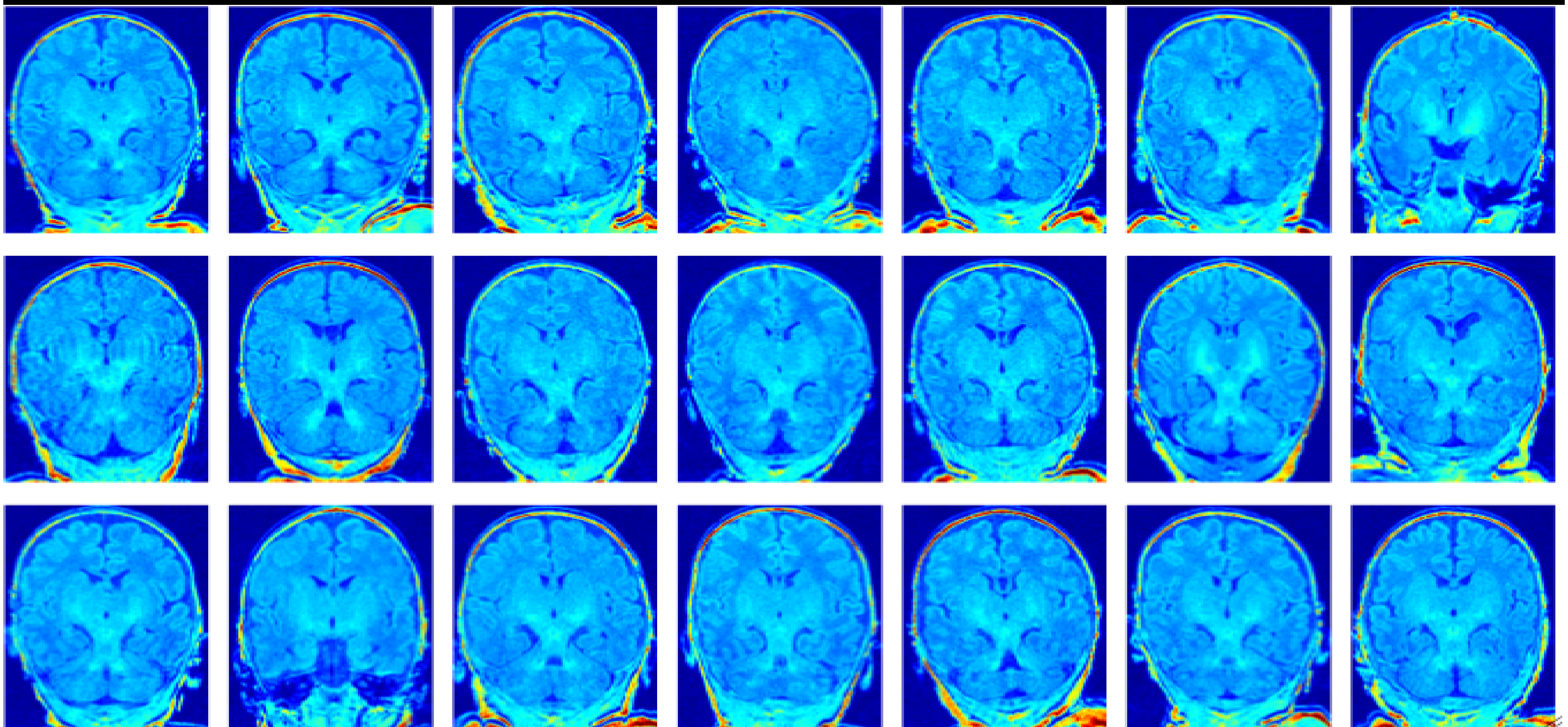

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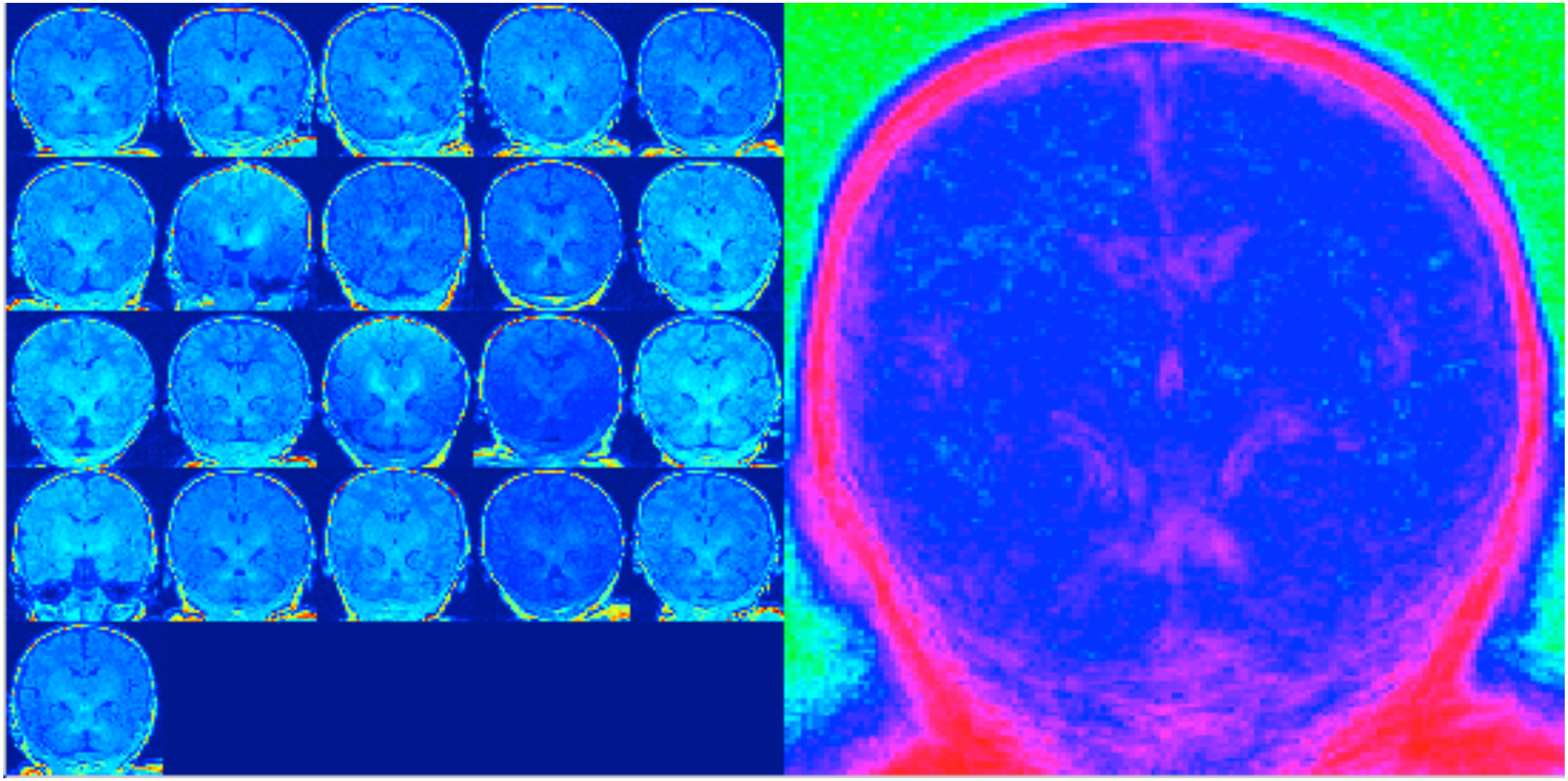
MRI Bias Removal



Summary

- Remove source of variability
  - MR bias removal
  - MR anatomical alignment
  - ERP signal alignment
  - Better alignment for recognition (hyper-features)
- Model a source of variability
  - Form factorized models (learning from one example)
- Define points of high saliency and repeatability (anchor points) for difficult registration problems