Non-rigid Registration of Longitudinal Brain Tumor Treatment MRI

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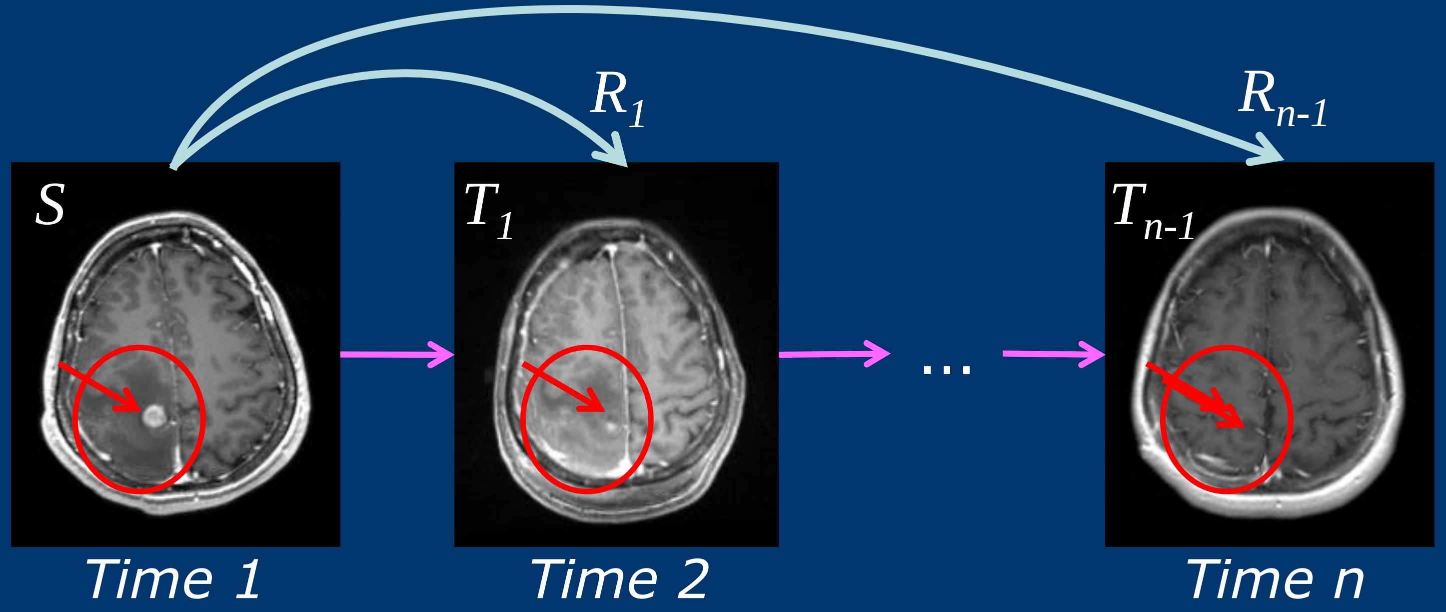
Image Registration Goal

- Align longitudinal brain tumor treatment MRI



- Challenge: Missing Correspondences
  - Changes in tumors, edema, resection…

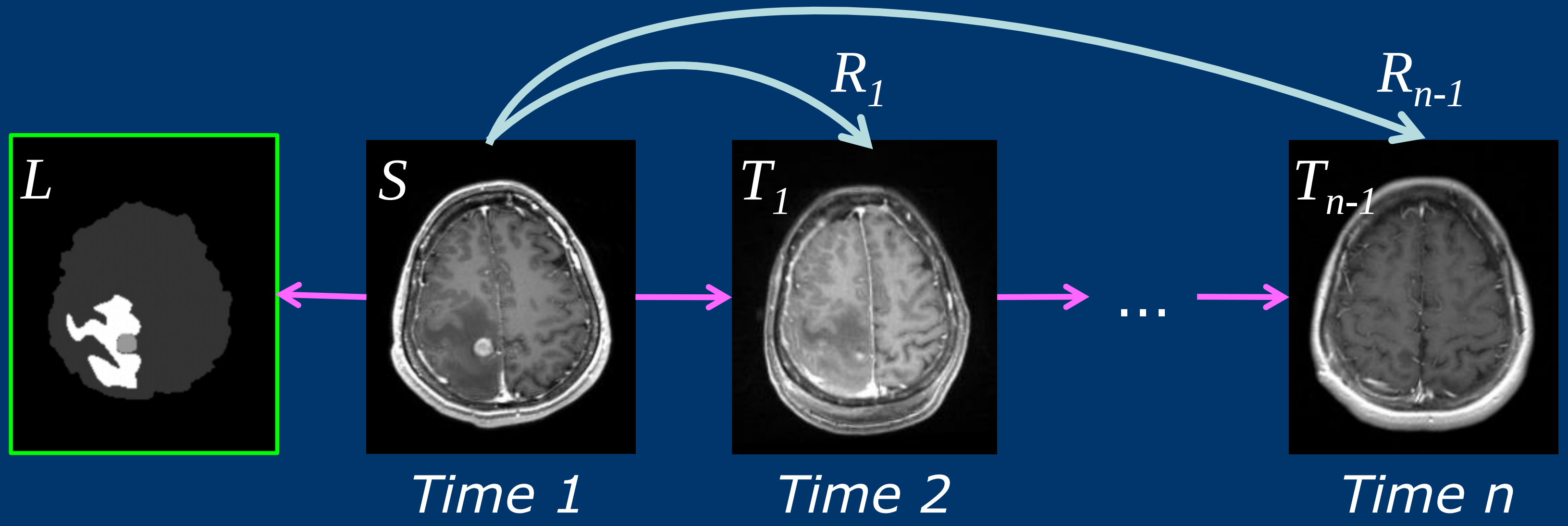
Some Approaches to Handle Missing Correspondences

- First extract points for matching[1]
- Simulate tumor growth in normal brain[2]
- Adapted demons registration[3]
- Simultaneously estimate missing data[4]
  - No prior information
- Our recent work aligning brain resection MRI[5]

→ NOW: extend to longitudinal brain tumors, with
  - Intensity information
  - Allowing larger deformations near lesion

[1]Liu et al., ISBI 2010; [2]Zacharaki et al., Neuroimage 2009; [3]Risholm et al., IPMI 2009
[4]Periaswamy and Farid, MedIA 2006; [5]Chitphakdithai and Duncan, MICCAI 2010

Registration Framework: Setup



- Include "hidden" label map L to indicate matching vs. missing correspondences
- Maximum a posteriori framework:

$$\hat{R} = \arg\max_{R} \log \sum_{L} p(R, L \mid S, T)$$

Registration Framework: EM Algorithm

- E-Step: Label Map Weights $p\left(L(\mathbf{x})=l \mid S,T,R^k\right)=$

$$\frac{\overbrace{p\left(T\left(R^k(\mathbf{x})\right)\mid S,R^k L(\mathbf{x})=l\right)}^{\textit{Likelihood}}\overbrace{p\left(S(\mathbf{x})\mid L(\mathbf{x})=l\right)}^{\textit{Intensity Prior}}\overbrace{p\left(L(\mathbf{x})=l\right)}^{\textit{Label Map Prior}}}{\sum_{l'} p\left(T\left(R^k(\mathbf{x})\right)\mid S,R^k,L(\mathbf{x})=l'\right)p\left(S(\mathbf{x})\mid L(\mathbf{x})=l'\right)p\left(L(\mathbf{x})=l'\right)}$$

- M-Step: Update registration $R^{k+1}=$

$$\arg\max_R\left[\sum_{\mathbf{x}\in S}\sum_{l\in L}\overbrace{p\left(L(\mathbf{x})=l\mid S,T,R^k\right)}^{\textit{E-Step Weights}}\log\overbrace{p\left(T\left(R(\mathbf{x})\right)\mid S,R,L(\mathbf{x})=l\right)}^{\textit{Likelihood}}\right.$$
$$\left.+\sum_{\mathbf{x}\in S}\log\underbrace{p\left(R(\mathbf{x})\mid L^{k+1}\right)}_{\textit{Transformation Prior}}\right]$$

Probability Models: Likelihood

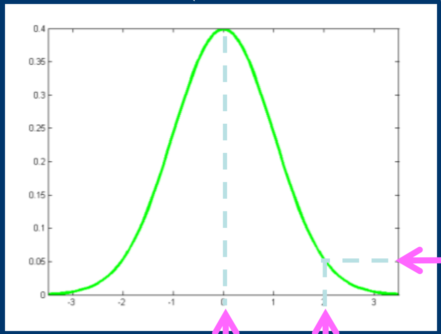
- Likelihood acts like similarity measure

$$p\left(T\left(R(\mathbf{x})\right)\mid S,R,L(\mathbf{x})=l\right)\sim\begin{cases} N\left(S(\mathbf{x}),\sigma_t\right) & ,l=\text{valid tissue}\\ N\left(S(\mathbf{x}),\sigma_b\right) & ,l=\text{background}\\ Unif\left(\frac{1}{C}\right) & ,l=\text{abnormal class}\end{cases}$$

- Automatically update σ_t and C:

$$\sigma_t^{k+1}=\sqrt{\frac{\sum_{x\in S} p\left(L(\mathbf{x})=l\mid S,T,R^k\right)\left(T\left(R^k(\mathbf{x})\right)-S(\mathbf{x})\right)^2}{\sum_{x\in S} p\left(L(\mathbf{x})=l\mid S,T,R^k\right)}}$$

$Normal\left(S(x),\sigma_t^{k+1}\right)$



$\frac{1}{C^{k+1}}$

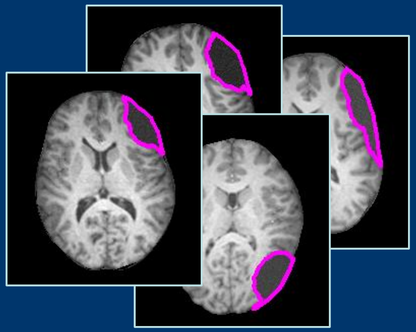
$S(x)$ $+2\sigma_t^{k+1}$

Probability Models: Intensity Prior

- Assume MRI signal characterized by tissue type
  → Different distribution for intensities given label

$$p\left(S\left(\mathbf{x}\right)|L\left(\mathbf{x}\right)=l\right)\sim\begin{cases}Unif\left(\frac{1}{K}\right) & ,l=\text{valid tissue}\\ N\left(0,\sigma_b\right) & ,l=\text{background}\\ N\left(\mu_a,\sigma_a\right) & ,l=\text{abnormal class}\end{cases}$$

Training set



→

Abnormal class parameters

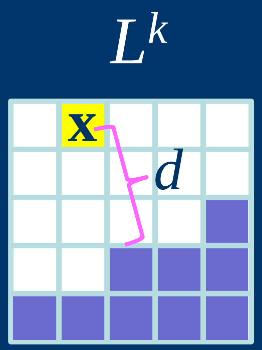
$\boxed{\mu_a,\sigma_a}$

Probability Models: Transformation Prior

- Transformation Model: FFDs based on uniform cubic B-splines
- Want to tolerate greater deformation near "abnormal regions" in current map estimate L^k
- Model $R(\mathbf{x}) | L^k \sim N(\mu_{\mathbf{x}}, \sigma_{\mathbf{x}})$
  - $\mu_{\mathbf{x}}$ = Position of voxel $\mathbf{x}$
  - Increased d → Decreased $\sigma_{\mathbf{x}}$

$$\sigma_{\mathbf{x}}{}^2 = \begin{cases} \sigma_{\min}^2 + \frac{d_{tol} - d}{d_{tol}} \left(\sigma_{\max}^2 - \sigma_{\min}^2 \right) & , d \le d_{tol} \\ \sigma_{\min}^2 & , d > d_{tol} \end{cases}$$

  - Variances updated every M-step



= Abnormal Class

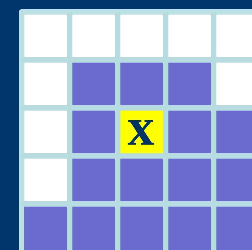
Probability Models: Label Map Prior

- Impose Markov random field onto label map

- Use mean-field approximation and Potts smoothing model:

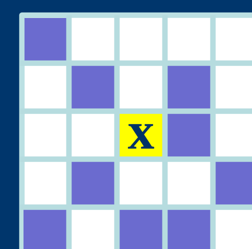
$$p\left(L(\mathbf{x})=l\right) \approx \frac{1}{Z'_{\mathbf{x}}(\beta)} \exp\left[\beta \sum_{\mathbf{n} \in N(\mathbf{x})} \delta\left(l, L^k(\mathbf{n})\right)\right],$$

$$L^k(\mathbf{n}) = \arg\max\, p\left(L(\mathbf{x}) = l \mid S, T, R^{k-1}\right)$$



Higher

$p\left(L(\mathbf{x}) = \blacksquare\right)$



Lower

$p\left(L(\mathbf{x}) = \blacksquare\right)$

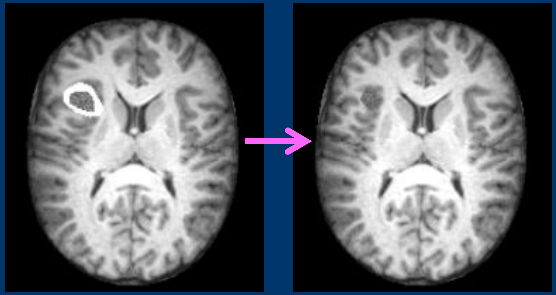
- Update β^{k+1} every M-step

$$\arg\max_{\beta} \sum_{\mathbf{x} \in S} \sum_{l \in L} p\left(L(\mathbf{x}) = l \mid S, T, R^k\right)\left[\log p\left(L(\mathbf{x}) = l \mid \beta\right) + \log p(\beta)\right]$$

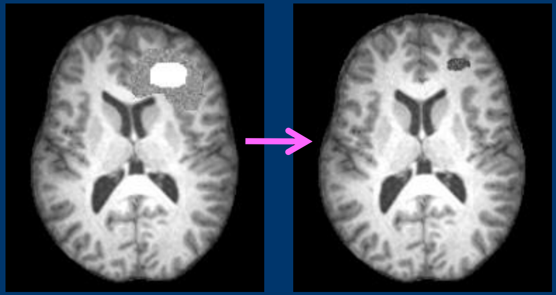
Normal with small μ, σ

Synthetic Examples: Data and Experiments

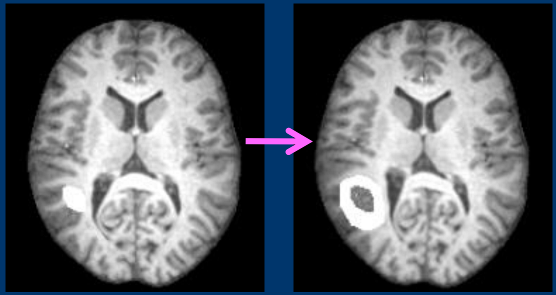
- 3 Sample Series:



Active Tumor Shrinks



Edema + Tumor Resected



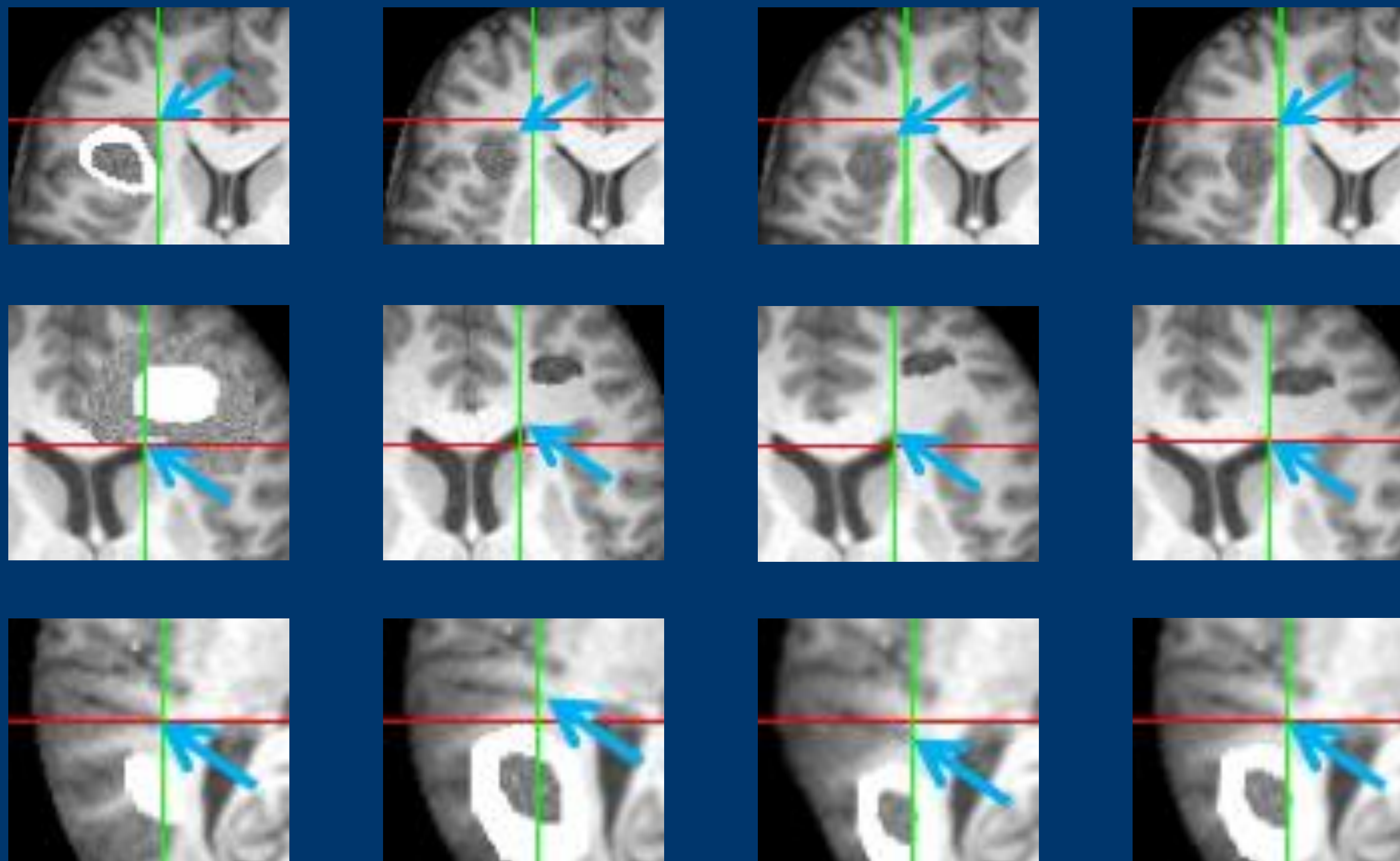
Active Tumor Grows

- Compared our method (*RALE*) to "standard" non-rigid registration[1] (*SNRR*)

  * Both use:
  - Voxel intensity-based similarity
  - FFD transformation model

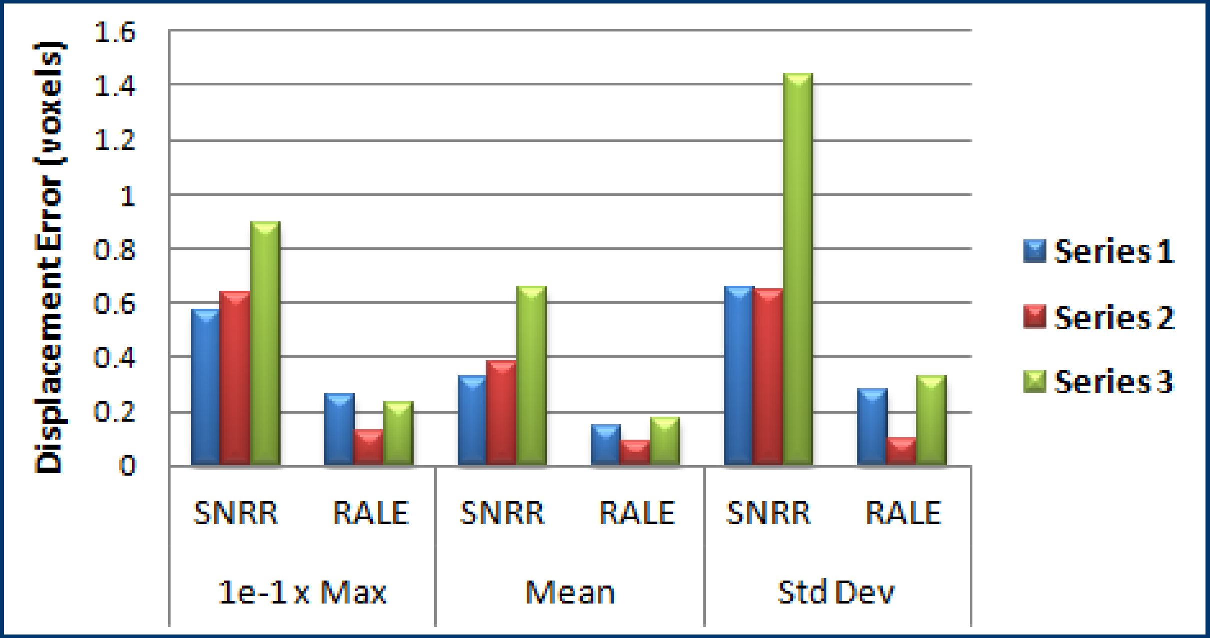
[1]Rueckert et al., TMI 1999

Synthetic Examples: Sample Results



Synthetic Examples: Registration Errors

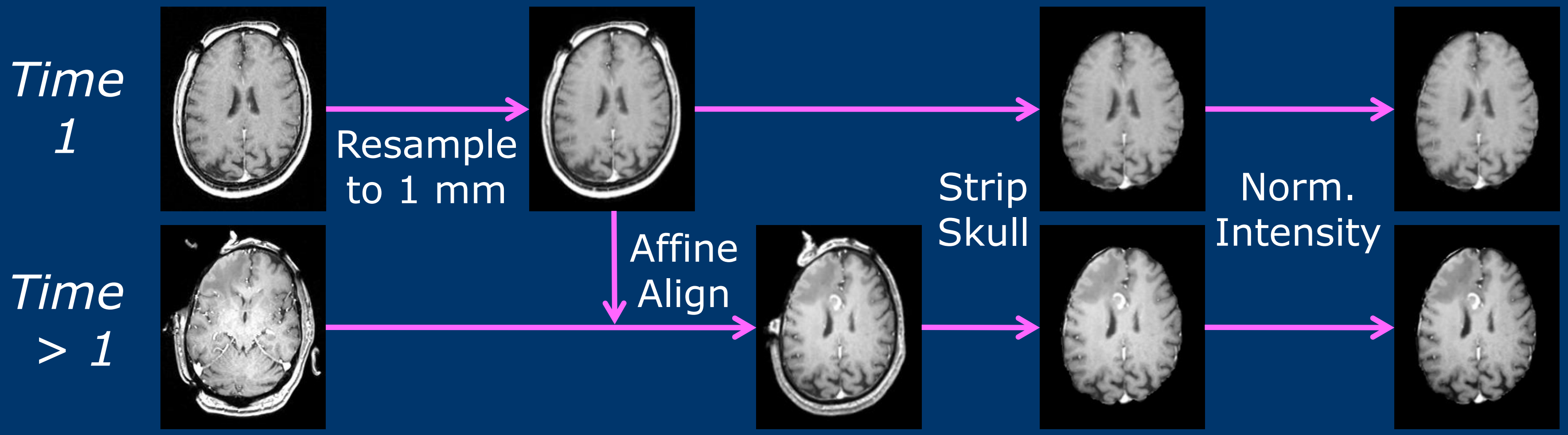
Average Displacement Field Errors



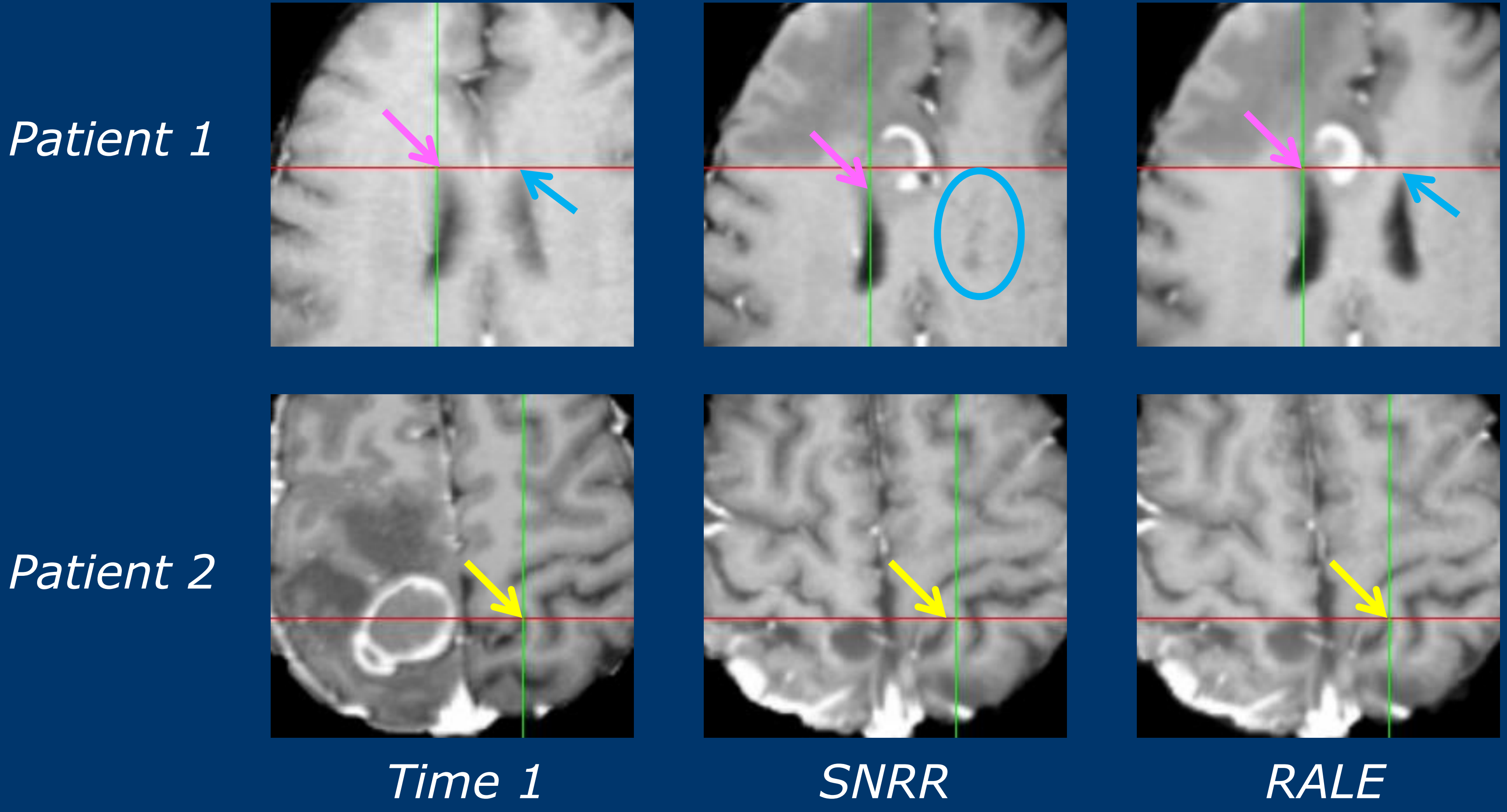
RALE significantly reduced each error measure ($p < 0.05$)

Patient Examples: Data Preparation

- Patient 1 (4 images): Right frontal lesion, Gamma knife treatment, resection
- Patient 2 (4 images): Right parietal lesion, pre-treatment studies, resection, post-op
- Pre-processing



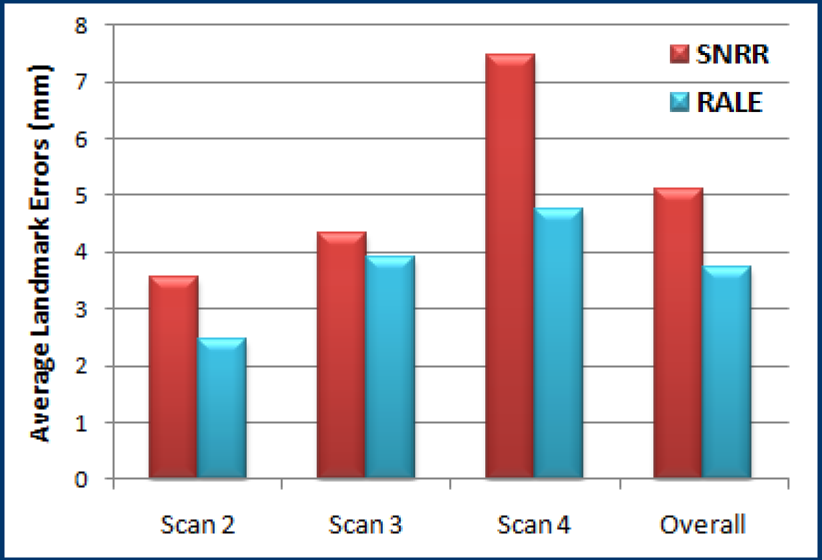
Patient Examples: Sample Results



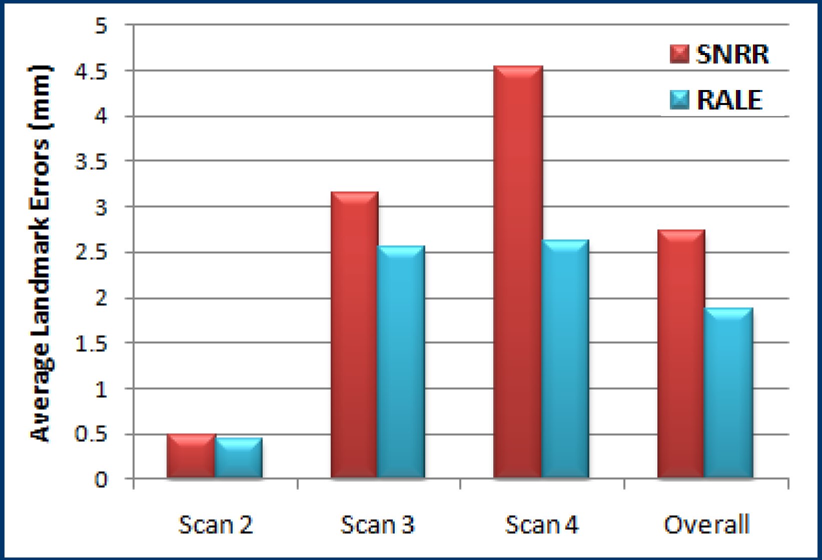
Patient Examples: Registration Errors

Measured 7 Landmarks Highly Affected by Lesion in Each Patient

Patient 1



Patient 2

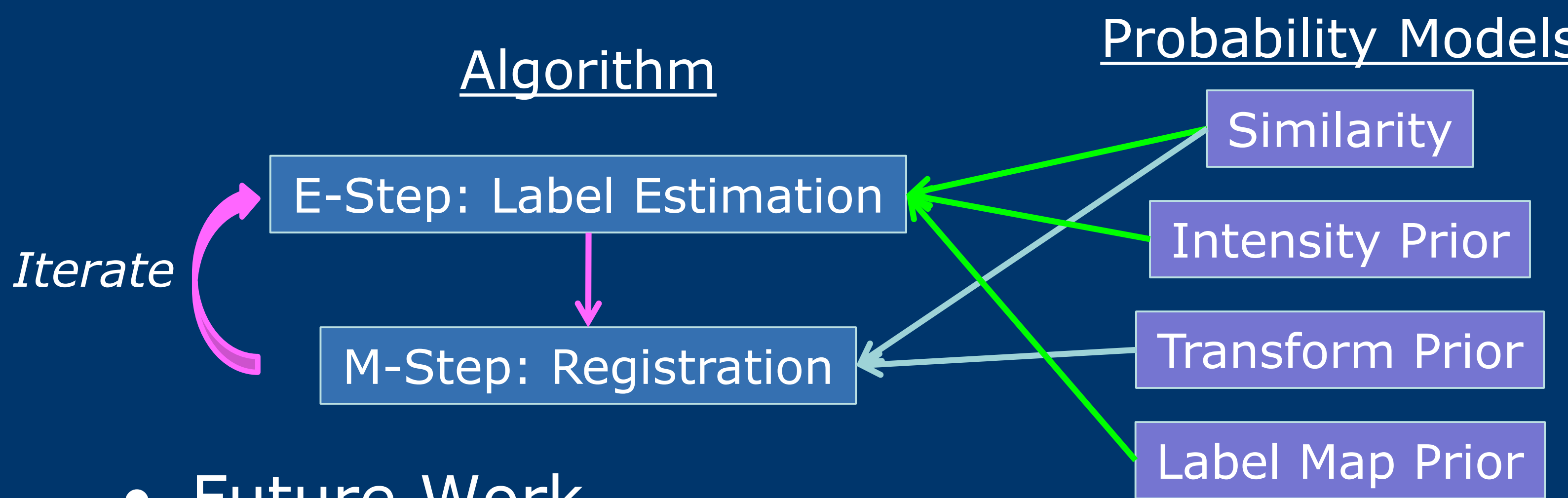


Overall Average Errors	SNRR	3.91 mm
	RALE	2.79 mm

* RALE significantly increased accuracy ($p<2e-6$)

Conclusions and Future Work

- Contributions
  - Registration method for aligning longitudinal brain tumor treatment images



- Future Work
  - Difficulty distinguishing abnormal regions
    → May include prior spatial information

Thank You!

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  - Todd Constable (MRI Acquisition)
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