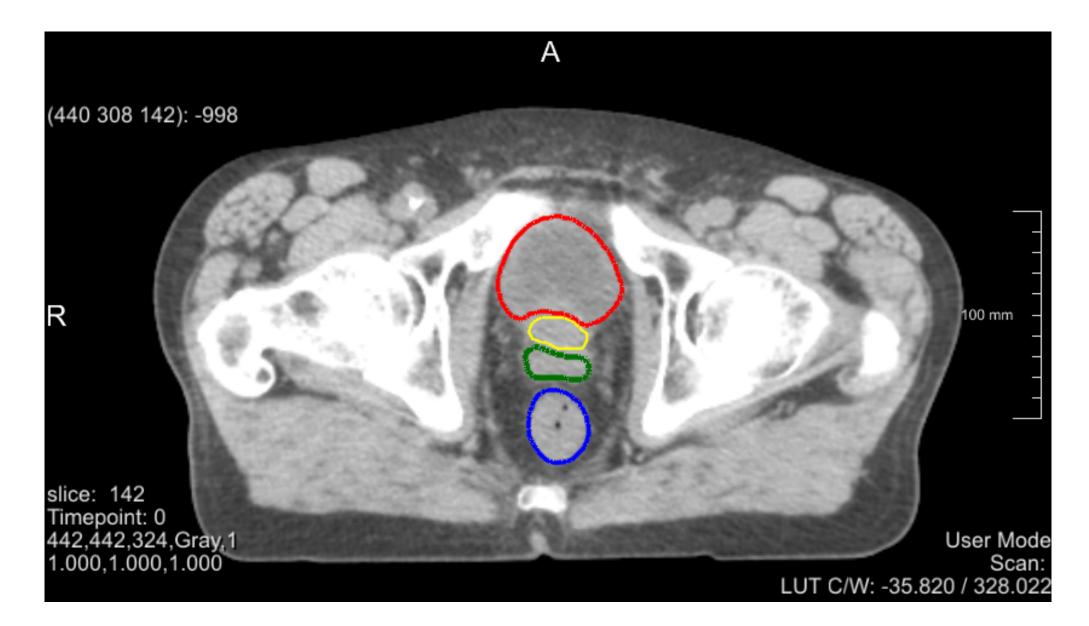
A Cross-Stitch Architecture for Joint Registration and Segmentation in Adaptive Radiotherapy

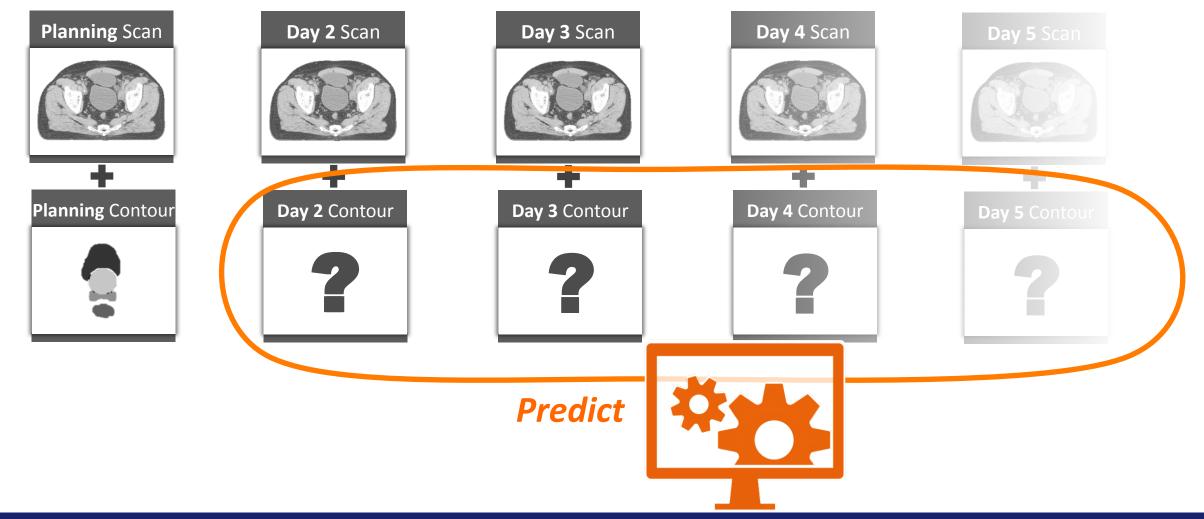
Laurens Beljaards¹, Mohamed S. Elmahdy², Fons Verbeek¹, Marius Staring^{2,3}



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- ² Division of Image Processing, Department of Radiology, Leiden University Medical Center
- ³ Department of Radiation Oncology, Leiden University Medical Center



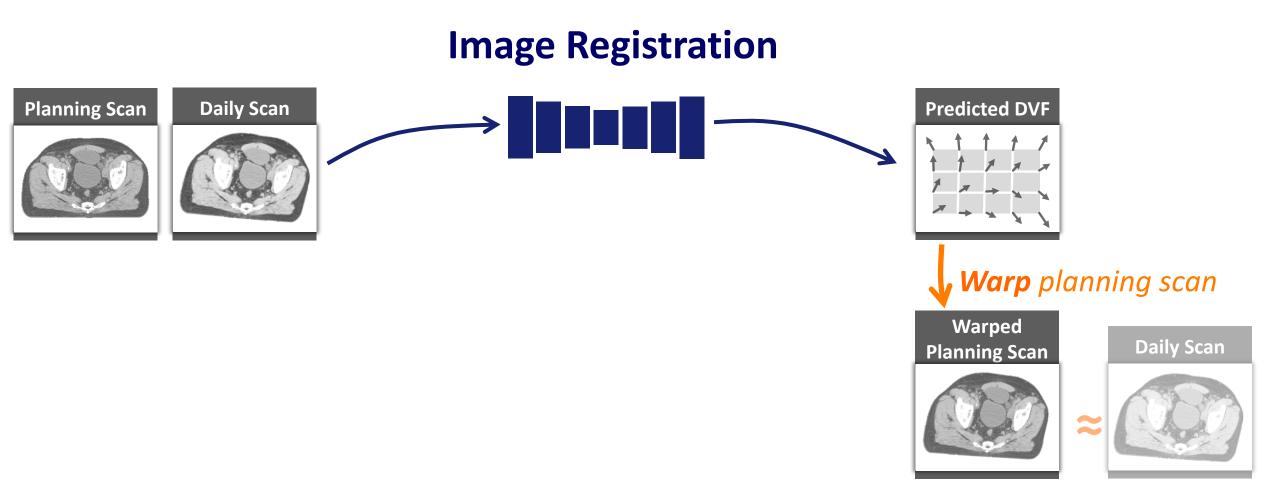
• Online Adaptive Radiotherapy: Time intensive



Generating Contours

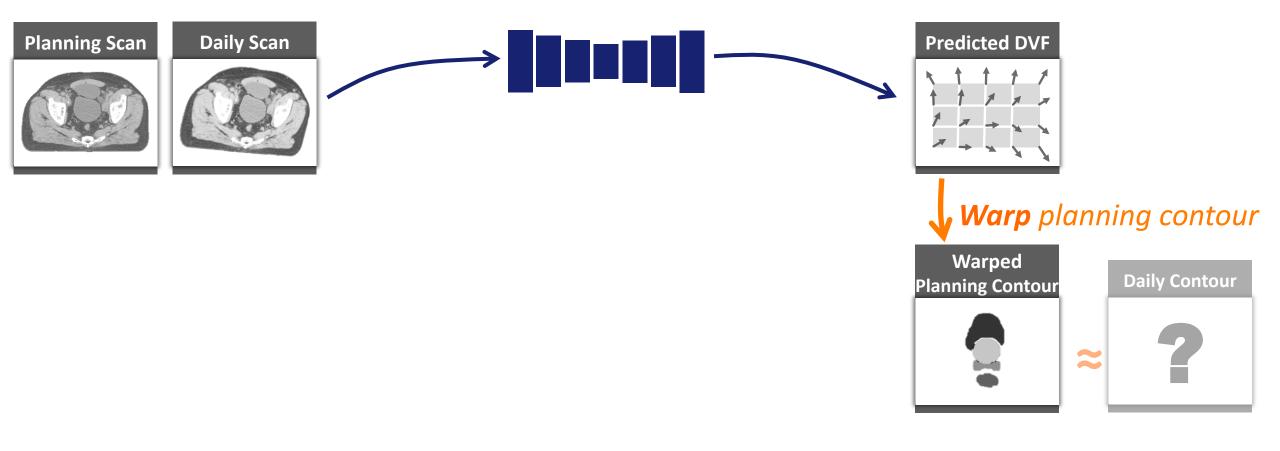


Generating Contours



Generating Contours

Contour Propagation



Overview

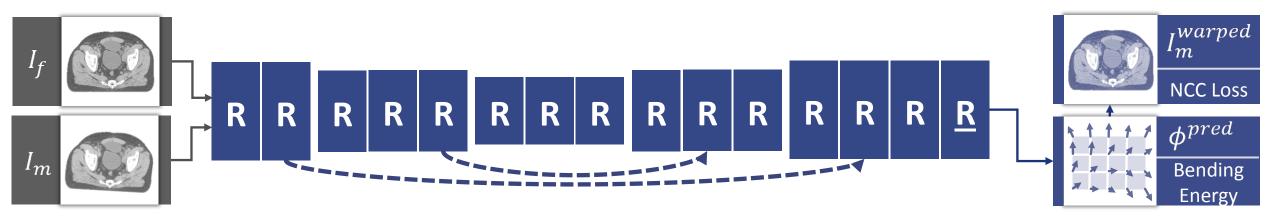
- **Registration** with contour propagation:
 - Prior knowledge of the patient's anatomy (Planning scan & contour)
- Segmentation:
 - Robust to organ **deformations**

Overview

- Registration with contour propagation: Prior knowledge of the patient's anatomy (Planning scan & contour)
- Segmentation:
 - Robust to organ deformations
- Joining the two methods to exploit their strengths
- A) Joint-Registration-Segmentation (JRS) through loss for contour propagation
- B) We combine Segmentation and Registration in one joint network

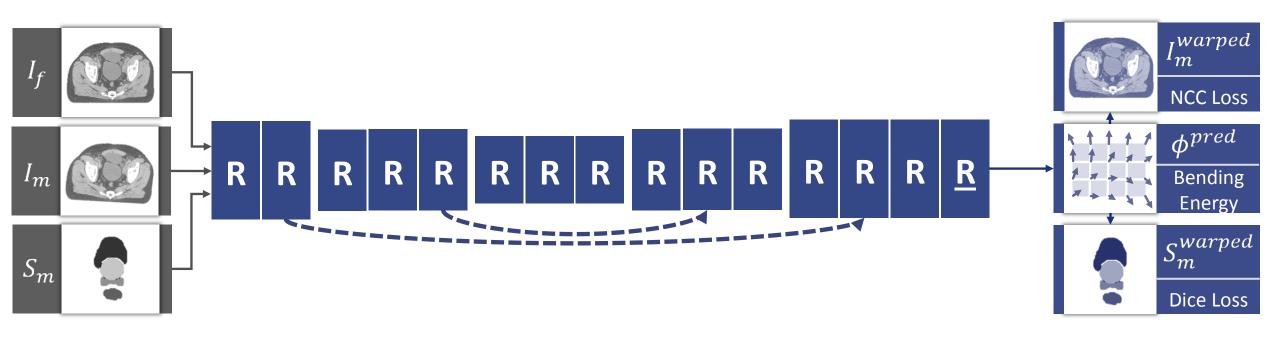
Segmentation and Registration Networks





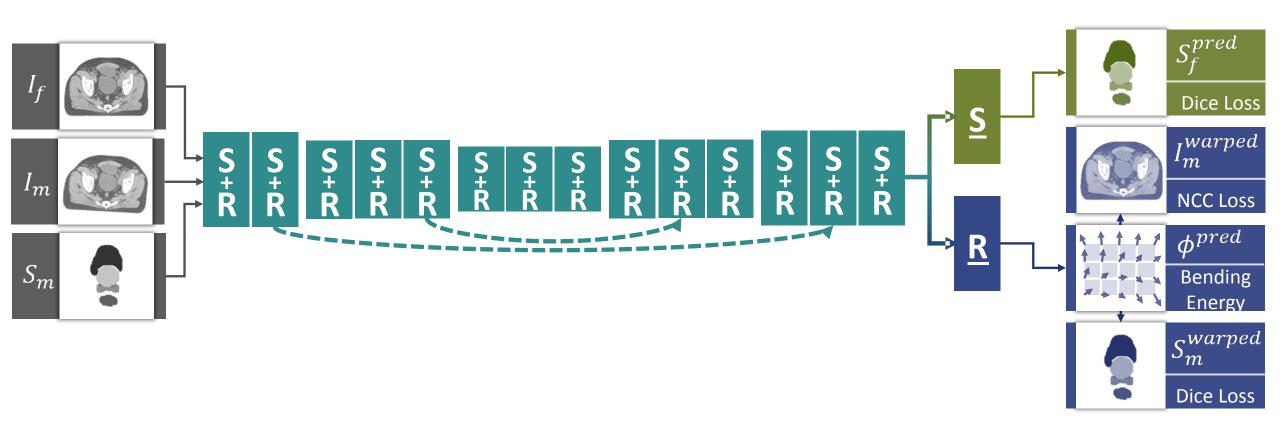
| | Prostate | Seminal vesicles | Rectum | Bladder |
|--------------|--------------------|-----------------------------|----------------------------------|----------------------------------|
| | $\mu\pm\sigma$ | $\mu \pm \sigma$ | $\mu\pm\sigma$ | $\mu \pm \sigma$ |
| Segmentation | 1.49 ± 0.3 | 2.50 ± 2.6 | 3.39 ± 2.2 | $\textbf{1.60} \pm \textbf{1.1}$ |
| Registration | $\bf 1.43 \pm 0.8$ | $\boldsymbol{1.71 \pm 1.4}$ | $\textbf{2.44} \pm \textbf{1.1}$ | 3.40 ± 2.3 |

JRS-Registration Network



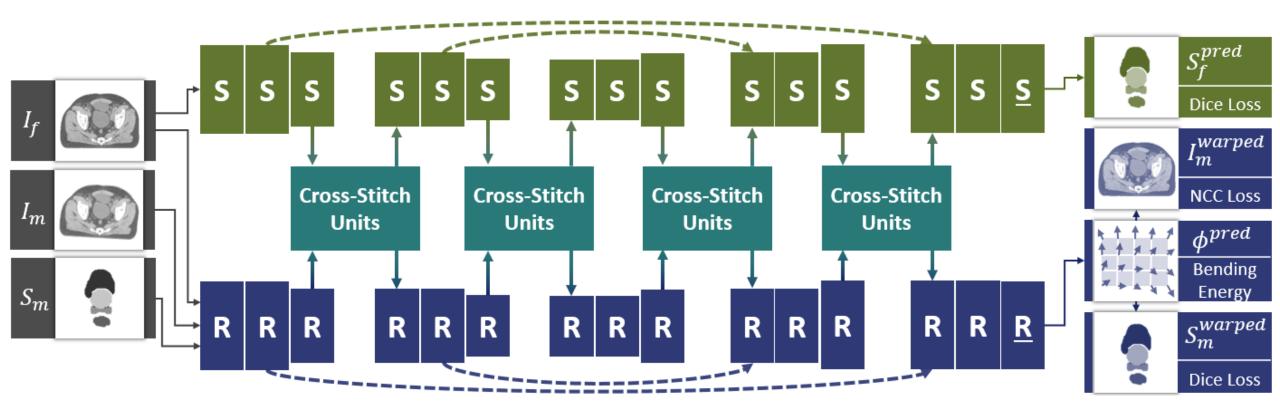
| | Prostate | Seminal vesicles | Rectum | Bladder |
|------------------|----------------------------------|--------------------|----------------------------------|----------------------------------|
| | $\mu\pm\sigma$ | $\mu \pm \sigma$ | $\mu \pm \sigma$ | $\mu \pm \sigma$ |
| Segmentation | 1.49 ± 0.3 | 2.50 ± 2.6 | 3.39 ± 2.2 | $\textbf{1.60} \pm \textbf{1.1}$ |
| Registration | 1.43 ± 0.8 | 1.71 ± 1.4 | 2.44 ± 1.1 | 3.40 ± 2.3 |
| JRS-Registration | $\textbf{1.20} \pm \textbf{0.4}$ | $\bf 1.35 \pm 0.7$ | $\textbf{2.08} \pm \textbf{1.0}$ | 2.63 ± 2.3 |

Fully Hard Parameter Sharing Network



| | | Prostate | Seminal vesicles | Rectum | Bladder |
|--------------------|--------------|----------------|--------------------|----------------------------------|--------------------------------|
| | Output Path | $\mu\pm\sigma$ | $\mu \pm \sigma$ | $\mu\pm\sigma$ | $\mu\pm\sigma$ |
| Segmentation | | 1.49 ± 0.3 | 2.50 ± 2.6 | 3.39 ± 2.2 | 1.60 ± 1.1 |
| Registration | | 1.43 ± 0.8 | 1.71 ± 1.4 | 2.44 ± 1.1 | 3.40 ± 2.3 |
| JRS-Registration | | 1.20 ± 0.4 | 1.35 ± 0.7 | 2.08 ± 1.0 | 2.63 ± 2.3 |
| Fully Hard Sharing | Segmentation | 1.14 ± 0.4 | 1.73 ± 2.1 | $\textbf{1.91} \pm \textbf{0.9}$ | $\textbf{1.04}\pm\textbf{0.7}$ |
| | Registration | 1.20 ± 0.3 | $\bf 1.33 \pm 0.7$ | 2.16 ± 1.1 | 2.56 ± 1.9 |

Cross-Stitch Network



Results in terms of MSD

• + denotes a significant difference (at p = 0.05) with the cross-stitch network

| | | Prostate | Seminal vesicles | Rectum | Bladder |
|--------------------|--------------|---------------------------|---------------------------|---------------------------|---------------------------|
| | Output Path | $\mu\pm\sigma$ | $\mu\pm\sigma$ | $\mu\pm\sigma$ | $\mu\pm\sigma$ |
| Segmentation | | $1.49 \pm 0.3^{\dagger}$ | $2.50\pm2.6^{\dagger}$ | $3.39 \pm 2.2^{\dagger}$ | $1.60 \pm 1.1^{\dagger}$ |
| Registration | | $1.43 \pm 0.8^{\dagger}$ | $1.71 \pm 1.4^{\dagger}$ | $2.44 \pm 1.1^{\dagger}$ | $3.40 \pm 2.3^{\dagger}$ |
| JRS-Registration | | $1.20 \pm 0.4^{\dagger}$ | 1.35 ± 0.7 | $2.08 \pm 1.0^{\dagger}$ | $2.63 \pm 2.3^{\dagger}$ |
| Fully Hard Sharing | Segmentation | $1.14\pm0.4^{\dagger}$ | 1.73 ± 2.1 | 1.91 ± 0.9 | $1.04 \pm 0.7^{\dagger}$ |
| | Registration | $1.20\pm0.3^{\dagger}$ | 1.33 ± 0.7 | $2.16 \pm 1.1^{\dagger}$ | $2.56 \pm 1.9^{\dagger}$ |
| Cross-Stitch | Segmentation | $\boldsymbol{1.06\pm0.3}$ | $\boldsymbol{1.27\pm0.4}$ | $\boldsymbol{1.76\pm0.8}$ | $\boldsymbol{0.91\pm0.4}$ |
| | Registration | 1.10 ± 0.3 | 1.30 ± 0.6 | 2.00 ± 1.0 | 2.45 ± 2.1 |

Comparison with State-of-the-Art Methods

- "Elastix"⁽¹⁾: Conventional iterative method using Elastix software¹ with MI similarity measure
- *"JRS-GAN"*⁽²⁾: An **unsupervised GAN** to jointly perform deformable image registration and segmentation
- "Hybrid"⁽³⁾: A hybrid learning and iterative approach. It uses domain specific strategies to further improve the registration

¹ S. Klein, M. Staring, K. Murphy, M.A. Viergever, J.P.W. Pluim. elastix: a toolbox for intensity based medical image registration, IEEE Transactions on Medical Imaging, vol. 29, no. 1, pp. 196 - 205, January 2010

² Mohamed S. Elmahdy, Jelmer Wolterink, et al. Adversarial Optimization for Joint Registration and Segmentation in Prostate CT Radiotherapy. In Lecture Notes in Computer Science (pp. 366–374). Springer, 2019

³ Mohamed S. Elmahdy, Thyrza Jagt, et al. Robust contour propagation using deep learning and image registration for online adaptive proton therapy of prostate cancer. Medical physics, 2019

Results – Validation Set (HMC Dataset)

- Results in terms of MSD on the validation set (HMC dataset)
- + denotes a significant difference (at p = 0.05) with the cross-stitch network

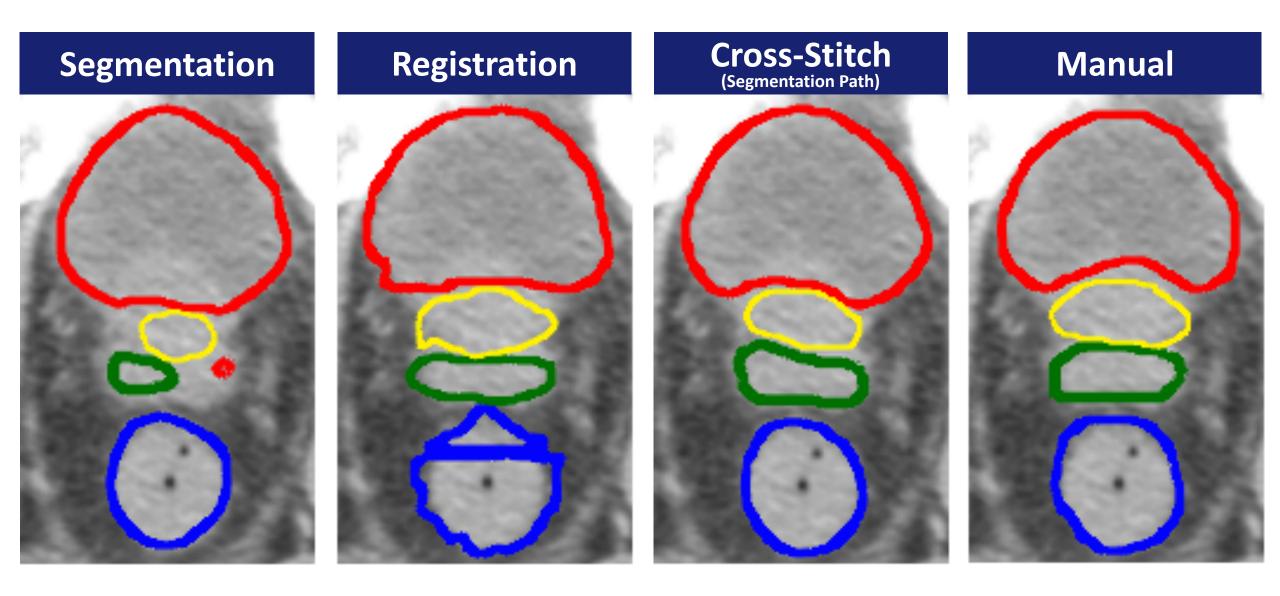
| | | Prostate | | Seminal vesicles | | Rectum | | Bladder | |
|--------------|--------------|----------------------------------|--------|--------------------------|--------|--------------------------|--------|---------------------------|--------|
| | Output Path | $\mu \pm \sigma$ | Median | $\mu \pm \sigma$ | Median | $\mu \pm \sigma$ | Median | $\mu \pm \sigma$ | Median |
| Cross-Stitch | Segmentation | $\textbf{1.06} \pm \textbf{0.3}$ | 0.99 | 1.27 ± 0.4 | 1.15 | $\bf 1.76 \pm 0.8$ | 1.47 | $\boldsymbol{0.91\pm0.4}$ | 0.82 |
| | Registration | 1.10 ± 0.3 | 1.06 | 1.30 ± 0.6 | 1.13 | 2.00 ± 1.0 | 1.75 | 2.45 ± 2.1 | 1.81 |
| Elastix | | $1.73\pm0.7^{\dagger}$ | 1.59 | $2.71 \pm 1.6^{\dagger}$ | 2.45 | $3.69 \pm 1.2^{\dagger}$ | 3.50 | $5.26\pm2.6^{\dagger}$ | 4.72 |
| JRS-GAN | | $1.14\pm0.3^{\dagger}$ | 1.04 | $1.75\pm1.3^{\dagger}$ | 1.44 | $2.17\pm1.1^\dagger$ | 1.89 | $2.25\pm1.9^\dagger$ | 1.54 |
| Hybrid | | $1.27\pm0.3^{\dagger}$ | 1.25 | $1.47 \pm 0.5^{\dagger}$ | 1.32 | $2.03\pm0.6^{\dagger}$ | 1.85 | $1.75 \pm 1.0^{\dagger}$ | 1.26 |

Results – Independent Test Set (EMC Dataset)

- Results in terms of MSD on the **independent test set** (EMC dataset)
- The networks have **not been retrained** or fine-tuned on this dataset

| | Prostate | | Seminal vesicles | | Rectum | | Bladder | |
|---------------------------|--------------------------|--------|-----------------------------|--------|--------------------------|--------|-----------------------------|--------|
| Output Path | $\mu\pm\sigma$ | Median | $\mu\pm\sigma$ | Median | $\mu\pm\sigma$ | Median | $\mu\pm\sigma$ | Median |
| Segmentation | $3.18\pm1.8^\dagger$ | 2.57 | $9.33 \pm 10.1^{\dagger}$ | 5.82 | $5.79\pm3.4^{\dagger}$ | 5.18 | $\boldsymbol{1.88 \pm 1.5}$ | 1.50 |
| Registration | $2.01 \pm 2.5^{\dagger}$ | 1.18 | $2.86\pm5.2^{\dagger}$ | 1.18 | $2.89 \pm 2.5^{\dagger}$ | 2.23 | $5.98 \pm 4.7^{\dagger}$ | 4.44 |
| Cross-Stitch Segmentation | 1.88 ± 2.2 | 1.21 | 4.73 ± 8.0 | 1.42 | 3.61 ± 5.0 | 2.18 | 2.45 ± 2.4 | 1.24 |
| Registration | 1.82 ± 2.4 | 1.09 | 2.45 ± 5.0 | 1.02 | 2.57 ± 2.3 | 2.10 | 4.93 ± 4.1 | 2.69 |
| Elastix | 1.42 ± 0.7 | 1.17 | $2.07\pm2.6^{\dagger}$ | 1.24 | $3.20 \pm 1.6^{\dagger}$ | 3.07 | $5.30\pm5.1^{\dagger}$ | 3.27 |
| Hybrid | $1.55\pm0.6^{\dagger}$ | 1.36 | $\boldsymbol{1.65 \pm 1.3}$ | 1.22 | 2.65 ± 1.6 | 2.36 | $3.81 \pm 3.6^{\dagger}$ | 2.26 |

Visual Examples



Conclusion

- Combined segmentation and registration through loss and architecture
- Fully hard-sharing network and cross-stitch network

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- Good performance when compared to state-of-the-art methods

Conclusion

- Combined segmentation and registration through loss and architecture
- Fully hard-sharing network and cross-stitch network
- Superior accuracy over separate networks
- Good performance when compared to state-of-the-art methods
- Future work:

Generalization across datasets Third task, next to registration and segmentation tasks