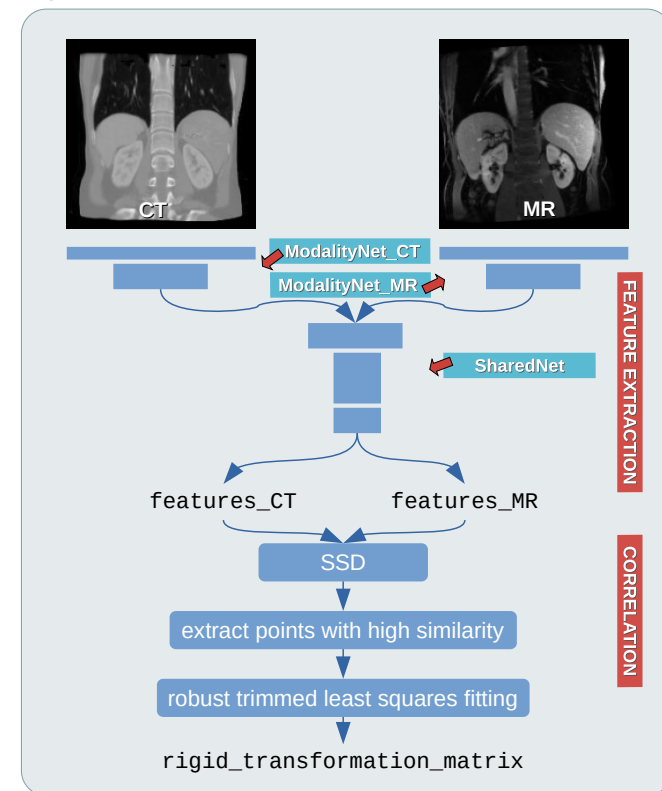
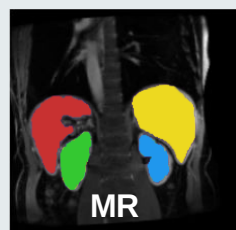
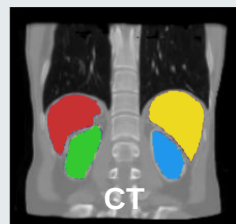


**Image 1 (fixed):** from trainset, modality A  
**Image 2 (moving):** from trainset, modality B  
**Image 3:** random synthetic transform, modality B

**implementation details, open source code, image data:**

[github.com/multimodallelearning/learning\\_without\\_metric](https://github.com/multimodallelearning/learning_without_metric)





## Experiments:

16 **paired** abdominal CT and MR scans from collections of the TCIA project <sup>[1][2][3]</sup>

### pre-processing:

- reorientation
- resampling to isotropic resolution of 2 mm
- cropping/padding to volume dimensions of  $192 \times 160 \times 192$

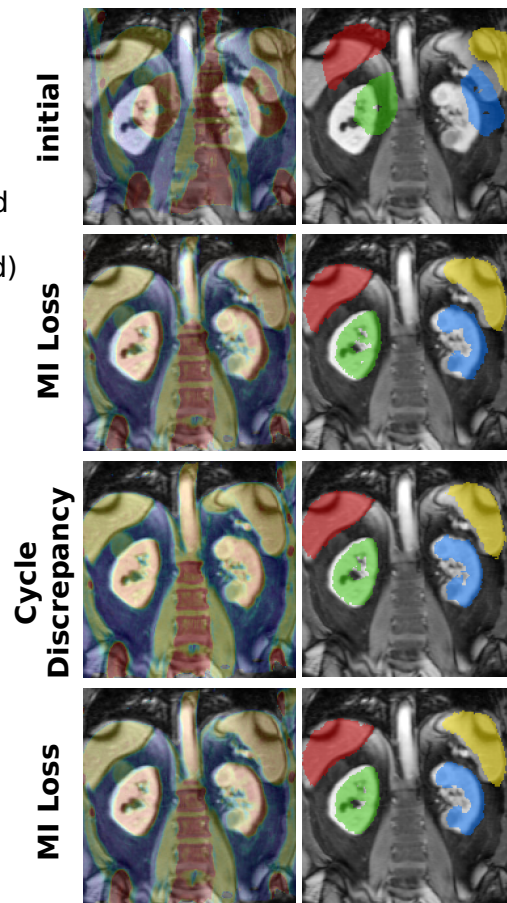
**augmentation:** random rigid transformations

**evaluation:** labels for 4 abdominal organs

### result visualisation:

**left:** fixed MRI and jet colourmap overlay of (warped) moving CT

**right:** fixed MRI and (warped) moving CT labels



## Results:

Dice scores listed by anatomical structures:

	liver <span style="color: red;">■</span>	spleen <span style="color: yellow;">■</span>	lkidney <span style="color: blue;">■</span>	rkidney <span style="color: green;">■</span>	mean
initial	59.3	36.9	36.6	37.0	43.0
FeatCNN + MI Loss	74.7	62.5	67.9	67.4	68.1
FeatCNN + Cycle Discrepancy	78.5	69.7	71.6	74.9	73.8
FeatCNN + Label Loss	79.3	71.1	76.0	75.0	75.3

[1] K Clark, B Vendt, K Smith, et al. The cancer imaging archive (tcia): maintaining and operating a public information repository. Journal of digital imaging, 26(6), 2013.

[2] O Akin, P Elnajjar, M Heller, et al. Radiology data from the cancer genome atlas kidney renal clear cell carcinoma [tcga-kirc] collection. The Cancer Imaging Archive, 2016.

[3] M Linehan, R Gautam, S Kirk, et al. Radiology data from the cancer genome atlas cervical kidney renal papillary cell carcinoma [kirp] collection. The Cancer Imaging Archive, 2016.