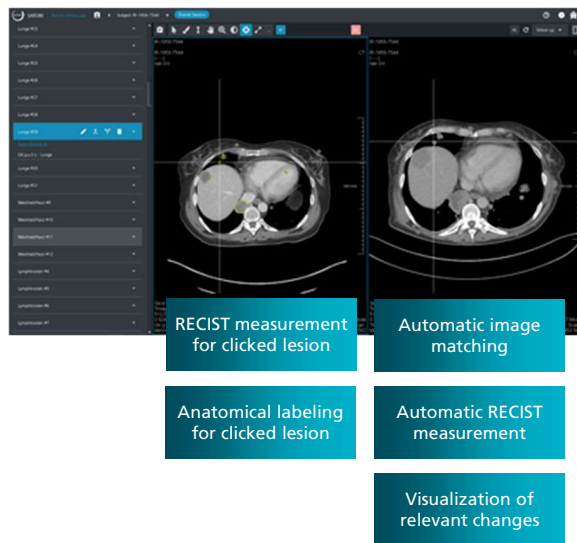


Motivation:

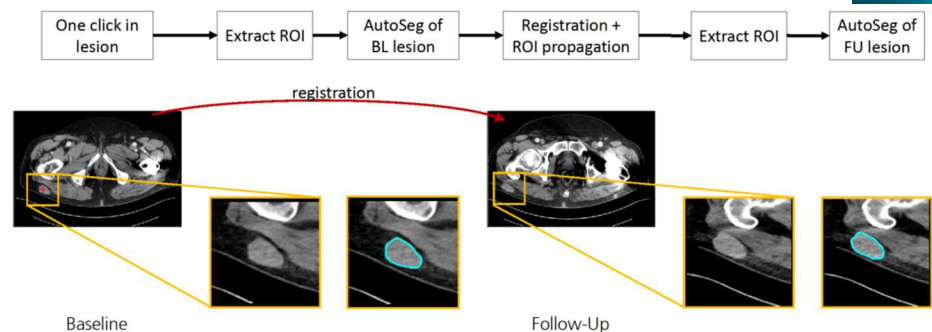
- Higher number of cancer patient + more successful and new therapies -> higher workload of radiologist
- Measurement of metastatic tumors on longitudinal CT scans is essential to evaluate efficiency of treatment
- In clinical routine, often only a visual inspection is possible
- Measurements are mostly not archived in a structured way

Our goal:

We make routine tumor follow-up quicker and more reliable through software-assisted workflows and lay the foundation for novel predictive imaging biomarkers.



Pipeline:



Dataset:

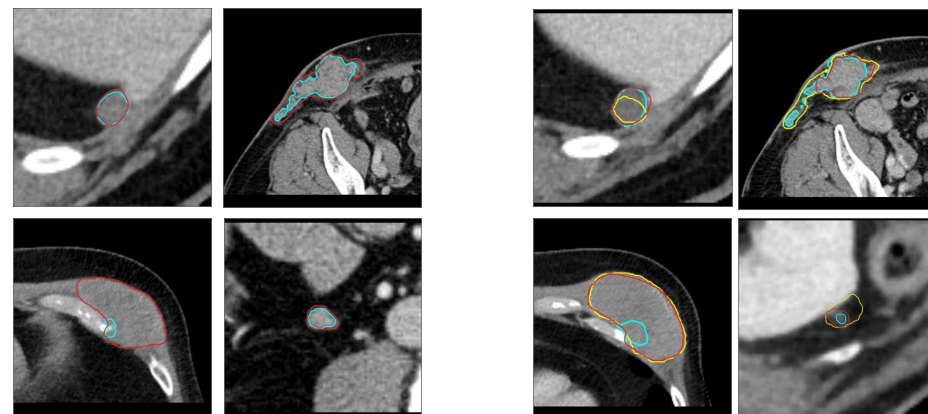
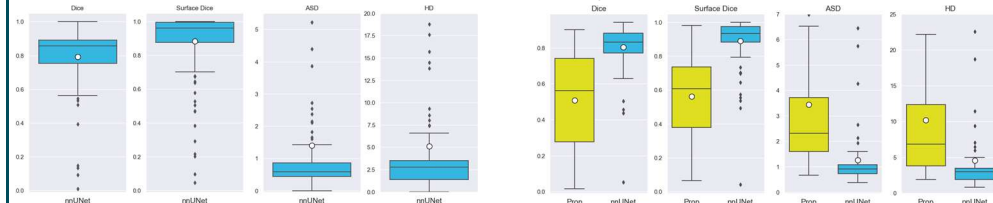
- 206 baseline and follow-up CT scan pairs with metastatic melanoma
- 163 training+validation cases with 2408 annotated **soft-tissue lesions** on baseline
- 43 test cases with 125 annotated soft-tissue lesions of baseline and follow-up

Results:

- Baseline:
- 120 of 125 lesions are segmented
 - Avg. Dice Score 0.79

Follow-Up:

- 15 of 25 disappeared lesions correctly not segmented
- 80 of 100 lesions are segmented
- Avg. Dice Score 0.8



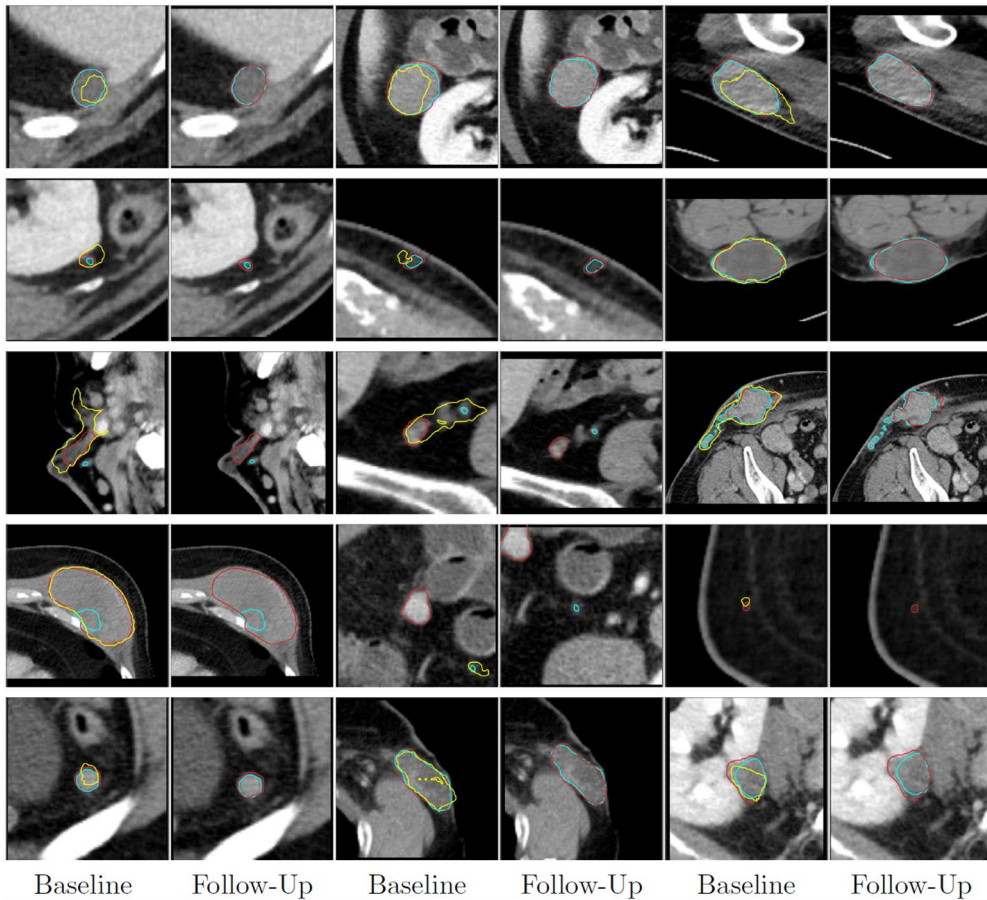
■ Manual Segmentation
■ nnUNet Segmentation
■ propagated Segmentation

Next:

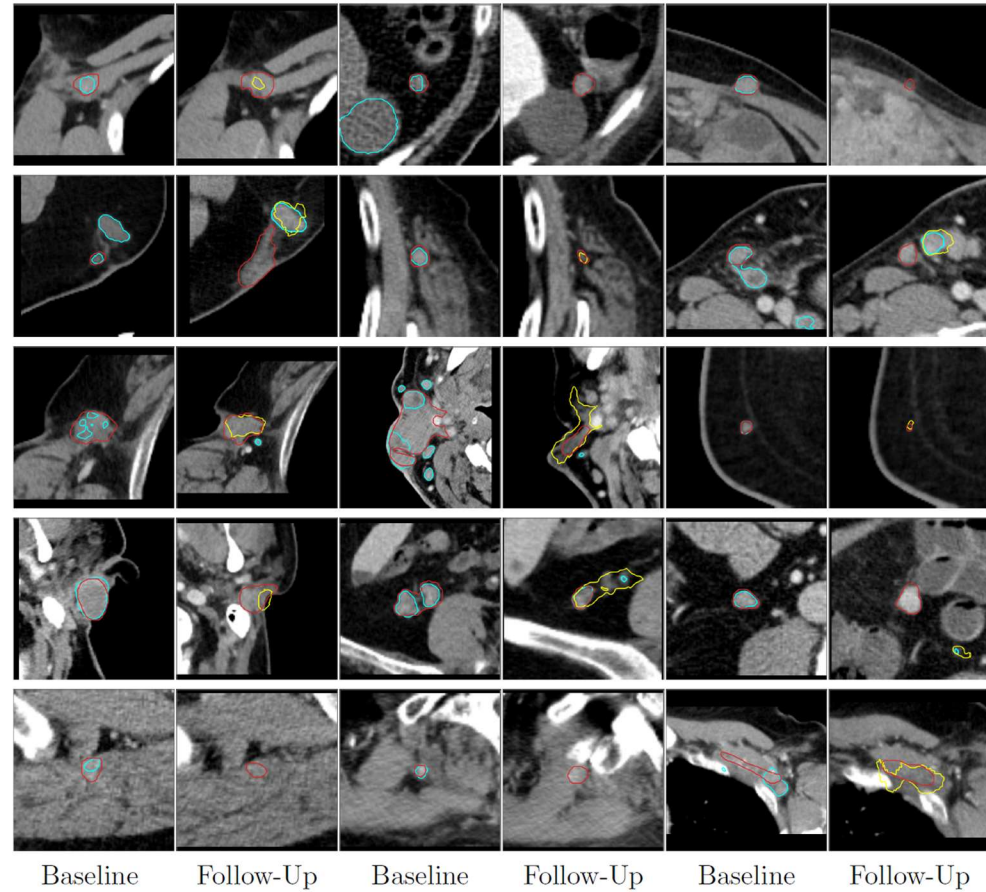
- Use knowledge about appearance of baseline lesion for follow-up segmentation
- Consider that lesions can split/merge over time
- Train pipeline for more lesion types
- Evaluate trained network for other tumor entities
- Evaluate whether the trained networks show a bias (scanner type, gender, ethnicity etc.)
- Use the software in the clinic



More visual results:



Failure Cases:



Manual Segmentation
nnUNet Segmentation
propagated Segmentation