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FACULTY OF ENGINEERING

A Guided Spatial Transformer Network for Histology Cell Differentiation

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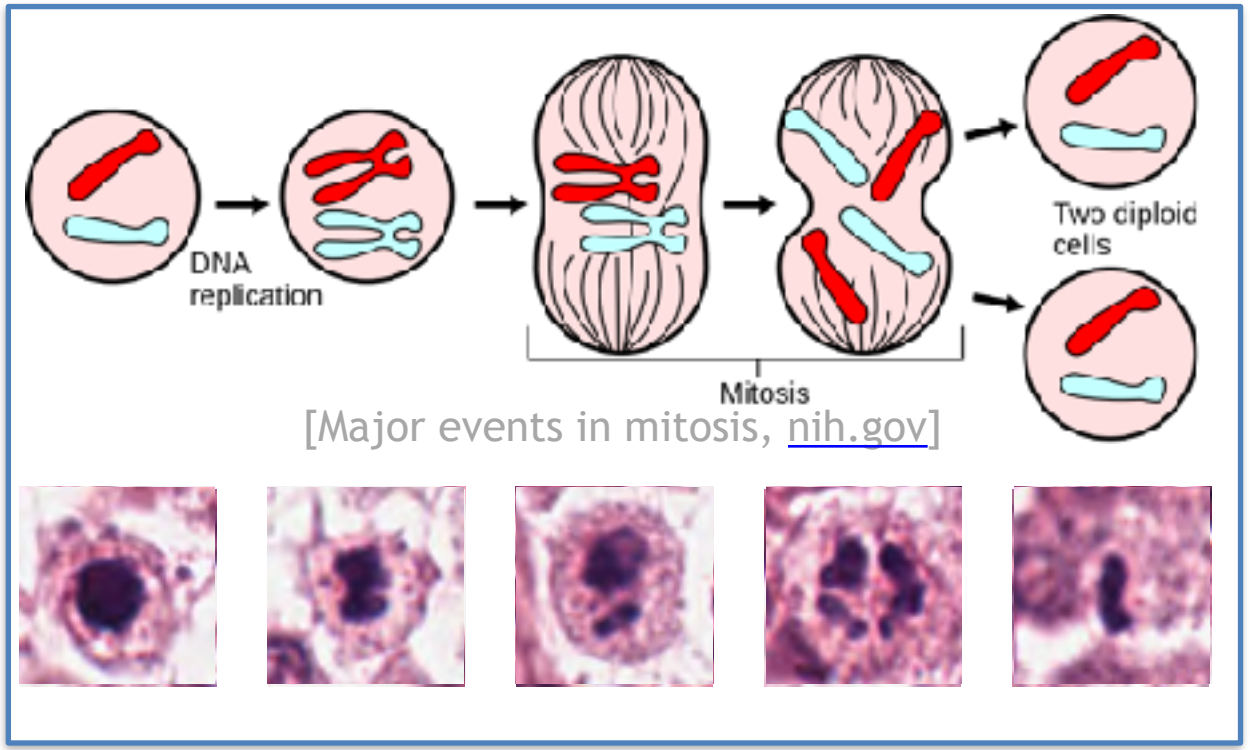
Motivation: Mitosis

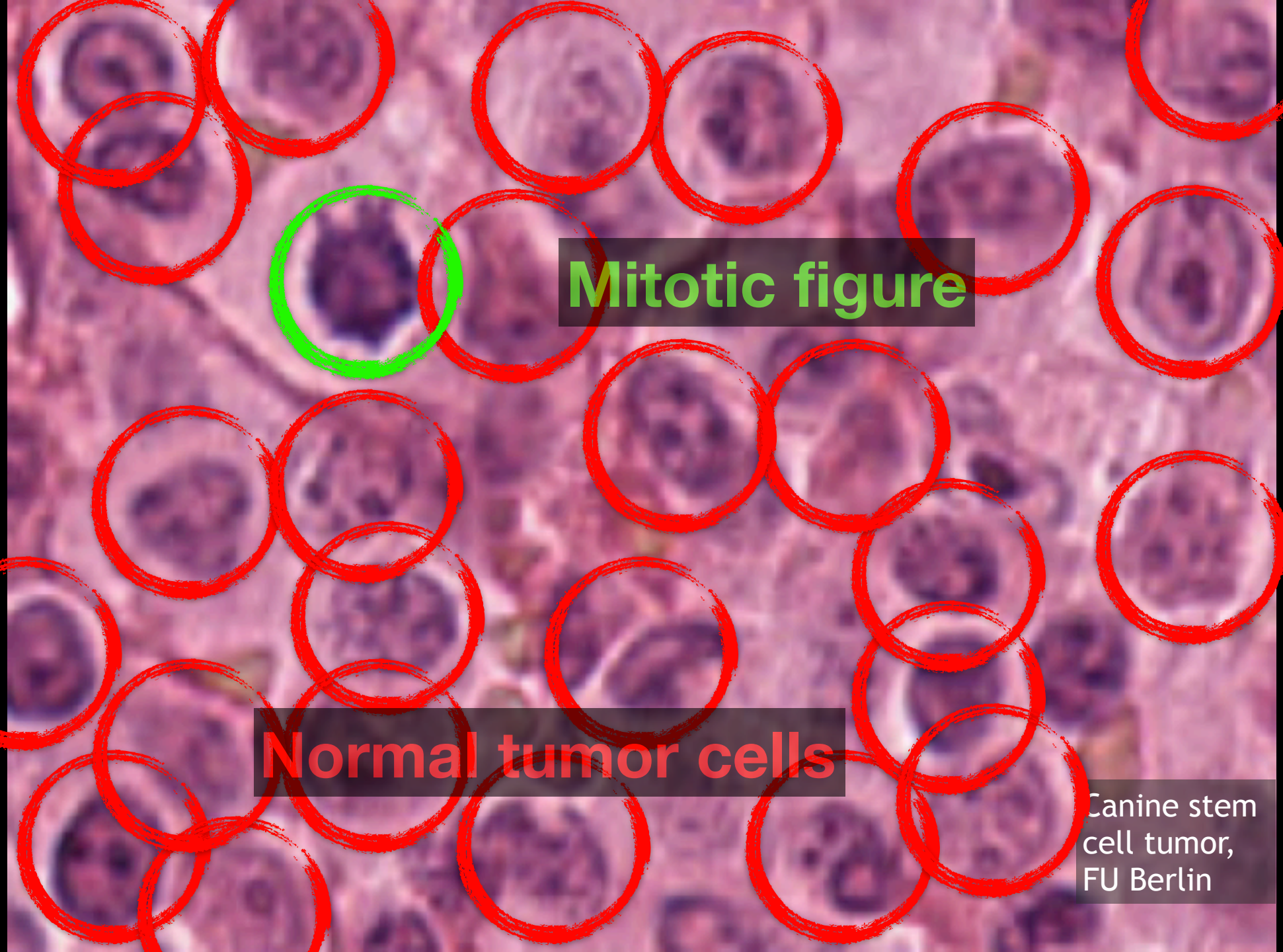
- Cell division, an important marker in tumor diagnostics
- Different phases in mitosis and differences in staining

  ⇨ High variance

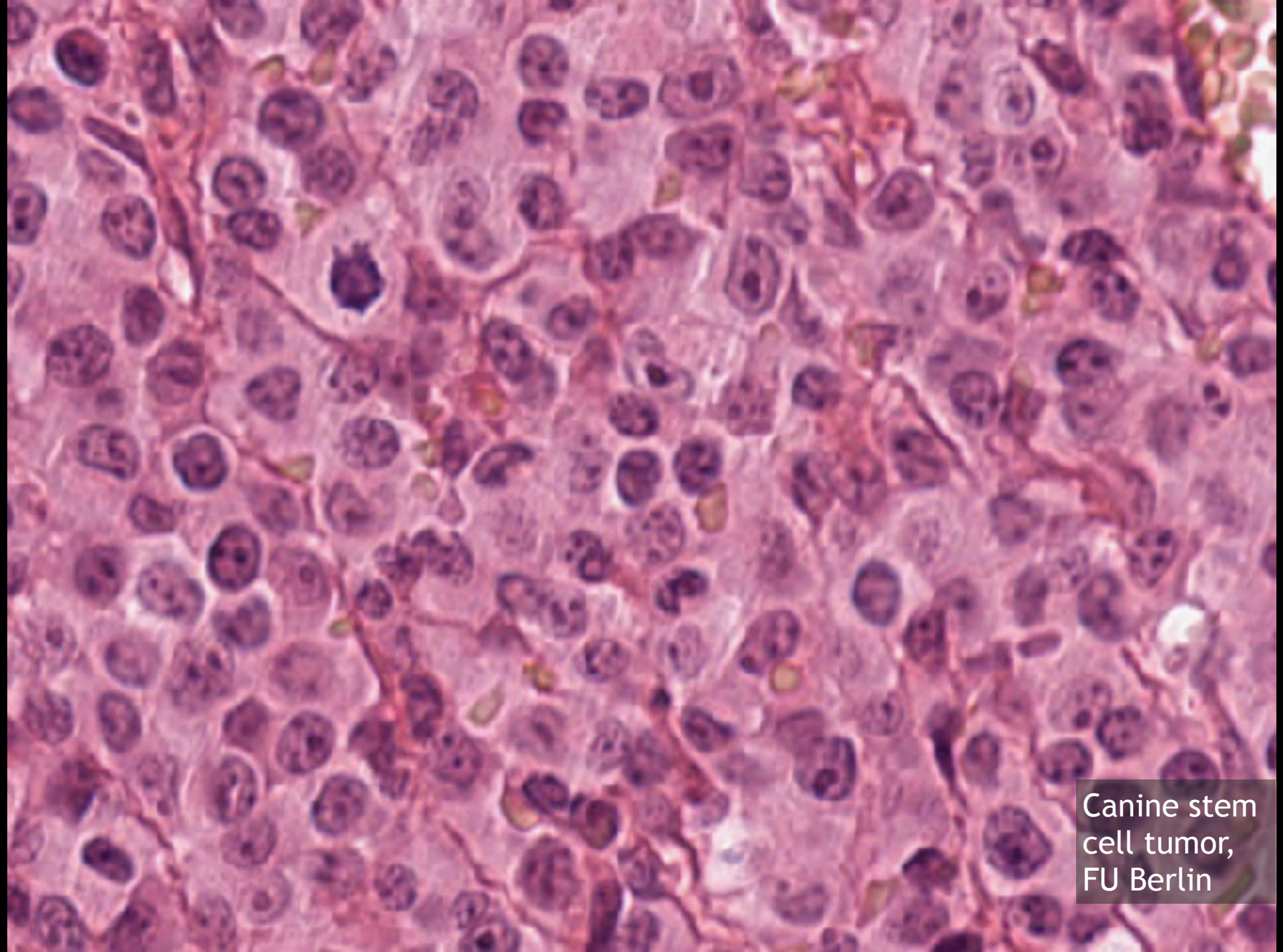
- Low intra-rater reliability in grading
- Sparsely distributed in histology slides



[Major events in mitosis, nih.gov]



Canine stem cell tumor, FU Berlin



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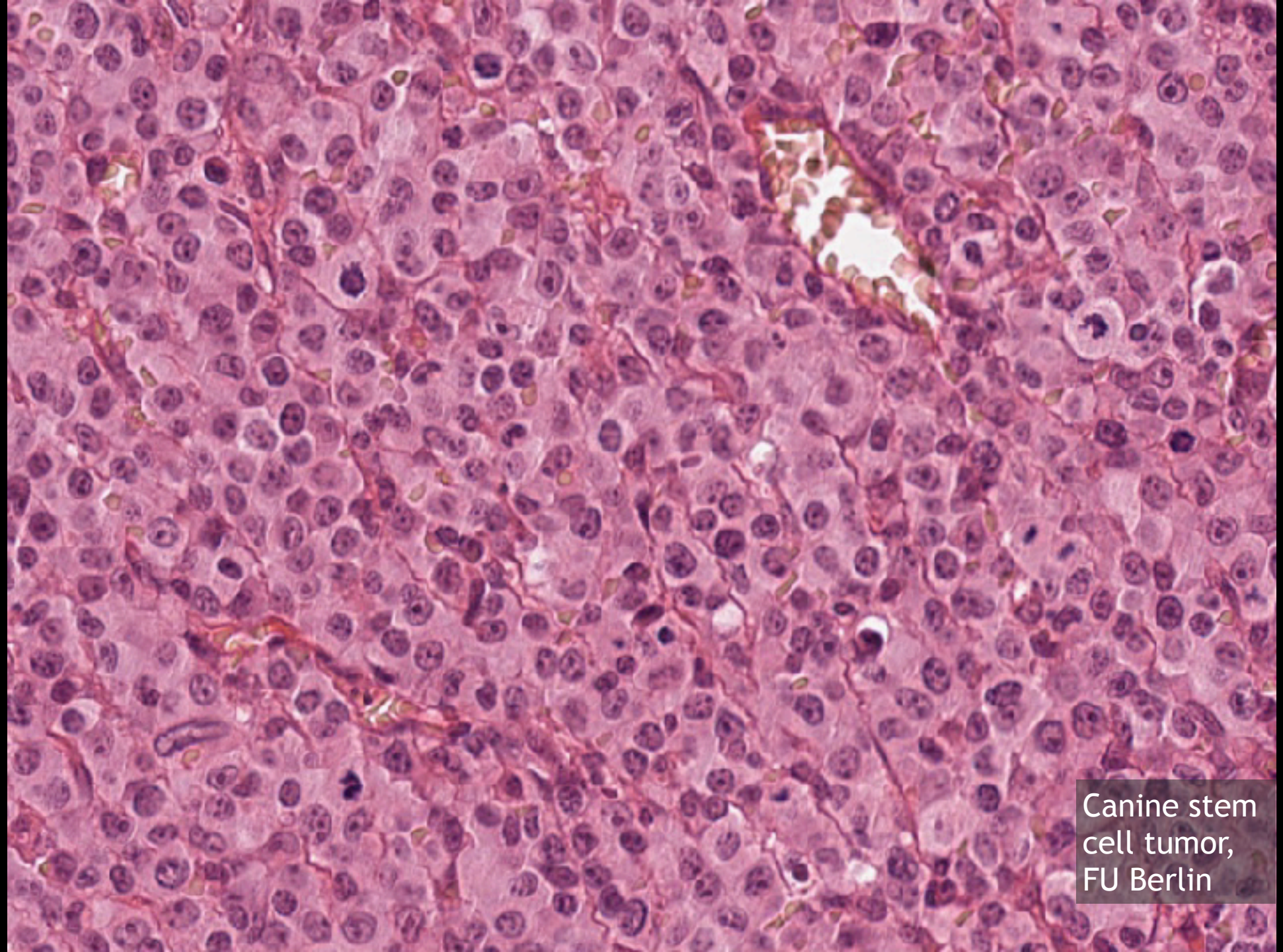
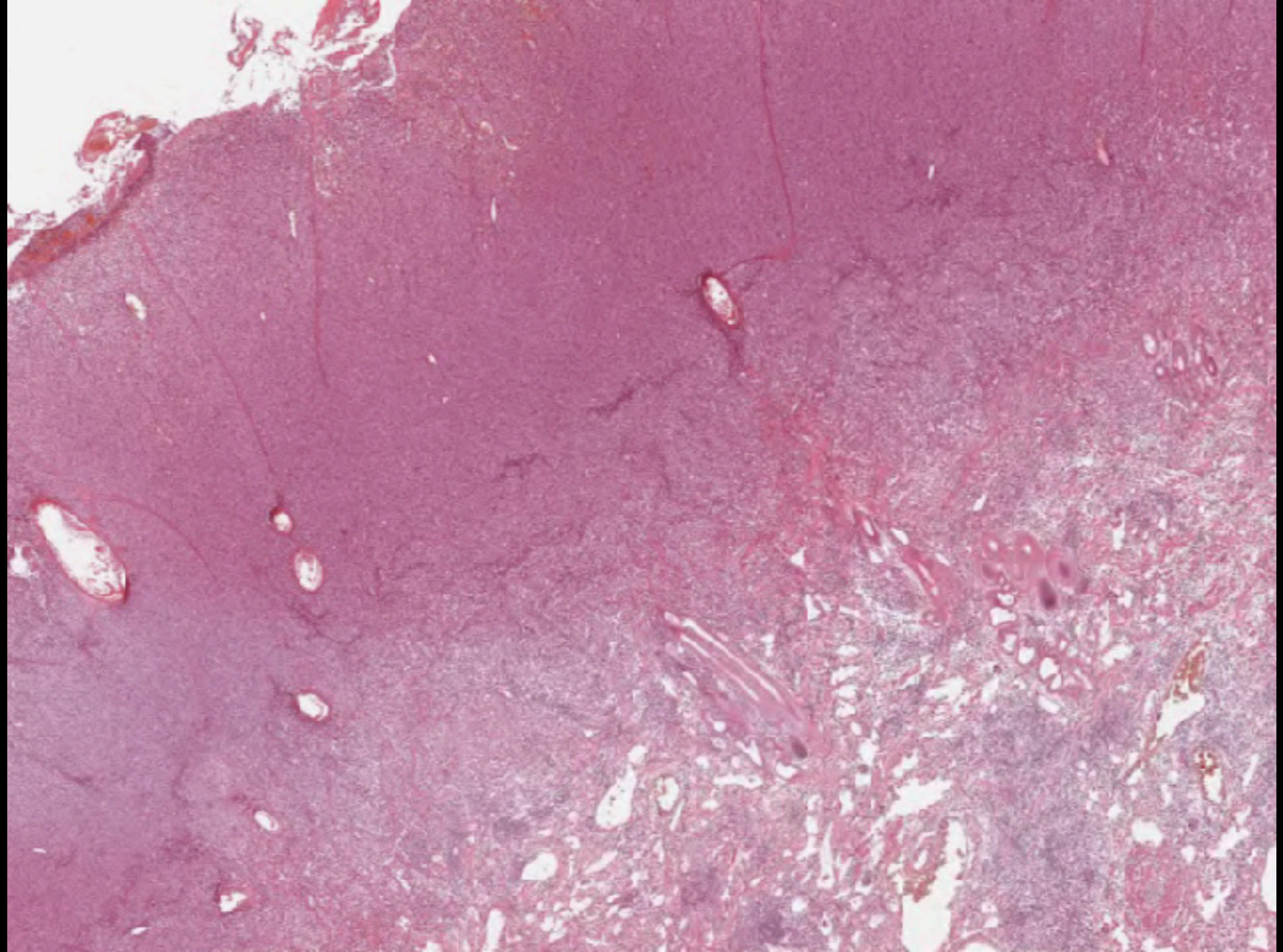
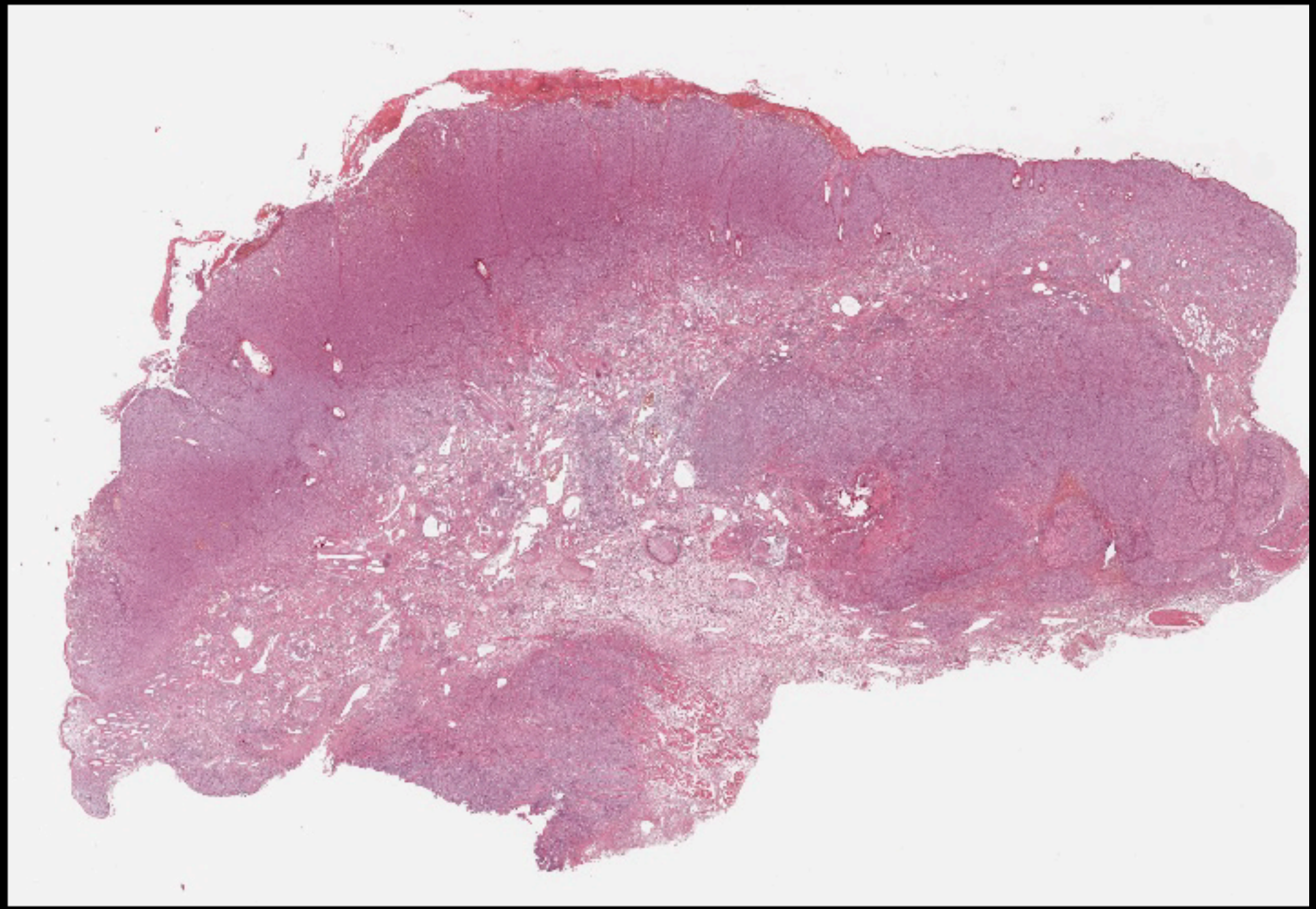


Canine stem cell tumor, FU Berlin





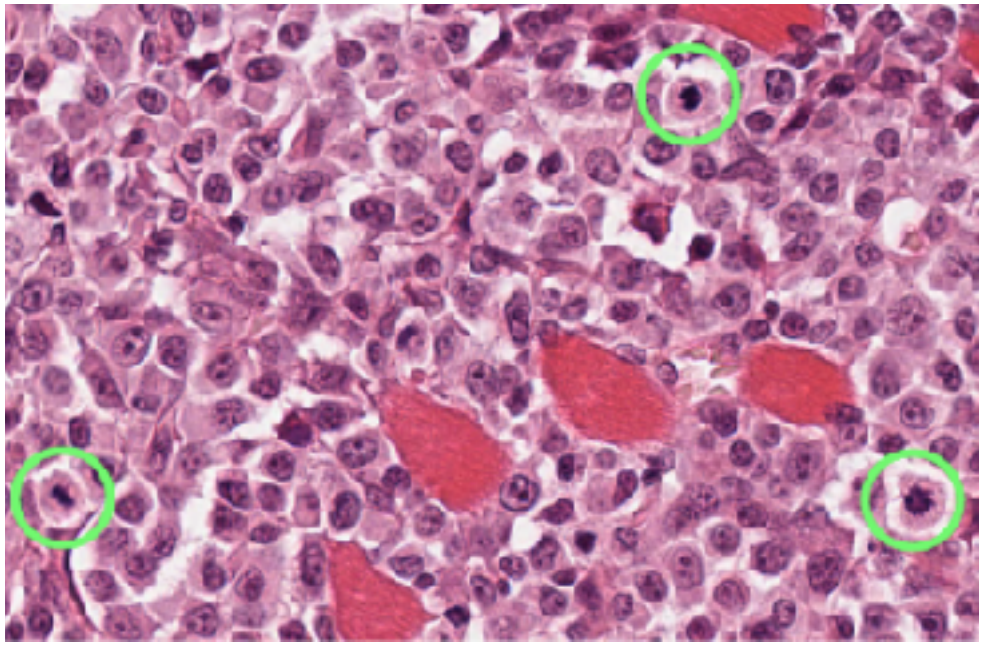
Our Data Set

Sparsely annotated dataset of **10k** cell annotations per type

Full annotations drastically increase workload in annotation task

Only mitotic cells with high certainty are annotated.

But: How to use the data?



cell types:
mitosis,
granulocyte,
normal cell

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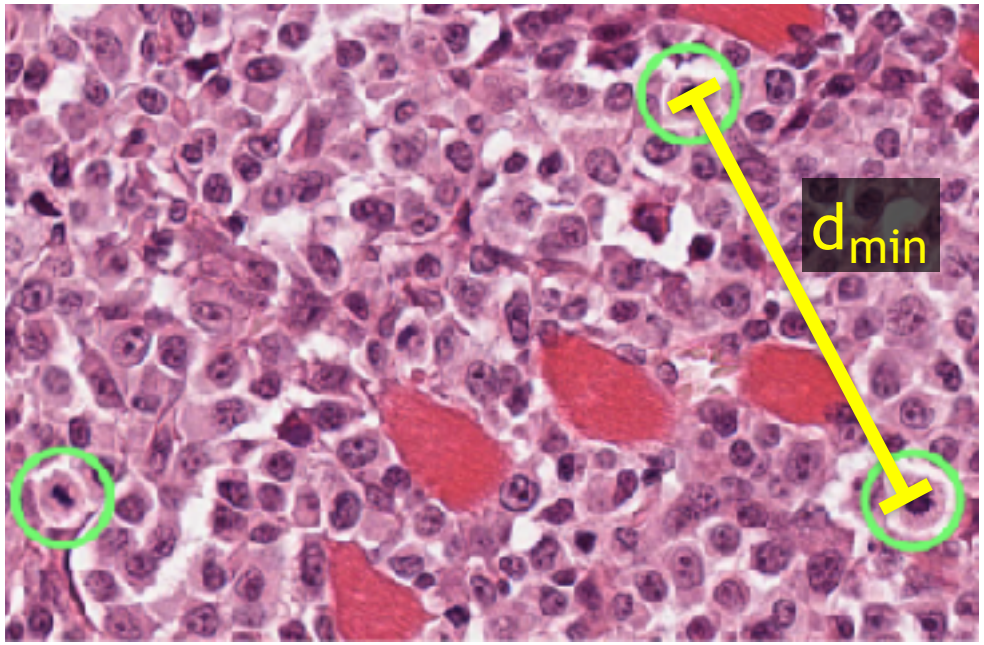
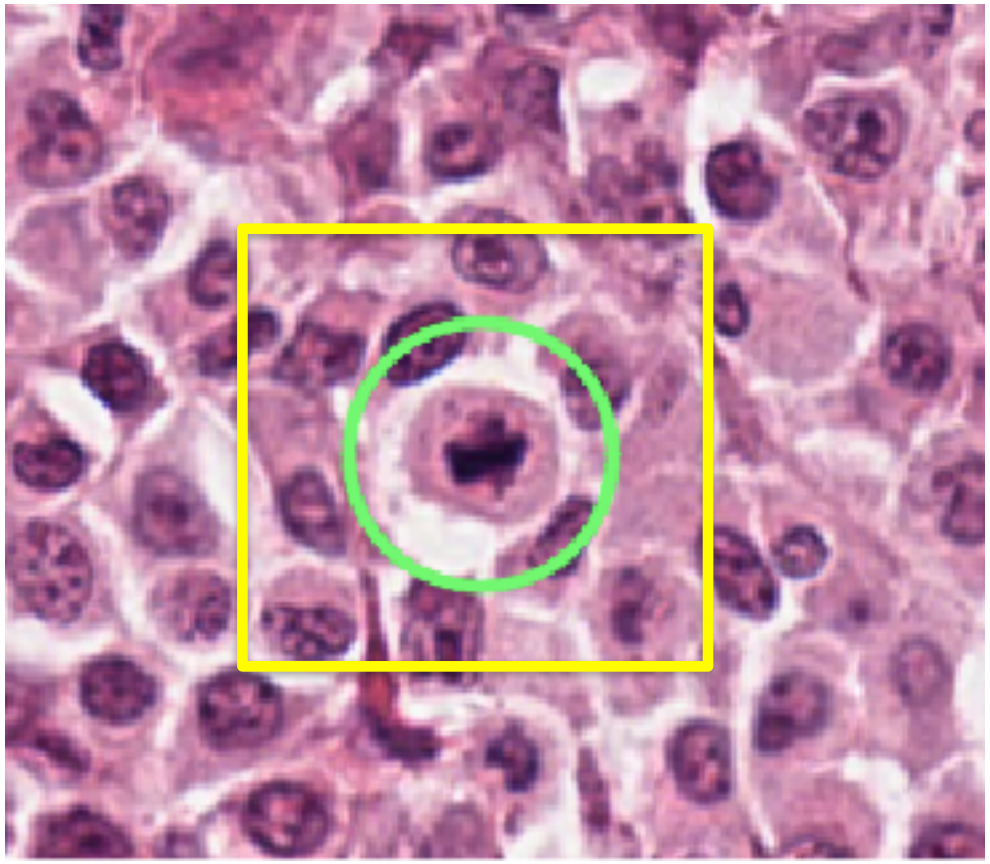


cell types: mitosis, granulocyte, normal cell

Assumption:
No two mitotic cells within a certain distance of each other.

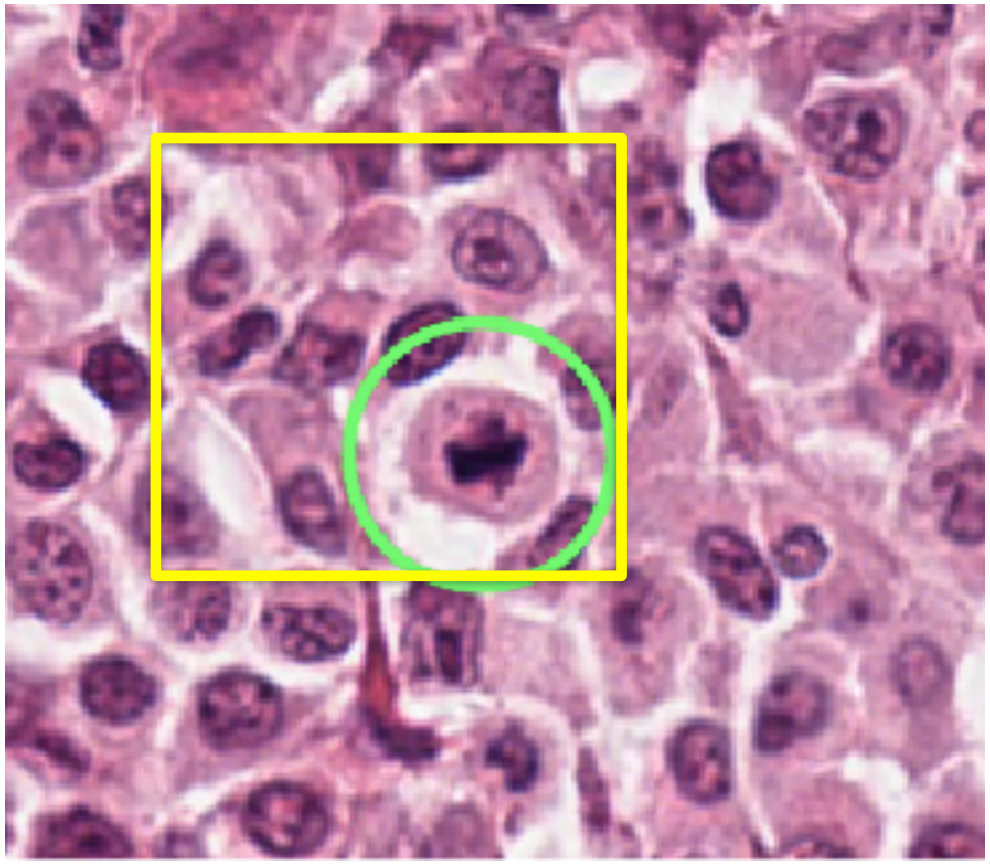
A Classification Task



Classes:
Mitotic cells | Granulocytes | Normal cells

	prec	rec	F1
granulocyte	0.94	0.96	0.95
mitosis	0.93	0.90	0.92
normal cell	0.95	0.96	0.96
average	0.94	0.94	0.94

Idea: Create a localization task and a classification task



Let's estimate the position of the cell and the cell type.

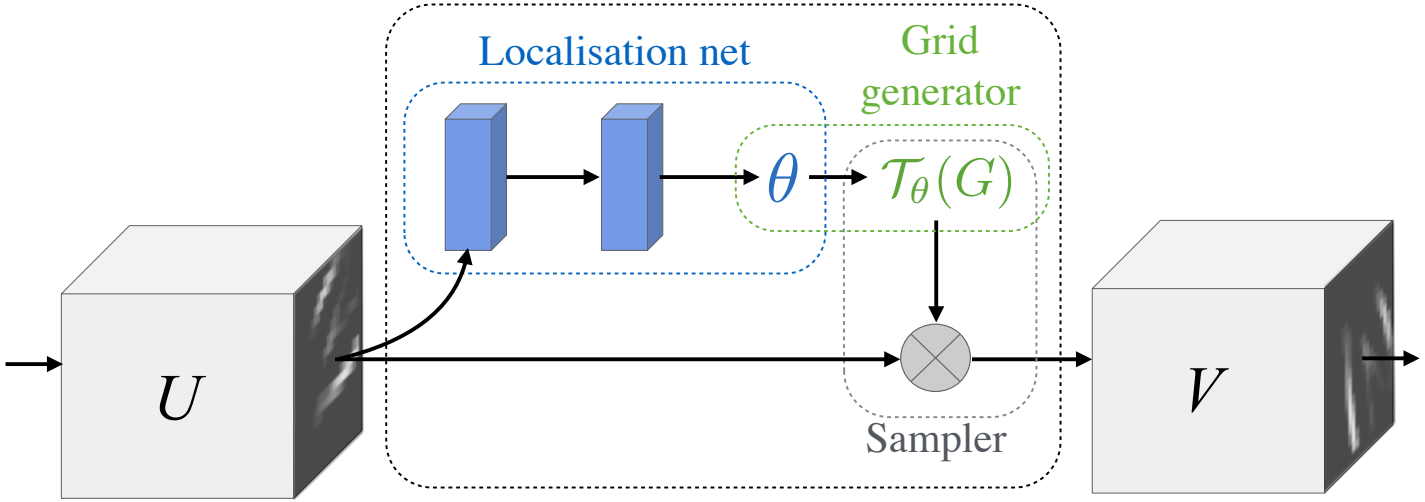
Classification and Localization task

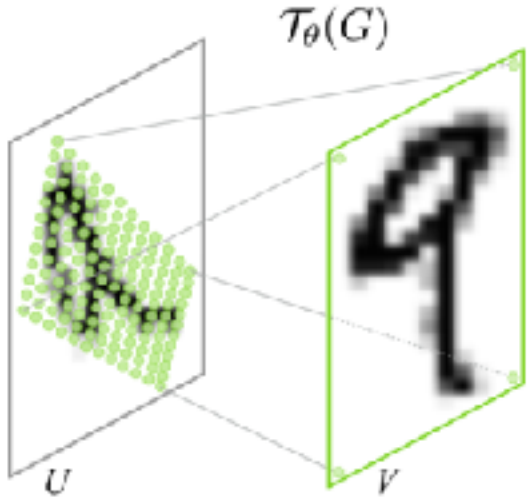
Classes:
Mitotic cells | Granulocytes | Normal cells

negative class

Spatial Transformer Networks [Jaderberg et al., 2015]

- Affine transform within the network

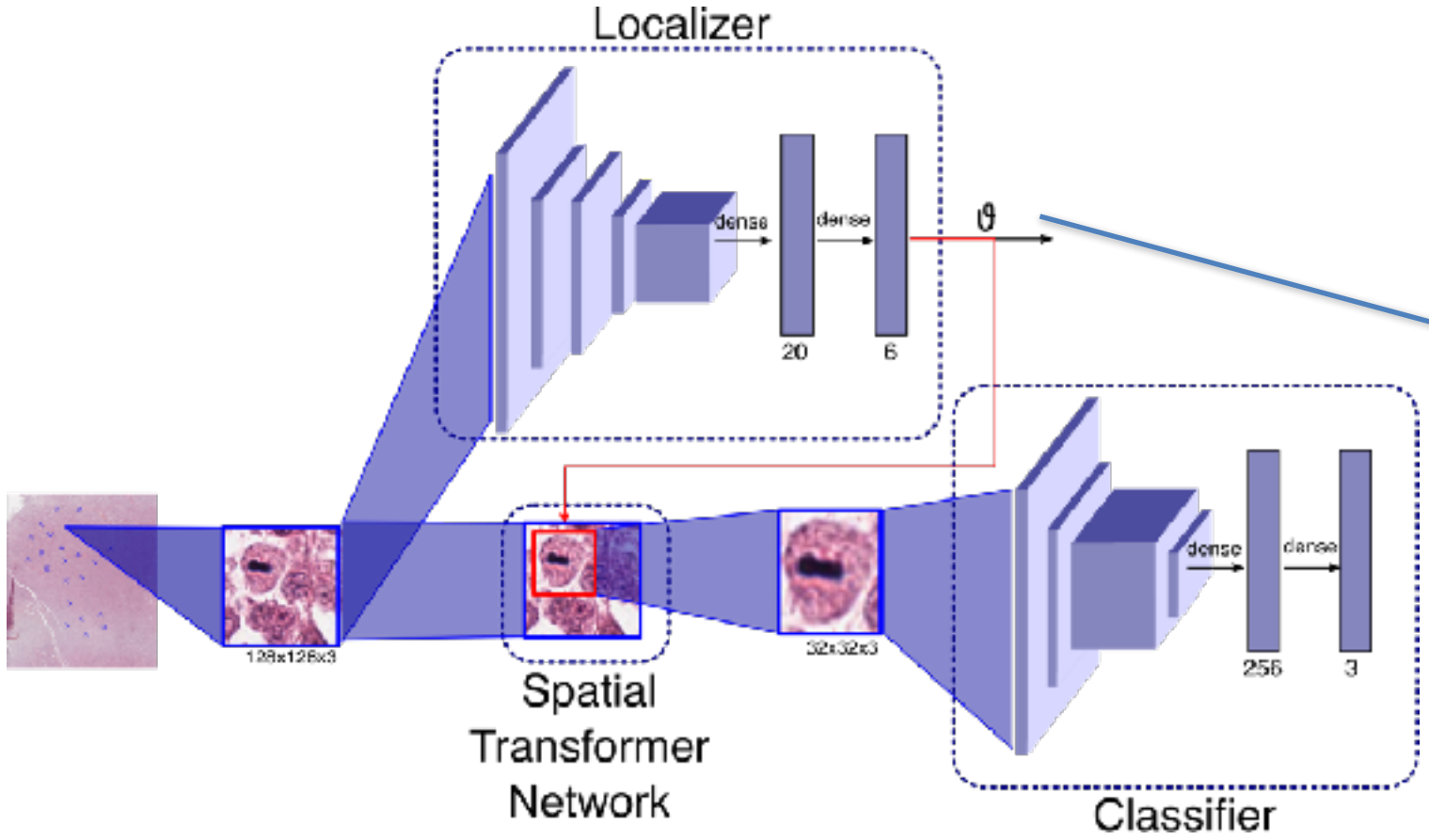




Jaderberg et al., 2015, on arXiV

- Transformation matrix is learned unsupervised within optimization of the classification task.

Spatial Transformer Network for Cell Detection



Standard CNN-approach (+ inception layers) for classification

Supervised training of the STN
==> focus on the cell

Loss function [Localizer]

Affine transform

$$\theta = \begin{bmatrix} \vartheta_s & 0 & \vartheta_x \\ 0 & \vartheta_s & \vartheta_y \end{bmatrix} \qquad \widehat{\theta} = \begin{bmatrix} \widehat{\vartheta_1} & \widehat{\vartheta_2} & \widehat{\vartheta_x} \\ \widehat{\vartheta_3} & \widehat{\vartheta_4} & \widehat{\vartheta_y} \end{bmatrix}$$

ground truth — estimate

$$\widehat{\vartheta_{s_x}} = \sqrt{\widehat{\vartheta_1}^2 + \widehat{\vartheta_3}^2}$$

$$\widehat{\vartheta_{s_y}} = \sqrt{\widehat{\vartheta_2}^2 + \widehat{\vartheta_4}^2}$$

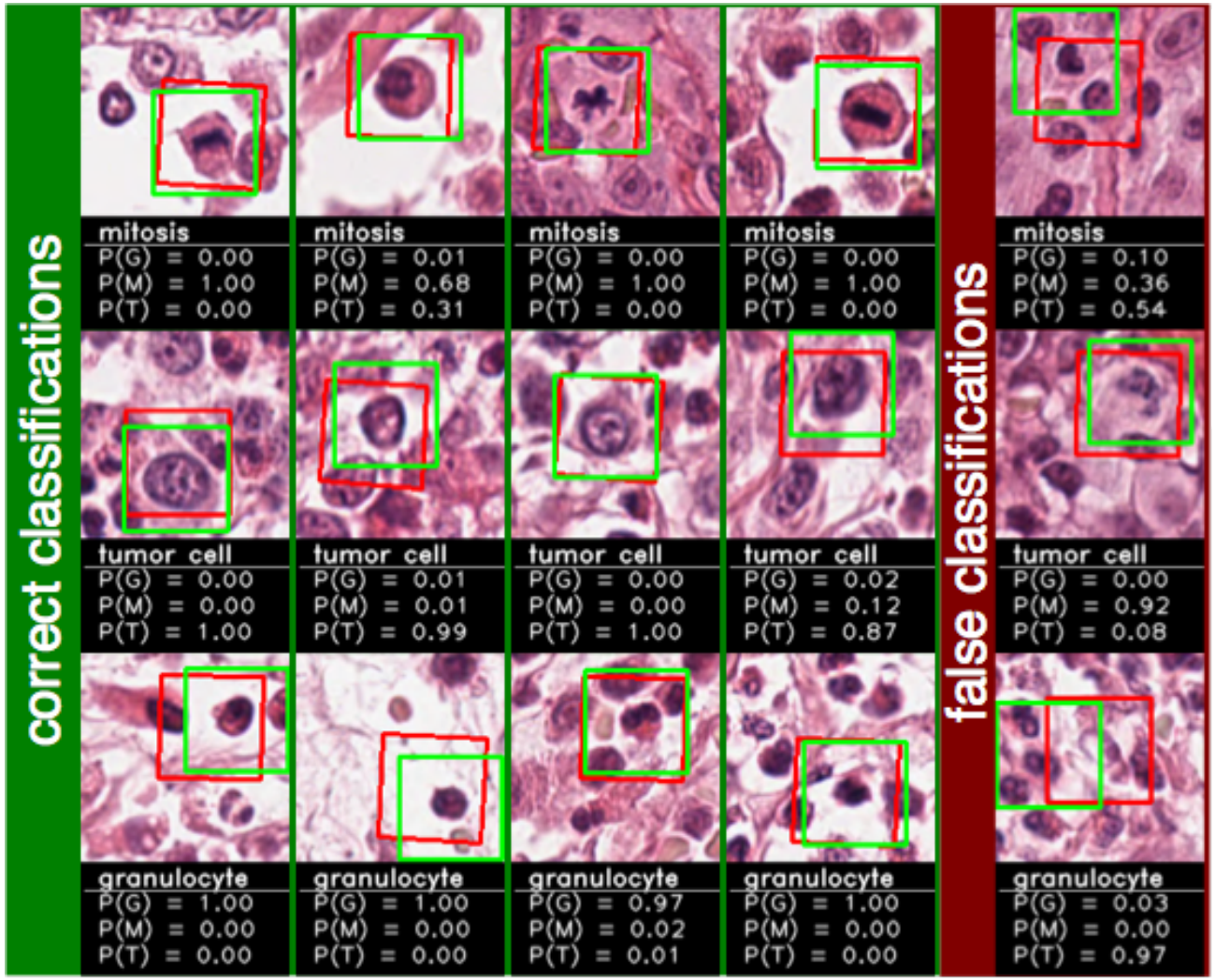
Scale estimate

position constraint — scale constr.

$$l_{\text{loc}} = \left|\widehat{\vartheta_x} - \vartheta_x\right|^2 + \left|\widehat{\vartheta_y} - \vartheta_y\right|^2 + \left|\widehat{\vartheta_{s_x}} - \vartheta_s\right|^2 + \left|\widehat{\vartheta_{s_y}} - \vartheta_s\right|^2 + \left|\widehat{\vartheta_1} - \widehat{\vartheta_4}\right|^2 + \left|\widehat{\vartheta_2} + \widehat{\vartheta_3}\right|^2$$

skew inhibition

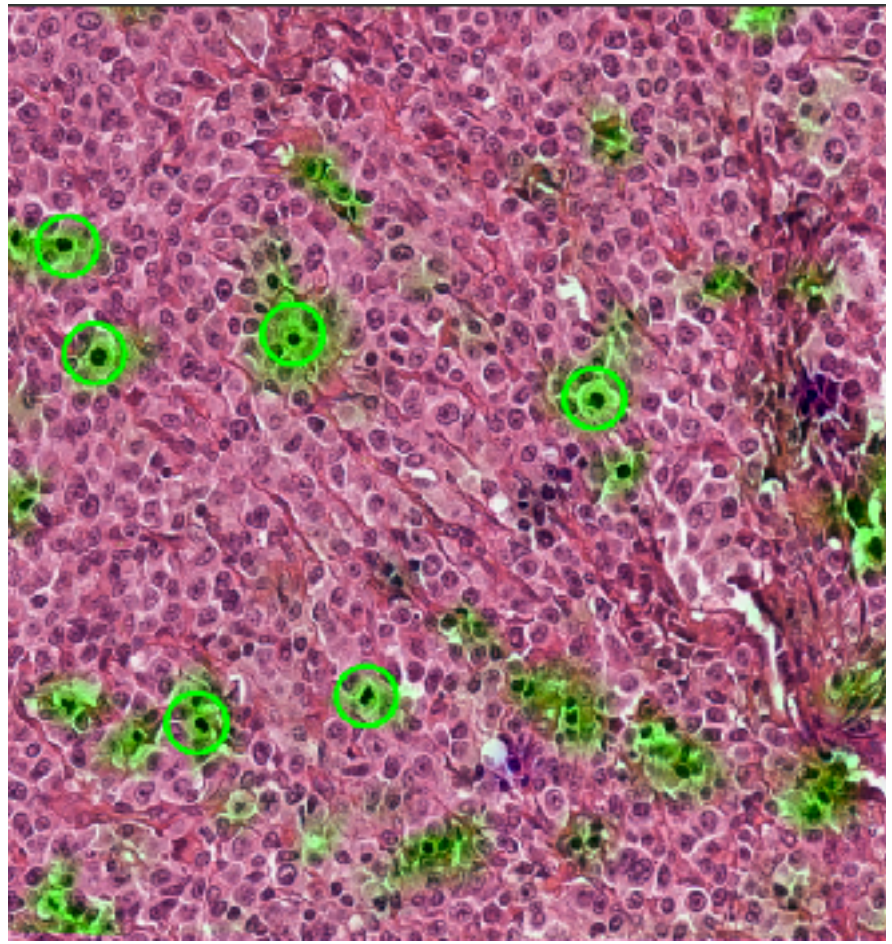
Results



approach	name	precision	recall	f1-score
CNN baseline	granulocytes	0.847	0.898	0.872
	mitotic figures	0.822	0.853	0.837
	normal t. cells	0.916	0.859	0.887
	avg / total	**0.870**	**0.868**	**0.869**
CNN-STN	granulocytes	0.912	0.925	0.918
	mitotic figures	0.891	0.889	0.890
	normal t. cells	0.932	0.924	0.928
	avg / total	**0.915**	**0.915**	**0.915**

Summary

Supervised STNs can be exploited for sparsely labeled image data



Outlook

Mitosis object detection in whole slide images