RADIOGENOMICS
learning GENOMIC CLASSES based on IMAGE FEATURES

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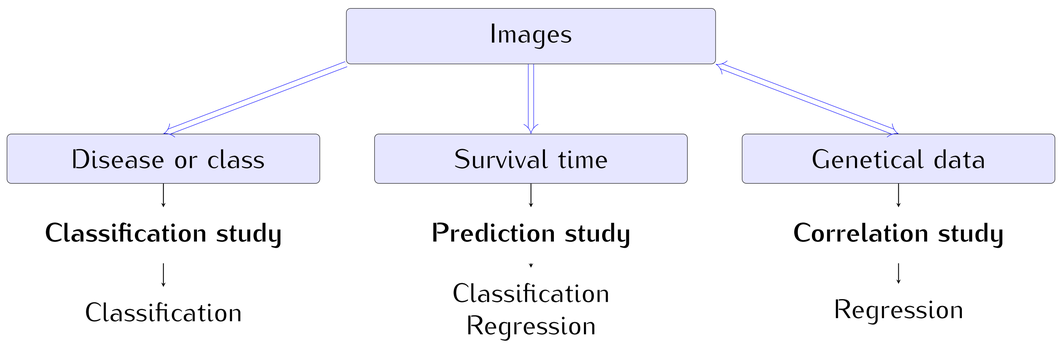
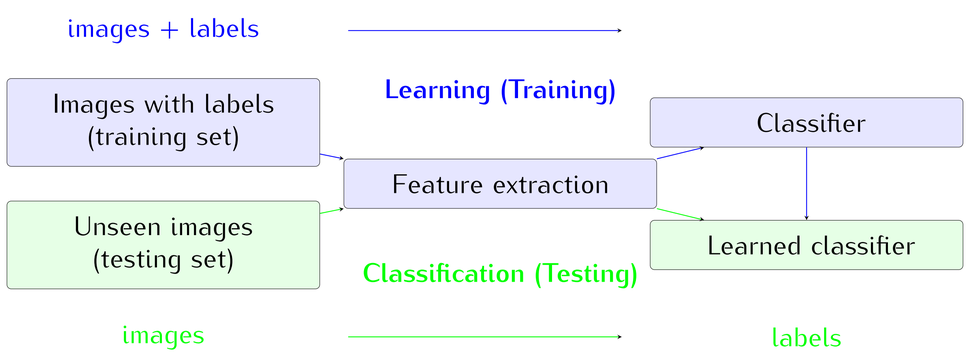
Radiogenomics – What are we learning?

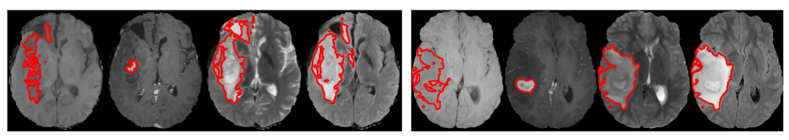
Three common radiogenomics approaches



Computer Aided Diagnosis – our application



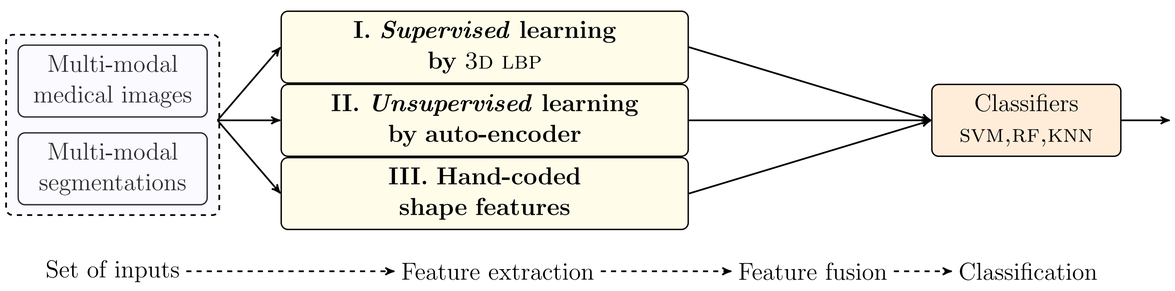
Images	MR brain tumor images	T1, T1c, T2, FLAIR
	tumor segmentations	edema, active core, necrotic core
Labels	genetic subclasses	CIMP codel, CIMP non-codel, CIMP neg



CIMP codel CIMP non-codel

Fig. 1: Data available for each patient: MR images, tumor segmentations and genetic subclass.

Feature extraction – Quantifying texture



I. Supervised learning by 3D Linear Binary Patterns

1. Spherical sampling: get neighbours
2. Create a neighbourhood function by:
   - 0: neighbour intensity < center intensity
   - 1: neighbour intensity > center intensity
3. Get frequency components of spherical harmonics for the neighbourhood function

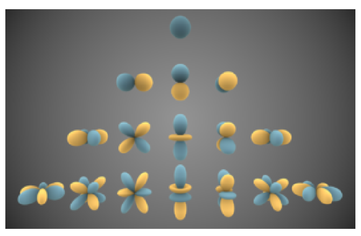
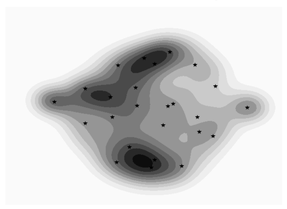


Fig. 2: Spherical harmonics (order 1-4).

Feature generation

Using the training set:

1. Calculate LBPs for all tumor voxels
2. Learn n common patterns



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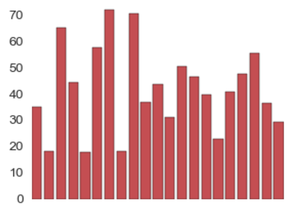
In the test set:

cluster LBPs towards the n learned patterns



generated feature
= frequency of the n patterns
in the new image

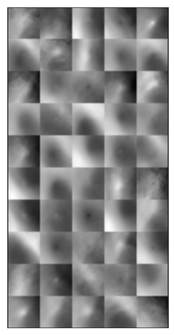


Fig. 3: Learnt texture patterns ($n = 25$).

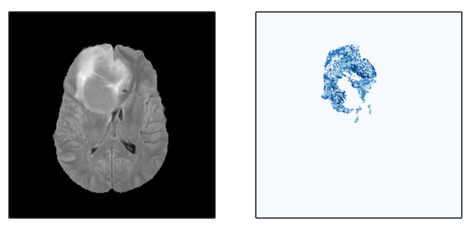


Fig. 4: LBP clustering of tumor voxels.

II. Unsupervised learning by auto-encoder

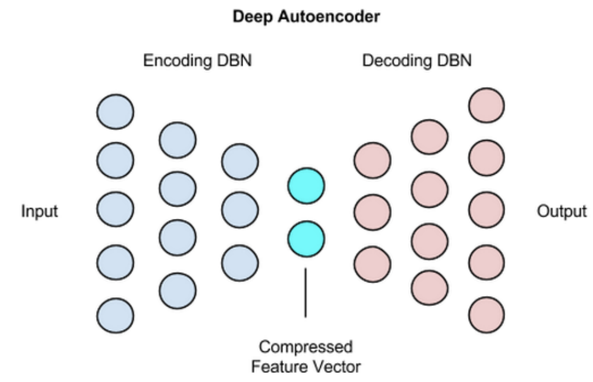
An **auto-encoder** is defined by encoder ϕ and decoder ψ transformations:

$$\phi : \mathbf{x} \in \mathbb{R}^d \rightarrow \mathbf{z} \in \mathbb{R}^p \quad (1)$$

$$\psi : \mathbf{z} \in \mathbb{R}^p \rightarrow \mathbf{x} \in \mathbb{R}^d \quad (2)$$

Here, $p << d$, in order to get a **compressed feature** representation.
The transformations ϕ and ψ are **learnt** through a **minimisation problem**:

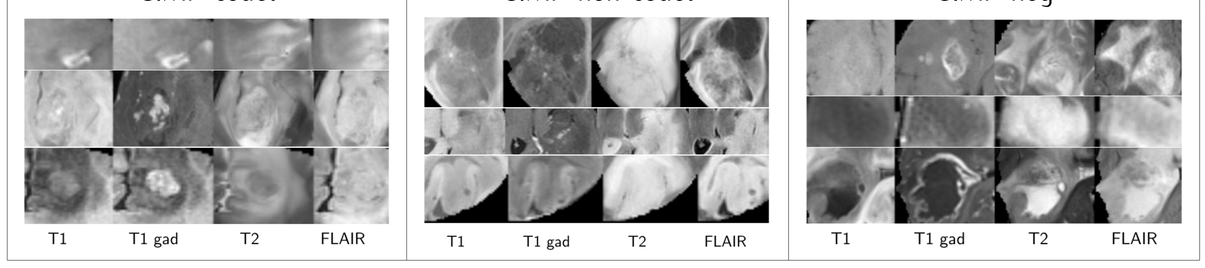
$$\underset{\phi,\psi}{\operatorname{argmin}} ||\mathbf{x} - (\psi \circ \phi)\mathbf{x}||^2 \quad (3)$$



Encoder ϕ 1 Decoder ψ 2

Classifiers – when p<<n . . .

Difficult classification task – human raters cannot differentiate



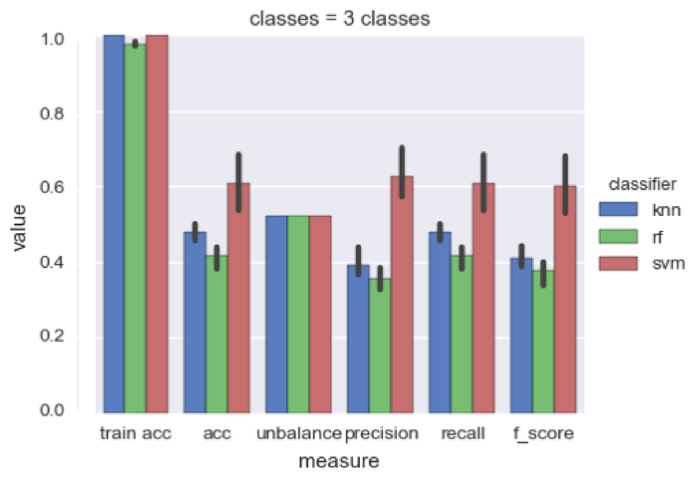


Fig. 5: Prediction results using LBP, HOG and auto-encoder features from T1, T1 gad, T2 and FLAIR.

We are looking for relations. In other words, we don't know how well the best possible classifier would perform!

Main problem: Curse of dimensionality

- Only 117 patients (= 117 labels)
- Every patient has 4 images (T1, T1 gad, T2 and FLAIR)
- Over 500 features per image
- ⇒ over 2000 features per label!

Next steps

- Smart feature selection to reduce dimension
- Patch-based deep learning approach to increase samples
- Testing on other datasets and other labels to look for more obvious relations
- Investigate specialized classifiers
- Add genetical metadata
- Look into semisupervised learning techniques

Literature

[1] Menze, B. H., Jakab, A., Bauer, S., et al.: The Multimodal Brain Tumor Image Segmentation Benchmark (BRATS). IEEE Trans. Med. Imag (2014)

[2] Menze, B.H., Van Leemput, K., Lashkari, D., et al.: A generative model for brain tumor segmentation in multi-modal images. Proc MICCAI 13(2), 151–159 (2010)

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[4] Banerjee, J., Moelker, A., Niessen, W. J., et al.: 3D LBP-Based Rotationally Invariant Region Description. ACCV Workshops (2012)