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Feature extraction from myelin-stained histological sections of the rat brain

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Introduction
Extracting meaningful features from histological images is a fundamental step to automate tissue analysis and classification. This feature extraction can be approached through nonlinear methods that can preserve complex biological structural information, or through linear methods that are directly interpretable and less computationally demanding. Understanding when nonlinear approaches provide meaningful advantages over linear alternatives is crucial for efficient analysis of large-scale brain datasets. In this work, we compare a nonlinear method, convolutional autoencoders (AEs), with a classical linear method, principal component analysis (PCA) to extract features from myelin-stained sections of the rat brain.

Methods
We used myelin-stained sections from 13 rat brains, which were scanned at 0.013 mm^2/px resolution. Both methods, AEs and PCA, were trained on patches from 9 brains (420 images) and tested on the remaining 4 brains (194 images). For each method, we tested two input patch sizes: 128x128 pixels and 256x256 pixels, with both configurations compressing the input to 256 features. We evaluated AEs and PCA on: 1) reconstruction quality both quantitatively (mean square error, MSE) and qualitatively; and 2) the biological relevance of the extracted features through clustering.

Results
PCA models were trained in less than 3 CPU days, while AEs training required 6 GPU days for 128x128 pixel patches and 9 GPU days for 256x256 pixel patches. AEs training used early stopping, halting when the validation error stopped improving for 10 consecutive iterations. PCA achieved lower MSE compared to AEs for both input patch sizes, but visual assessment revealed that AEs better preserved axonal structures while PCA produced smoother, more averaged reconstructions. When evaluating feature clustering, both methods obtained nearly identical clustering results using Gaussian Mixture Models. The clustering successfully separated white matter regions from grey matter areas, while also identifying subtypes within each tissue class based on myelin density and axonal distribution patterns.

Conclusions
Both PCA and AEs effectively extract features from myelin histology images. While PCA produces smaller MSE, AEs preserve fine textural details that may be critical for certain biological analyses. Despite these differences, clustering results converge, indicating both methods capture meaningful tissue organization through distinct strategies. For resource-constrained applications, PCA offers biologically meaningful compression with significantly reduced computational overload. AEs should be preferred when preserving structural details is essential. Future work could explore different clustering techniques to better understand how each method's feature space relates to specific biological questions.

Primary author: ESTELA DALMAU, Melina (University of Eastern Finland)

Co-authors: SALO, Raimo (A.I. Virtanen Institute for Molecular Sciences, University of Eastern Finland, Kuopio, Finland); SAN MARTÍN MOLINA, Isabel (Immunology Program/Imaging Facility, Babraham Institute, Babraham Research Campus, Cambridge, United Kingdom); KOLEHMAINEN, Ville (Department of Applied Physics, University of Eastern Finland, Kuopio, Finland); TOHKA, Jussi (University of Eastern Finland); SIERRA, Alejandra (University of Eastern Finland)

Presenter: ESTELA DALMAU, Melina (University of Eastern Finland)

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