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Michael Biehl <m.biehl@rug.nl>
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Degree programme

Degree programme	Thesis type
Computing Science	Bachelor's Thesis

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Original title

Iterative Subspace Correction Procedure for Generalized Matrix Learning Vector Quantization in Biomedicine

Abstract of thesis

Neurodegenerative diseases are challenging to diagnose accurately due to their incurable nature and overlapping symptoms. One potential solution is to use a trained Generalized Matrix Learning Vector Quantization (GMLVQ) system on patients's FDG-PET scans to differentiate between different neurodegenerative diseases. In this thesis, we explore a modified method incorporating iterative subspace corrections. The GMLVQ system is trained on homogeneous healthy control cohorts, allowing extraction of vectors highlighting centre differences. By ignoring these in our feature space, we aim to eliminate the centre-specific variance present in the data. The method's

performance is assessed by using artificial data sets of increasing complexity, generated as Gaussian clusters, and evaluating it based on the known characteristics used to generate them. The results showed that the iterative method successfully aligned the subspace with the ground truth centre direction in simple cases, maintaining a high accuracy in disease classification and arbitrary classification in centre identification. In complex cases, the iterative method struggled to accurately capture the underlying differences. Larger data sets generally improved performance, but complexity posed challenges in classification accuracy. The centre-wise z-scored data approach demonstrated better adaptability, achieving high disease classification accuracy and arbitrary centre classification across different complexities.

Number of pages	111
Language of the thesis	English
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