A pseudo-Voigt component model for high-resolution recovery of constituent spectra in Raman spectroscopy

Raman spectroscopy is a well-known analytical technique for identifying and analyzing chemical species. Since Raman scattering is a weak effect, surface-enhanced Raman spectroscopy (SERS) is often employed to amplify the signal. SERS signal surface mapping is a common method for detecting trace amounts of target molecules. Since the method produces large amounts of data and, in the case of very low concentrations, low signal-to-noise (SNR) ratio, ability to extract relevant spectral features is crucial. We propose a pseudo-Voigt model as a constrained source separation model, that is able to directly and reliably identify the Raman modes, with overall performance similar to the state of the art non-negative matrix factorization approach. However, the model provides better interpretation and is a step towards enabling the use of SERS in detection of trace amounts of molecules in real-life settings.

Bayesian Modelling of Functional Whole Brain Connectivity

This thesis deals with parcellation of whole-brain functional magnetic resonance imaging (fMRI) using Bayesian inference with mixture models tailored to the fMRI data. In the three included papers and manuscripts, we analyze two different approaches to modeling fMRI signal; either we accept the prevalent strategy of standardizing of fMRI time series and model data using directional statistics or we model the variability in the signal across the brain and across multiple
subjects. In either case, we use Bayesian nonparametric modeling to automatically learn from the fMRI data the number of functional units, i.e. parcels. We benchmark the proposed mixture models against state of the art methods of brain parcellation, both probabilistic and non-probabilistic.

The time series of each voxel are most often standardized using z-scoring which projects the time series data onto a hypersphere. This underlying manifold is often ignored and the data is modeled using Gaussian distributions. In one contribution, we show that using a mixture model based on the directional distribution, the von Mises-Fisher distribution, increase the reliability of inferred parcellations.

We develop a mixture model for modeling time-series using a Gaussian Process as a prior that is informed of the temporal dynamics of the data expected from the blood oxygenation level dependent (BOLD) signal. In two contributions, we explore the potential of this modeling framework. In the first, we show that this mixture model can delineate regions of task activation that can then be identified unsupervised. This forms a promising framework for unsupervised identification of task activated when the task design is unknown. In the final contribution, we evaluate the performance of the mixture model on the problem of clustering whole-brain fMRI. Based on both simulations on synthetic data and analysis of two fMRI datasets, we show that the model provides improved reliability of clustering compared to traditional clustering methods. Furthermore, the inferred parcellations provide the foundation for a method for increasing the reliability and sensitivity in analyses of task activation and for determining the networks of functionally connectivity in fMRI.

The proposed mixture models form promising tools for brain parcellation and we hope the methods can provide a nudge towards using probabilistic models for fMRI parcellation.

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Difference-of-Convex optimization for variational kl-corrected inference in dirichlet process mixtures
Variational methods for approximate inference in Bayesian models optimise a lower bound on the marginal likelihood, but the optimization problem often suffers from being nonconvex and high-dimensional. This can be alleviated by working in a collapsed domain where a part of the parameter space is marginalized. We consider the KL-corrected collapsed variational bound and apply it to Dirichlet process mixture models, allowing us to reduce the optimization space considerably. We find that the variational bound exhibits consistent and exploitable structure, allowing the application of difference-of-convex optimization algorithms. We show how this yields an interpretable fixed-point update algorithm in the collapsed setting for the Dirichlet process mixture model. We connect this update formula to classical coordinate ascent updates, illustrating that the proposed improvement surprisingly reduces to the traditional scheme.

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Examination of heterogeneous societies: Identifying subpopulations by contrasting cultures
The recent development of data analytic tools rooted around the Multi-Group Latent Class Analysis (MGLCA) has enabled the examination of heterogeneous datasets in a cross-cultural context. Although the MGLCA is considered as an established and popular cross-cultural data analysis approach, the infinite relational model (IRM) is a new and disruptive type of unsupervised clustering approach that has been developed recently by cognitive psychologists and computer scientists. In this article, an extended version of the IRM coined the multinominal IRM—or mIRM in short—is applied to a cross-cultural analysis of survey data available from the World Value Survey organization. Specifically, the present work analyzes response patterns of the Portrait Value Questionnaire (PVQ) representing Schwartz’s 10 basic values of Japanese and Swedes. The applied model exposes heterogeneous structures of the two societies consisting of fine-grained response patterns expressed by the respective subpopulations and extracts latent typological structures contrasting and highlighting similarities and differences between these two societies. In the final section, we discuss similarities and differences identified between the MGLCA and the mIRM approaches, which indicate potential applications and contributions of the mIRM and the general IRM framework for future cross-cultural data analyses.
Infinite von Mises-Fisher Mixture Modeling of Whole Brain fMRI Data

Cluster analysis of functional magnetic resonance imaging (fMRI) data is often performed using gaussian mixture models, but when the time series are standardized such that the data reside on a hypersphere, this modeling assumption is questionable. The consequences of ignoring the underlying spherical manifold are rarely analyzed, in part due to the computational challenges imposed by directional statistics. In this letter, we discuss a Bayesian von Mises-Fisher (vMF) mixture model for data on the unit hypersphere and present an efficient inference procedure based on collapsed Markov chain Monte Carlo sampling. Comparing the vMF and gaussian mixture models on synthetic data, we demonstrate that the vMF model has a slight advantage inferring the true underlying clustering when compared to gaussian-based models on data generated from both a mixture of vMFs and a mixture of gaussians subsequently normalized. Thus, when performing model selection, the two models are not in agreement. Analyzing multisubject whole brain resting-state fMRI data from healthy adult subjects, we find that the vMF mixture model is considerably more reliable than the gaussian mixture model when comparing solutions across models trained on different groups of subjects, and again we find that the two models disagree on the optimal number of components. The analysis indicates that the fMRI data support more than a thousand clusters, and we confirm this is not a result of overfitting by demonstrating better prediction on data from held-out subjects. Our results highlight the utility of using directional statistics to model standardized fMRI data and demonstrate that whole brain segmentation of fMRI data requires a very large number of functional units in order to adequately account for the discernible statistical patterns in the data.

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Large Scale Computing for the Modelling of Whole Brain Connectivity

The human brain constitutes an impressive network formed by the structural and functional connectivity patterns between billions of neurons. Modern functional and diffusion magnetic resonance imaging (fMRI and dMRI) provides unprecedented opportunities for exploring the functional and structural organization of the brain in continuously increasing resolution. From these images, networks of structural and functional connectivity can be constructed. Bayesian stochastic block modelling provides a prominent data-driven approach for uncovering the latent organization, by clustering the networks into groups of nodes with a shared connectivity pattern. Modelling the brain in great detail on a whole-brain scale
is essential to fully understand the underlying organization of the brain and reveal the relations between structure and function, that allows sophisticated cognitive behaviour to emerge from ensembles of neurons. Relying on Markov Chain Monte Carlo (MCMC) simulations as the workhorse in Bayesian inference however poses significant computational challenges, especially when modelling networks at the scale and complexity supported by high-resolution whole-brain MRI. In this thesis, we present how to overcome these computational limitations and apply Bayesian stochastic block models for un-supervised data-driven clustering of whole-brain connectivity in full image resolution. We implement high-performance software that allows us to efficiently apply stochastic blockmodelling with MCMC sampling on large complex networks. To obtain the necessary computational performance, we find that both hardware and model specific properties must be taken into consideration - to an extend not supported by generic modelling tools. Computational overhead is reduced by an approach, where key values are cached to avoid re-computations, while tablelookups are utilized for frequently computed special functions. The efficient memory-management of C++ is utilized to implement dedicated data-structures, optimized to facilitate performance-critical operations related to the inference procedure. Furthermore, the software is based on a modular design, which allows us to couple and explore different models and sampling procedures in runtime, still being applied to full-sized data. Using the implemented tools, we demonstrate that the models successfully can be applied for clustering whole-brain connectivity networks. Without being informed of spatial information, the data-driven models can discover spatial homogeneous regions that are meaningful and in agreement with existing anatomical atlases. We further demonstrate that structural and functional connectivity share information, allowing us to jointly model both modalities. For limited, noisy fMRI data we find that integrating structural information aids in discovering the functional organization better than using the fMRI data alone. Though structure and function describes very different properties of the brain, we find that probabilistic modelling provides an intuitive data-driven approach for uncovering the latent organization in connectivity networks. We find that the stochastic block models can be computationally scaled to model wholebrain connectivity, and by doing so allows us to better utilize the full potential of high-resolution MRI and advances our understanding of both the functional and structural organization of the entire brain.

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Modeling dynamic functional connectivity using a wishart mixture model
Dynamic functional connectivity (dFC) has recently become a popular way of tracking the temporal evolution of the brains functional integration. However, there does not seem to be a consensus on how to choose the complexity, i.e. number of brain states, and the time-scale of the dynamics, i.e. the window length. In this work we use the Wishart Mixture Model (WMM) as a probabilistic model for dFC based on variational inference. The framework admits arbitrary window lengths and number of dynamic components and includes the static one-component model as a special case. We exploit that the WMM framework provides model selection by quantifying models generalization to new data. We use this to quantify the number of states within a prespecified window length. We further propose a heuristic procedure for choosing the window length based on contrasting for each window length the predictive performance of dFC models to their static counterparts and choosing the window length having largest difference as most favorable for characterizing dFC. On synthetic data we find that generalizability is influenced by window length and signal-to-noise ratio. Too long windows cause dynamic states to be mixed together whereas short windows are more unstable and influenced by noise and we find that our heuristic correctly identifies an adequate level of complexity. On single subject resting state fMRI data we find that dynamic models generally outperform static models and using the proposed heuristic points to a windowlength of around 30 seconds provides largest difference between the predictive likelihood of static and dynamic FC.

General information
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Modeling Structural Brain Connectivity

The human brain consists of a gigantic complex network of interconnected neurons. Together all these connections determine who we are, how we react and how we interpret the world. Knowledge about how the brain is connected can further our understanding of the brain's structural organization, help improve diagnosis, and potentially allow better treatment of a wide range of neurological disorders.

Tractography based on diffusion magnetic resonance imaging is a unique tool to estimate this "structural connectivity" of the brain non-invasively and in vivo. During the last decade, brain connectivity has increasingly been analyzed using graph theoretic measures adopted from network science and this characterization of the brain's structural connectivity has been shown to be useful for the classification of populations, such as healthy and diseased subjects. The structural connectivity of the brain estimated using tractography is, however, derived by integrating noisy estimates of the local fiber orientation in each voxel, entailing biases and limitations in the estimated connections and resulting in noisy graphs.

In this thesis, the ability of stochastic block models to extract the latent organization of structural brain connectivity graphs is investigated. It is found that both the stochastic block model and its non-parametric extension, the infinite relational model, are able to reliably extract a clustering that better accounts for structural connectivity than cortical atlases based solely upon surface morphology. Furthermore, a statistical prediction framework to quantify the ability of a cortical parcellation to account for structural connectivity is proposed. It is tested on two commonly used cortical atlases that are both based on surface morphology, as well as on a recently proposed cortical parcellation by Glasser et al. (2016) that is based on both task and resting-state functional magnetic resonance imaging, cortical thickness and myelin. It is found that all three atlases capture the structural connectivity much better than random, but also that the parcellation based on multiple modalities is superior to those solely based on surface morphology.

The generation of structural brain connectivity graphs comprises a comprehensive processing pipeline, with various experimenter-defined parameters. The settings of these parameters are, however, unclear and this subjective aspect complicates the cross-comparison of studies investigating structural brain connectivity derived from tractography. Even though scan acquisition parameters, i.e. spatial resolution, angular resolution and b-value, are often discussed as possible factors influencing the final result, the impact of these factors on the derived structural connectivity graph has not yet been investigated. Herein, structural connectivity graphs, generated using different combinations of the three aforementioned acquisition parameters, are validated by comparison to a connectivity graph derived using invasive tracer injections in monkeys. It is found that the choice of acquisition parameters influences the derived structural connectivity graph and that higher angular resolution is always beneficial. Surprisingly, it is also found that higher spatial resolution does not improve the derived graph, but further investigation is needed to confirm this result.

General information

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Scalable group level probabilistic sparse factor analysis

Many data-driven approaches exist to extract neural representations of functional magnetic resonance imaging (fMRI) data, but most of them lack a proper probabilistic formulation. We propose a scalable group level probabilistic sparse factor analysis (psFA) allowing spatially sparse maps, component pruning using automatic relevance determination (ARD) and subject specific heteroscedastic spatial noise modeling. For task-based and resting state fMRI, we show that the sparsity constraint gives rise to components similar to those obtained by group independent component analysis. The noise modeling shows that noise is reduced in areas typically associated with activation by the experimental design. The psFA model identifies sparse components and the probabilistic setting provides a natural way to handle parameter uncertainties. The variational Bayesian framework easily extends to more complex noise models than the presently considered.

Whole-brain functional connectivity predicted by indirect structural connections

Modern functional and diffusion magnetic resonance imaging (fMRI and dMRI) provide data from which macro-scale networks of functional and structural whole brain connectivity can be estimated. Although networks derived from these two modalities describe different properties of the human brain, they emerge from the same underlying brain organization, and functional communication is presumably mediated by structural connections. In this paper, we assess the structure-function relationship by evaluating how well functional connectivity can be predicted from structural graphs. Using high-resolution whole brain networks generated with varying density, we contrast the performance of several non-parametric link predictors that measure structural communication flow. While functional connectivity is not well predicted directly by structural connections, we show that superior predictions can be achieved by taking indirect structural pathways into account. In particular, we find that the length of the shortest structural path between brain regions is a good predictor of
functional connectivity in sparse networks (density less than one percent), and that this improvement comes from integrating indirect pathways comprising up to three steps. Our results support the existence of important indirect relationships between structure and function, extending beyond the immediate direct structural connections that are typically investigated.

**Bayesian latent feature modeling for modeling bipartite networks with overlapping groups**

Bi-partite networks are commonly modelled using latent class or latent feature models. Whereas the existing latent class models admit marginalization of parameters specifying the strength of interaction between groups, existing latent feature models do not admit analytical marginalization of the parameters accounting for the interaction strength within the feature representation. We propose a new binary latent feature model that admits analytical marginalization of interaction strengths such that model inference reduces to assigning nodes to latent features. We propose a constraint inspired by the notion of community structure such that the edge density within groups is higher than between groups. Our model further assumes that entities can have different propensities of generating links in one of the modes. The proposed framework is contrasted on both synthetic and real bi-partite networks to the infinite relational model and the infinite Bernoulli mixture model. We find that the model provides a new latent feature representation of structure while in link-prediction performing close to existing models. Our current extension of the notion of communities and collapsed inference to binary latent feature representations in bipartite networks provides a new framework for accounting for structure in bi-partite networks using binary latent feature representations providing interpretable representations that well characterize structure as quantified by link prediction.
Completely random measures for modelling block-structured sparse networks

Many statistical methods for network data parameterize the edge-probability by attributing latent traits to the vertices such as block structure and assume exchangeability in the sense of the Aldous-Hoover representation theorem. Empirical studies of networks indicate that many real-world networks have a power-law distribution of the vertices which in turn implies the number of edges scale slower than quadratically in the number of vertices. These assumptions are fundamentally irreconcilable as the Aldous-Hoover theorem implies quadratic scaling of the number of edges. Recently Caron and Fox [2014] proposed the use of a different notion of exchangeability due to Kallenberg [2006] and obtained a network model which admits power-law behaviour while retaining desirable statistical properties, however this model does not capture latent vertex traits such as block-structure. In this work we re-introduce the use of block-structure for network models obeying allenberg’s notion of exchangeability and thereby obtain a model which admits the inference of block-structure and edge inhomogeneity. We derive a simple expression for the likelihood and an efficient sampling method. The obtained model is not significantly more difficult to implement than existing approaches to block-modelling and performs well on real network datasets.

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Authors: Herlau, T. (Intern), Schmidt, M. N. (Intern), Mørup, M. (Intern)
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Surface-enhanced Raman spectroscopic study of DNA and 6-mercapto-1-hexanol interactions using large area mapping

The emergence of 2D SERS substrates with large areas of hot spots has enabled data to be gathered at large scale. This work presents a statistical tool for analysing large amounts of SERS data by utilizing a peak-fitting model in a specific spectral range. By analysing the distributions of Raman intensities and peak positions it is possible to directly inspect the interplay between DNA and 6-mercapto-1-hexanol on gold covered nanopillars. It is demonstrated that optimised functionalization parameters can be extracted from the Raman spectra directly. Using the peak-fitting approach it is possible to avoid miss-interpretation of intensity histograms, where contamination might contribute with an enhanced background and not a peak.

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Organisations: Department of Micro- and Nanotechnology, Department of Applied Mathematics and Computer Science, Cognitive Systems, Nanoprobes, Copenhagen Center for Health Technology, Surface Engineering, Center for Intelligent Drug Delivery and Sensing Using Microcontainers and Nanomechanics
Authors: Frøhling, K. B. (Intern), Alstrøm, T. S. (Intern), Bache, M. (Intern), Schmidt, M. S. (Intern), Schmidt, M. N. (Intern), Larsen, J. (Intern), Jakobsen, M. H. (Intern), Boisen, A. (Intern)
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The influence of hyper-parameters in the infinite relational model

The infinite relational model (IRM) is a Bayesian nonparametric stochastic block model, a generative model for random networks parameterized for uni-partite undirected networks by a partition of the node set and symmetric matrix of inter-partition link probabilities. The prior for the node clusters is the Chinese restaurant process, and the link probabilities are, in the most simple setting, modeled as iid. with a common symmetric Beta prior. More advanced priors such as separate asymmetric Beta priors for links within and between clusters have also been proposed. In this paper we investigate the importance of these priors for discovering latent clusters and for predicting links. We compare fixed symmetric priors and fixed asymmetric priors based on the empirical distribution of links with a Bayesian hierarchical approach where the parameters of the priors are inferred from data. On synthetic data, we show that the hierarchical Bayesian approach can infer the prior distributions used to generate the data. On real network data we demonstrate that using asymmetric priors significantly improves predictive performance and heavily influences the number of extracted partitions.
Nonparametric modeling of dynamic functional connectivity in fMRI data

Dynamic functional connectivity (FC) has in recent years become a topic of interest in the neuroimaging community. Several models and methods exist for both functional magnetic resonance imaging (fMRI) and electroencephalography (EEG), and the results point towards the conclusion that FC exhibits dynamic changes. The existing approaches modeling dynamic connectivity have primarily been based on time-windowing the data and k-means clustering. We propose a nonparametric generative model for dynamic FC in fMRI that does not rely on specifying window lengths and number of dynamic states. Rooted in Bayesian statistical modeling we use the predictive likelihood to investigate if the model can discriminate between a motor task and rest both within and across subjects. We further investigate what drives dynamic states using the model on the entire data collated across subjects and task/rest. We find that the number of states extracted are driven by subject variability and preprocessing differences while the individual states are almost purely defined by either task or rest. This questions how we in general interpret dynamic FC and points to the need for more research on what drives dynamic FC.

Numerical approximations for speeding up MCMC inference in the infinite relational model

The infinite relational model (IRM) is a powerful model for discovering clusters in complex networks; however, the computational speed of Markov chain Monte Carlo inference in the model can be a limiting factor when analyzing large networks. We investigate how using numerical approximations of the log-Gamma function in evaluating the likelihood of the IRM can improve the computational speed of MCMC inference, and how it affects the performance of the model. Using an ensemble of networks generated from the IRM, we compare three approximations in terms of their generalization performance measured on test data. We demonstrate that the computational time for MCMC inference can be reduced by a factor of two without affecting the performance, making it worthwhile in practical situations when on a computational budget.
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Statistical analysis of large areas of Raman mapped DNA functionalized gold coated silicon nanopillar SERS substrates

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Unsupervised segmentation of task activated regions in fMRI
Functional Magnetic Resonance Imaging has become a central measuring modality to quantify functional activation of the brain in both task and rest. Most analysis used to quantify functional activation requires supervised approaches as employed in statistical parametric mapping (SPM) to extract maps of task induced functional activations. This requires strong knowledge and assumptions on the BOLD response as a function of activation while smoothing in general enhances the statistical power but at the cost of spatial resolution. We propose a fully unsupervised approach for the extraction of task activated functional units in multi-subject fMRI data that exploits that regions of task activation are consistent across subjects and can be more reliably inferred than regions that are not activated. We develop a non-parametric Gaussian mixture model that apriori assumes activations are smooth using a Gaussian Process prior while assuming the segmented functional maps are the same across subjects but having individual time-courses and noise variances. To improve inference we propose an enhanced split-merge procedure. We find that our approach well extracts the induced activity of a finger tapping fMRI paradigm with maps that well corresponds to a supervised group SPM analysis. We further find interesting regions that are not activated time locked to the paradigm. Demonstrating that we in a fully unsupervised manner are able to extract the task-induced activations forms a promising framework for the analysis of task fMRI and resting-state data in general where strong knowledge of how the task induces a BOLD response is missing.
Cross-categorization of legal concepts across boundaries of legal systems: in consideration of inferential links

This work contrasts Giovanni Sartor’s view of inferential semantics of legal concepts (Sartor in Artif Intell Law 17:217–251, 2009) with a probabilistic model of theory formation (Kemp et al. in Cognition 114:165–196, 2010). The work further explores possibilities of implementing Kemp’s probabilistic model of theory formation in the context of mapping legal concepts between two individual legal systems. For implementing the legal concept mapping, we propose a cross-categorization approach that combines three mathematical models: the Bayesian Model of Generalization (BMG; Tenenbaum and Griffiths in Behav Brain Sci 4:629–640, 2001), the probabilistic model of theory formation, i.e., the Infinite Relational Model (IRM) first introduced by Kemp et al. (The twenty-first national conference on artificial intelligence, 2006, Cognition 114:165–196, 2010) and its extended model, i.e., the normal-IRM (n-IRM) proposed by Herlau et al. (IEEE International Workshop on Machine Learning for Signal Processing, 2012). We apply our cross-categorization approach to datasets where legal concepts related to educational systems are respectively defined by the Japanese- and the Danish authorities according to the International Standard Classification of Education. The main contribution of this work is the proposal of a conceptual framework of the cross-categorization approach that, inspired by Sartor (Artif Intell Law 17:217–251, 2009), attempts to explain reasoner’s inferential mechanisms.
Community structure in resting state complex networks

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Discovering hierarchical structure in normal relational data
Hierarchical clustering is a widely used tool for structuring and visualizing complex data using similarity. Traditionally, hierarchical clustering is based on local heuristics that do not explicitly provide assessment of the statistical saliency of the extracted hierarchy. We propose a non-parametric generative model for hierarchical clustering of similarity based on multifurcating Gibbs fragmentation trees. This allows us to infer and display the posterior distribution of hierarchical structures that comply with the data. We demonstrate the utility of our method on synthetic data and data of functional brain connectivity.

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Improving the robustness of Surface Enhanced Raman Spectroscopy based sensors by Bayesian Non-negative Matrix Factorization

Due to applications in areas such as diagnostics and environmental safety, detection of molecules at very low concentrations has attracted recent attention. A powerful tool for this is Surface Enhanced Raman Spectroscopy (SERS) where substrates form localized areas of electromagnetic “hot spots” where the signal-to-noise (SNR) ratio is greatly amplified. However, at low concentrations hot spots with target molecules bound are rare. Furthermore, traditional detection relies on having uncontaminated sensor readings which is unrealistic in a real world detection setting. In this paper, we propose a Bayesian Non-negative Matrix Factorization (NMF) approach to identify locations of target molecules. The proposed method is able to successfully analyze the spectra and extract the target spectrum. A visualization of the loadings of the basis vector is created and the results show a clear SNR enhancement. Compared to traditional data processing, the NMF approach enables a more reproducible and sensitive sensor.

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Infinite-degree-corrected stochastic block model

In stochastic block models, which are among the most prominent statistical models for cluster analysis of complex networks, clusters are defined as groups of nodes with statistically similar link probabilities within and between groups. A recent extension by Karrer and Newman [Karrer and Newman, Phys. Rev. E 83, 016107 (2011)] incorporates a node degree correction to model degree heterogeneity within each group. Although this demonstrably leads to better performance on several networks, it is not obvious whether modeling node degree is always appropriate or necessary. We formulate the degree corrected stochastic block model as a nonparametric Bayesian model, incorporating a parameter to control the amount of degree correction that can then be inferred from data. Additionally, our formulation yields principled ways of inferring the number of groups as well as predicting missing links in the network that can be used to quantify the model’s predictive performance. On synthetic data we demonstrate that including the degree correction yields better performance on both recovering the true group structure and predicting missing links when degree heterogeneity is present, whereas performance is on par for data with no degree heterogeneity within clusters. On seven real networks (with no ground truth group structure available) we show that predictive performance is about equal whether or not degree correction is included; however, for some networks significantly fewer clusters are discovered when correcting for degree, indicating that the data can be more compactly explained by clusters of heterogeneous degree nodes.

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Joint Iterative Carrier Synchronization and Signal Detection Employing Expectation Maximization

In this paper, joint estimation of carrier frequency, phase, signal means and noise variance, in a maximum likelihood sense, is performed iteratively by employing expectation maximization. The parameter estimation is soft decision driven and allows joint carrier synchronization and data detection. The algorithm is tested in a mixed line rate optical transmission scenario employing dual polarization 448 Gb/s 16-QAM signal surrounded by eight on-off keying channels in a 50 GHz grid. It is shown that joint carrier synchronization and data detection are more robust towards optical transmitter impairments and nonlinear phase noise, compared to digital phase-locked loop (PLL) followed by hard decisions. Additionally, soft decision driven joint carrier synchronization and detection offers an improvement of 0.5 dB in terms of input power compared to hard decision digital PLL based carrier synchronization and demodulation.

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Nonparametric Bayesian Clustering of Structural Whole Brain Connectivity in Full Image Resolution

Diffusion magnetic resonance imaging enables measuring the structural connectivity of the human brain at a high spatial resolution. Local noisy connectivity estimates can be derived using tractography approaches and statistical models are necessary to quantify the brain’s salient structural organization. However, statistically modeling these massive structural connectivity datasets is a computational challenging task. We develop a high-performance inference procedure for the infinite relational model (a prominent non-parametric Bayesian model for clustering networks into structurally similar groups) that defines structural units at the resolution of statistical support. We apply the model to a network of structural brain connectivity in full image resolution with more than one hundred thousand regions (voxels in the gray-white matter boundary) and around one hundred million connections. The derived clustering identifies in the order of one thousand salient structural units and we find that the identified units provide better predictive performance than predicting using the full graph or two commonly used atlases. Extracting structural units of brain connectivity at the full image resolution can aid in understanding the underlying connectivity patterns, and the proposed method for large scale data driven generation of structural units provides a promising framework that can exploit the increasing spatial resolution of neuro-imaging technologies.

Non-parametric Bayesian graph models reveal community structure in resting state fMRI

Modeling of resting state functional magnetic resonance imaging (rs-fMRI) data using network models is of increasing interest. It is often desirable to group nodes into clusters to interpret the communication patterns between nodes. In this study we consider three different nonparametric Bayesian models for node clustering in complex networks. In particular, we test their ability to predict unseen data and their ability to reproduce clustering across datasets. The three generative models considered are the Infinite Relational Model (IRM), Bayesian Community Detection (BCD), and the Infinite Diagonal Model (IDM). The models define probabilities of generating links within and between clusters and the difference between the models lies in the restrictions they impose upon the between-cluster link probabilities. IRM is the most flexible model with no restrictions on the probabilities of links between clusters. BCD restricts the between-cluster link probabilities to be strictly lower than within-cluster link probabilities to conform to the community structure typically seen in social networks. IDM only models a single between-cluster link probability, which can be interpreted as a background noise probability. These probabilistic models are compared against three other approaches for node clustering, namely Infomap, Louvain modularity, and hierarchical clustering. Using 3 different datasets comprising healthy volunteers' rs-fMRI we found that the BCD model was in general the most predictive and reproducible model. This suggests that rs-fMRI data exhibits community structure and furthermore points to the significance of modeling heterogeneous between-cluster link probabilities.
Nonparametric statistical structuring of knowledge systems using binary feature matches

Structuring knowledge systems with binary features is often based on imposing a similarity measure and clustering objects according to this similarity. Unfortunately, such analyses can be heavily influenced by the choice of similarity measure. Furthermore, it is unclear at which level clusters have statistical support and how this approach generalizes to the structuring and alignment of knowledge systems. We propose a non-parametric Bayesian generative model for structuring binary feature data that does not depend on a specific choice of similarity measure. We jointly model all combinations of binary matches and structure the data into groups at the level in which they have statistical support. The model naturally extends to structuring and aligning an arbitrary number of systems. We analyze three datasets on educational concepts and their features and demonstrate how the proposed model can both be used to structure each system separately or to jointly align two or more systems. The proposed method forms a promising new framework for the statistical modeling and alignment of structure across an arbitrary number of systems.

Analysis of Conceptualization Patterns across Groups of People

This paper analyzes patterns of conceptualizations possessed by different groups of subjects. The eventual goal of this work is to dynamically learn and structure semantic representations for groups of people sharing domain knowledge. In this paper, we conduct a survey for collecting data representing semantic representations of 34 subjects with different profiles in gender and educational background. The collected data is analyzed by an approach combining two extended versions of the Infinite Relational Model (Kemp et al. 2006) [1]: multiarray Infinite Relational Model (Mørup et al. 2010) [2] and normal Infinite Relational Model (Herlau et al. 2012) [3]. Results indicate that the employed approach not only localizes similar patterns of conceptualization within a group of subjects having a common profile, but also identifies differences in conceptualization across different subject groups.
Analysis of Subjective Conceptualizations Towards Collective Conceptual Modelling

This work is conducted as a preliminary study for a project where individuals' conceptualizations of domain knowledge will thoroughly be analyzed across 150 subjects from 6 countries. The project aims at investigating how humans' conceptualizations differ according to different types of mother languages, cultural backgrounds, gender, generations, etc., when domain-specific terms are expressed in a common language, i.e. English. In this work, we analyze a publicly available dataset [De Deyne, 2008] representing semantic structures of domain knowledge possessed by four subjects. The application of a non-parametric relational model, Infinite Relational Model [Kemp, 2006] co-clusters concept-feature relations, which identifies a common semantic structural grid across the four subjects considered. Through this common grid, the individual semantic structures possessed by the respective subjects are further contrasted to each other. The results show that the identified common grid visualizes subject specific patterns among the extracted concept-feature clusters. The work further discusses our future perspectives for modeling a collective ontology across subjects according to different subjects' profiles.

Comparing Structural Brain Connectivity by the Infinite Relational Model

The growing focus in neuroimaging on analyzing brain connectivity calls for powerful and reliable statistical modeling tools. We examine the Infinite Relational Model (IRM) as a tool to identify and compare structure in brain connectivity graphs by contrasting its performance on graphs from the same subject versus graphs from different subjects. The inferred structure is most consistent between graphs from the same subject, however, the model is able to predict links in graphs from different subjects on par with results within a subject. The framework proposed can be used as a statistical modeling tool for the identification of structure and quantification of similarity in graphs of brain connectivity in general.
Large scale inference in the Infinite Relational Model: Gibbs sampling is not enough
The stochastic block-model and its non-parametric extension, the Infinite Relational Model (IRM), have become key tools for discovering group-structure in complex networks. Identifying these groups is a combinatorial inference problem which is usually solved by Gibbs sampling. However, whether Gibbs sampling suffices and can be scaled to the modeling of large scale real world complex networks has not been examined sufficiently. In this paper we evaluate the performance and mixing ability of Gibbs sampling in the Infinite Relational Model (IRM) by implementing a high performance Gibbs sampler. We find that Gibbs sampling can be computationally scaled to handle millions of nodes and billions of links. Investigating the behavior of the Gibbs sampler for different sizes of networks we find that the mixing ability decreases drastically with the network size, clearly indicating a need for better sampling strategies.

Modeling Temporal Evolution and Multiscale Structure in Networks
Many real-world networks exhibit both temporal evolution and multiscale structure. We propose a model for temporally correlated multifurcating hierarchies in complex networks which jointly capture both effects. We use the Gibbs fragmentation tree as prior over multifurcating trees and a change-point model to account for the temporal evolution of each vertex. We demonstrate that our model is able to infer time-varying multiscale structure in synthetic as well as three real world time-evolving complex networks. Our modeling of the temporal evolution of hierarchies brings new insights into the changing roles and position of entities and possibilities for better understanding these dynamic complex systems.
Nonparametric Bayesian Modeling of Complex Networks: An Introduction

Modeling structure in complex networks using Bayesian nonparametrics makes it possible to specify flexible model structures and infer the adequate model complexity from the observed data. This article provides a gentle introduction to nonparametric Bayesian modeling of complex networks: Using an infinite mixture model as running example, we go through the steps of deriving the model as an infinite limit of a finite parametric model, inferring the model parameters by Markov chain Monte Carlo, and checking the model’s fit and predictive performance. We explain how advanced nonparametric models for complex networks can be derived and point out relevant literature.

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  Scopus rating (2010): SJR 2.986 SNIP 5.144
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Unsupervised knowledge structuring Application of Infinite Relational Models to the FCA visualization

This work presents a conceptual framework for learning an ontological structure of domain knowledge, which combines Jaccard similarity coefficient with the Infinite Relational Model (IRM) by (Kemp et al. 2006) and its extended model, i.e. the normal-Infinite Relational Model (n-IRM) by (Herlau et al. 2012). The proposed approach is applied to a dataset where legal concepts related to the Japanese educational system are defined by the Japanese authorities according to the International Standard Classification of Education (ISCED). Results indicate that the proposed approach effectively structures features for defining groups of concepts in several levels (i.e., concept, category, abstract category levels) from which an ontological structure is systematically visualized as a lattice graph based on the Formal Concept Analysis (FCA) by (Ganter and Wille 1997).

Bayesian community detection.

Many networks of scientific interest naturally decompose into clusters or communities with comparatively fewer external than internal links; however, current Bayesian models of network communities do not exert this intuitive notion of communities. We formulate a nonparametric Bayesian model for community detection consistent with an intuitive definition of communities and present a Markov chain Monte Carlo procedure for inferring the community structure. A Matlab toolbox with the proposed inference procedure is available for download. On synthetic and real networks, our model detects communities consistent with ground truth, and on real networks, it outperforms existing approaches in predicting missing links. This suggests that community structure is an important structural property of networks that should be explicitly modeled.
Detecting Hierarchical Structure in Networks

Many real-world networks exhibit hierarchical organization. Previous models of hierarchies within relational data has focused on binary trees; however, for many networks it is unknown whether there is hierarchical structure, and if there is, a binary tree might not account well for it. We propose a generative Bayesian model that is able to infer whether hierarchies are present or not from a hypothesis space encompassing all types of hierarchical tree structures. For efficient inference we propose a collapsed Gibbs sampling procedure that jointly infers a partition and its hierarchical structure. On synthetic and real data we demonstrate that our model can detect hierarchical structure leading to better link-prediction than competing models. Our model can be used to detect if a network exhibits hierarchical structure, thereby leading to a better comprehension and statistical account the network.

Haussdorff and hellinger for colorimetric sensor array classification

Development of sensors and systems for detection of chemical compounds is an important challenge with applications in areas such as anti-terrorism, demining, and environmental monitoring. A newly developed colorimetric sensor array is able to detect explosives and volatile organic compounds; however, each sensor reading consists of hundreds of pixel values, and methods for combining these readings from multiple sensors must be developed to make a classification system. In this work we examine two distance based classification methods, K-Nearest Neighbor (KNN) and Gaussian process (GP) classification, which both rely on a suitable distance metric. We evaluate a range of different distance measures and propose a method for sensor fusion in the GP classifier. Our results indicate that the best choice of distance measure depends on the sensor and the chemical of interest.
Interactive 3D audio: Enhancing awareness of details in immersive soundscapes?

Spatial audio and the possibility of interacting with the audio environment is thought to increase listeners' attention to details in a soundscape. This work examines if interactive 3D audio enhances listeners' ability to recall details in a soundscape. Nine different soundscapes were constructed and presented in either mono, stereo, 3D, or interactive 3D, and performance was evaluated by asking factual questions about details in the audio. Results show that spatial cues can increase attention to background sounds while reducing attention to narrated text, indicating that spatial audio can be constructed to guide listeners' attention.

Joint Modelling of Structural and Functional Brain Networks

Functional and structural magnetic resonance imaging have become the most important noninvasive windows to the human brain. A major challenge in the analysis of brain networks is to establish the similarities and dissimilarities between functional and structural connectivity. We formulate a non-parametric Bayesian network model which allows for joint modelling and integration of multiple networks. We demonstrate the model's ability to detect vertices that share structure across networks jointly in functional MRI (fMRI) and diffusion MRI (dMRI) data. Using two fMRI and dMRI scans per subject, we establish significant structures that are consistently shared across subjects and data splits. This provides an unsupervised approach for modeling of structure-function relations in the brain and provides a general framework for multimodal integration.
Modelling dense relational data
Relational modelling classically consider sparse and discrete data. Measures of influence computed pairwise between temporal sources naturally give rise to dense continuous-valued matrices, for instance p-values from Granger causality. Due to asymmetry or lack of positive definiteness they are not naturally suited for kernel K-means. We propose a generative Bayesian model for dense matrices which generalize kernel K-means to consider off-diagonal interactions in matrices of interactions, and demonstrate its ability to detect structure on both artificial data and two real data sets.

Nonlinear impairment compensation using expectation maximization for dispersion managed and unmanaged PDM 16-QAM transmission
In this paper, we show numerically and experimentally that expectation maximization (EM) algorithm is a powerful tool in combating system impairments such as fibre nonlinearities, inphase and quadrature (I/Q) modulator imperfections and laser linewidth. The EM algorithm is an iterative algorithm that can be used to compensate for the impairments which have an imprint on a signal constellation, i.e. rotation and distortion of the constellation points. The EM is especially effective for combating non-linear phase noise (NLPN). It is because NLPN severely distorts the signal constellation and this can be tracked by the EM. The gain in the nonlinear system tolerance for the system under consideration is shown to be dependent on the transmission scenario. We show experimentally that for a dispersion managed polarization multiplexed 16-QAM system at 14 Gbaud a gain in the nonlinear system tolerance of up to 3 dB can be obtained. For, a dispersion unmanaged system this gain reduces to 0.5 dB.
Nonlinear Impairment Compensation Using Expectation Maximization for PDM 16-QAM Systems

We show experimentally that by using non-linear signal processing based algorithm, expectation maximization, nonlinear system tolerance can be increased by 2 dB. Expectation maximization is also effective in combating I/Q modulator nonlinearities and laser linewidth.

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Authors: Zibar, D. (Intern), Winther, O. (Intern), Franceschi, N. (Ekstern), Borkowski, R. (Intern), Caballero Jambrina, A. (Intern), Arlunno, V. (Intern), Schmidt, M. N. (Intern), Gonzales, N. G. (Ekstern), Mao, B. (Ekstern), Larsen, K. J. (Intern), Tafur Monroy, I. (Intern)
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Infinite multiple membership relational modeling for complex networks

Learning latent structure in complex networks has become an important problem fueled by many types of networked data originating from practically all fields of science. In this paper, we propose a new non-parametric Bayesian multiple-membership latent feature model for networks. Contrary to existing multiple-membership models that scale quadratically in the number of vertices the proposed model scales linearly in the number of links admitting multiple-membership analysis in large scale networks. We demonstrate a connection between the single membership relational model and multiple membership models and show on "real" size benchmark network data that accounting for multiple memberships improves the learning of latent structure as measured by link prediction while explicitly accounting for multiple membership result in a more compact representation of the latent structure of networks.

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Transformation invariant sparse coding
Sparse coding is a well established principle for unsupervised learning. Traditionally, features are extracted in sparse coding in specific locations, however, often we would prefer invariant representation. This paper introduces a general transformation invariant sparse coding (TISC) model. The model decomposes images into features invariant to location and general transformation by a set of specified operators as well as a sparse coding matrix indicating where and to what degree in the original image these features are present. The TISC model is in general overcomplete and we therefore invoke sparse coding to estimate its parameters. We demonstrate how the model can correctly identify components of non-trivial artificial as well as real image data. Thus, the model is capable of reducing feature redundancies in terms of pre-specified transformations improving the component identification.

Unmixing of Hyperspectral Images using Bayesian Non-negative Matrix Factorization with Volume Prior
Hyperspectral imaging can be used in assessing the quality of foods by decomposing the image into constituents such as protein, starch, and water. Observed data can be considered a mixture of underlying characteristic spectra (endmembers), and estimating the constituents and their abundances requires efficient algorithms for spectral unmixing. We present a Bayesian spectral unmixing algorithm employing a volume constraint and propose an inference procedure based on Gibbs sampling. We evaluate the method on synthetic and real hyperspectral data of wheat kernels. Results show that our method perform as good or better than existing volume constrained methods. Further, our method gives credible intervals for the endmembers and abundances, which allows us to assess the confidence of the results.
Infinite Multiple Membership Relational Modeling for Complex Networks

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Infinite Multiple Membership Relational Modeling for Complex Networks

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Infinite non-negative matrix factorization

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Organisations: Cognitive Systems, Department of Informatics and Mathematical Modeling
Authors: Schmidt, M. N. (Intern), Mørup, M. (Intern)
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Reversible jump MCMC for Bayesian NMF

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Single-channel source separation using non-negative matrix factorization

Single-channel source separation problems occur when a number of sources emit signals that are mixed and recorded by a single sensor, and we are interested in estimating the original source signals based on the recorded mixture. This problem, which occurs in many sciences, is inherently under-determined and its solution relies on making appropriate assumptions concerning the sources. This dissertation is concerned with model-based probabilistic single-channel source separation based on non-negative matrix factorization, and consists of two parts: i) three introductory chapters and ii) five published papers. The first part introduces the single-channel source separation problem as well as non-negative matrix factorization and provides a comprehensive review of existing approaches, applications, and practical algorithms. This serves to provide context for the second part, the published papers, in which a number of methods for single-channel source separation based on non-negative matrix factorization are presented. In the papers, the methods are applied to separating audio signals such as speech and musical instruments and separating different types of tissue in chemical shift imaging.

General information
Bayesian non-negative matrix factorization

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Publication: Research › Ph.D. thesis – Annual report year: 2009

Bayesian Nonnegative Matrix Factorization with Volume Prior for Unmixing of Hyperspectral Images
In hyperspectral image analysis the objective is to unmix a set of acquired pixels into pure spectral signatures (endmembers) and corresponding fractional abundances. The Non-negative Matrix Factorization (NMF) methods have received a lot of attention for this unmixing process. Many of these NMF based unmixing algorithms are based on sparsity regularization encouraging pure spectral endmembers, but this is not optimal for certain applications, such as foods, where abundances are not sparse. The pixels will theoretically lie on a simplex and hence the endmembers can be estimated as the vertices of the smallest enclosing simplex. In this context we present a Bayesian framework employing a volume constraint for the NMF algorithm, where the posterior distribution is numerically sampled from using a Gibbs sampling procedure. We evaluate the method on synthetical and real hyperspectral data of wheat kernels.

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Non-negative matrix factorization with Gaussian process priors

We present a general method for including prior knowledge in a nonnegative matrix factorization (NMF), based on Gaussian process priors.

We assume that the nonnegative factors in the NMF are linked by a strictly increasing function to an underlying Gaussian process specified by its covariance function. This allows us to find NMF decompositions that agree with our prior knowledge of the distribution of the factors, such as sparseness, smoothness, and symmetries. The method is demonstrated with an example from chemical shift brain imaging.
Reduction of Non-stationary Noise using a Non-negative Latent Variable Decomposition

We present a method for suppression of non-stationary noise in single channel recordings of speech. The method is based on a non-negative latent variable decomposition model for the speech and noise signals, learned directly from a noisy mixture. In non-speech regions an over complete basis is learned for the noise that is then used to jointly estimate the speech and the noise from the mixture. We compare the method to the classical spectral subtraction approach, where the noise spectrum is estimated as the average over non-speech frames. The proposed method significantly outperforms the classic approach, especially when the noise is highly non-stationary and at low signal-to-noise ratios.

Structured non-negative matrix factorization with sparsity patterns

We introduce a novel structured non-negative matrix factorization (SNMF) model that incorporates sparsity patterns in the basis matrix. The sparsity patterns are encoded as a set of binary assignment matrices, which are learned together with the other model parameters. This allows the model to learn basis matrices that exhibit block diagonal structures, which are common in many real-world applications. We propose an efficient optimization algorithm for the proposed model and demonstrate its effectiveness on a variety of benchmark datasets.

Bibliographical note

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Linear Regression on Sparse Features for Single-Channel Speech Separation

In this work we address the problem of separating multiple speakers from a single microphone recording. We formulate a linear regression model for estimating each speaker based on features derived from the mixture. The employed feature representation is a sparse, non-negative encoding of the speech mixture in terms of pre-learned speaker-dependent dictionaries. Previous work has shown that this feature representation by itself provides some degree of separation. We show that the performance is significantly improved when regression analysis is performed on the sparse, non-negative features, both compared to linear regression on spectral features and compared to separation based directly on the non-negative sparse features.

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Single-Channel Speech Separation using Sparse Non-Negative Matrix Factorization

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Main Research Area: Technical/natural sciences
Conference: Spoken Language Processing, ISCA International Conference on (INTERSPEECH), 01/01/2007
Electronic versions:
imm4511.pdf
Links:
http://www2.imm.dtu.dk/pubdb/p.php?4511
Source: orbit
Source-ID: 191568
Publication: Research - peer-review › Article in proceedings – Annual report year: 2007

Wind Noise Reduction using Non-negative Sparse Coding

We introduce a new speaker independent method for reducing wind noise in single-channel recordings of noisy speech. The method is based on non-negative sparse coding and relies on a wind noise dictionary which is estimated from an isolated noise recording. We estimate the parameters of the model and discuss their sensitivity. We then compare the algorithm with the classical spectral subtraction method and the Qualcomm-ICSI-OGI noise reduction method. We optimize the sound quality in terms of signal-to-noise ratio and provide results on a noisy speech recognition task.
General information
State: Published
Organisations: Cognitive Systems, Department of Informatics and Mathematical Modeling, IT University of Copenhagen
Authors: Schmidt, M. N. (Intern), Larsen, J. (Intern), Hsiao, F. (Ekstern)
Publication date: 2007

Host publication information
Title of host publication: Machine Learning for Signal Processing, IEEE International Workshop on
Publisher: IEEE
ISBN (Print): 978-1-4244-1566-3
Main Research Area: Technical/natural sciences
Electronic versions:
Schmidt.pdf
DOIs:
10.1109/MLSP.2007.4414345

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Source: orbit
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Publication: Research - peer-review › Article in proceedings – Annual report year: 2007

Wind Noise Reduction Using Non-negative Sparse Coding

General information
State: Published
Organisations: Cognitive Systems, Department of Informatics and Mathematical Modeling
Authors: Schmidt, M. N. (Intern), Larsen, J. (Intern), Hsiao, F. (Ekstern)
Publication date: 2007

Publication information
Original language: English
Main Research Area: Technical/natural sciences
Wind noise, single channel separation, NMF
Electronic versions:
imm5450.pdf
Source: orbit
Source-ID: 209993
Publication: Research › Sound/Visual production (digital) – Annual report year: 2007

Nonnegative Matrix Factor 2-D Deconvolution for Blind Single Channel Source Separation

General information
State: Published
Organisations: Cognitive Systems, Department of Informatics and Mathematical Modeling
Authors: Schmidt, M. N. (Intern), Mørup, M. (Intern)
Publication date: 2006

Host publication information
Title of host publication: ICA2006 : Source Separation and Independent Component Analysis, International Conference on (ICA)
Main Research Area: Technical/natural sciences
Conference: Source Separation and Independent Component Analysis, International Conference on (ICA), 01/01/2006
Electronic versions:
imm4061.pdf
Links:
http://www2.imm.dtu.dk/pubdb/p.php?4061
Source: orbit
Source-ID: 191569
Publication: Research - peer-review › Article in proceedings – Annual report year: 2006
Sparse Non-negative Matrix Factor 2-D Deconvolution

We introduce the non-negative matrix factor 2-D deconvolution (NMF2D) model, which decomposes a matrix into a 2-dimensional convolution of two factor matrices. This model is an extension of the non-negative matrix factor deconvolution (NMFD) recently introduced by Smaragdis (2004). We derive and prove the convergence of two algorithms for NMF2D based on minimizing the squared error and the Kullback-Leibler divergence respectively. Next, we introduce a sparse non-negative matrix factor 2-D deconvolution model that gives easy interpretable decompositions and devise two algorithms for computing this form of factorization. The developed algorithms have been used for source separation and music transcription.

General information
State: Published
Organisations: Cognitive Systems, Department of Informatics and Mathematical Modeling
Authors: Mørup, M. (Intern), Schmidt, M. N. (Intern)
Publication date: 2006

Sparse Non-negative Matrix Factor 2-D Deconvolution for Automatic Transcription of Polyphonic Music

We present a novel method for automatic transcription of polyphonic music based on a recently published algorithm for non-negative matrix factor 2-D deconvolution. The method works by simultaneously estimating a time-frequency model for an instrument and a pattern corresponding to the notes which are played based on a log-frequency spectrogram of the music.

General information
State: Published
Organisations: Cognitive Systems, Department of Informatics and Mathematical Modeling
Authors: Schmidt, M. N. (Intern), Mørup, M. (Intern)
Publication date: 2006

Sparse Non-negative Tensor 2D Deconvolution (SNTF2D) for multi channel time-frequency analysis

We recently introduced two algorithms for sparse non-negative matrix factor 2-D deconvolution (SNMF2D) that are useful for single channel source separation and music transcription. We here extend this approach to the analysis of the log-frequency spectrograms of a multichannel recording. The model proposed forms a non-negative tensor factor 2-D deconvolution (NTF2D) based on the parallel factor (PARAFAC) model. Two algorithms are given for NTF2D; one based on least squares the other on Kullback-Leibler divergence minimization. Both algorithms are extended to give sparse decompositions. The algorithms are demonstrated to successfully identify the components of both artificially generated as well as real stereo music.

General information
State: Published
Organisations: Cognitive Systems, Department of Informatics and Mathematical Modeling
Authors: Mørup, M. (Intern), Schmidt, M. N. (Intern)
Publication date: 2006
Projects:

**A Bayesian Approach to Neural Networks**
Department of Applied Mathematics and Computer Science  
Period: 15/03/2016 → 14/03/2019  
Number of participants: 3  
Phd Student: Jørgensen, Peter Bjørn (Intern)  
Supervisor: Mørup, Morten (Intern)  
Main Supervisor: Schmidt, Mikkel Nørgaard (Intern)  

**Financing sources**  
Source: Internal funding (public)  
Name of research programme: Institut stipendie (DTU)  
Project: PhD

**Modeling Temporal Dynamics in Functional Brain Connectivity**
Department of Applied Mathematics and Computer Science  
Period: 15/08/2015 → 14/08/2018  
Number of participants: 4  
Phd Student: Nielsen, Søren Føns Vind (Intern)  
Supervisor: Madsen, Kristoffer Hougaard (Intern)  
Schmidt, Mikkel Nørgaard (Intern)  
Main Supervisor: Mørup, Morten (Intern)  

**Financing sources**  
Source: Internal funding (public)  
Name of research programme: Samfinansieret - Andet  
Project: PhD

**Bayes on a Budget- Approximate inference for Bayesian Nonparametrics on a computational Budget**
Department of Applied Mathematics and Computer Science  
Period: 01/04/2015 → 31/03/2018  
Number of participants: 3  
Phd Student: Bonnevie, Rasmus (Intern)  
Supervisor: Mørup, Morten (Intern)  
Main Supervisor: Schmidt, Mikkel Nørgaard (Intern)  

**Financing sources**  
Source: Internal funding (public)  
Name of research programme: Institut stipendie (DTU)  
Project: PhD
Active Bayesian Sensing
Department of Applied Mathematics and Computer Science
Period: 01/03/2014 → 16/08/2017
Number of participants: 6
Phd Student:
Andersen, Michael Riis (Intern)
Supervisor:
Winther, Ole (Intern)
Main Supervisor:
Hansen, Lars Kai (Intern)
Examiner:
Schmidt, Mikkel Nørgaard (Intern)
Heskes, Tom (Ekstern)
Theodoridis, Sergios (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Offentlig finansiering

Relations
Publications:
Probabilistic models for structured sparsity
Project: PhD

Bayesian Modelling of Functional Whole Brain Connectivity
Department of Applied Mathematics and Computer Science
Period: 01/02/2014 → 14/06/2017
Number of participants: 7
Phd Student:
Røge, Rasmus (Intern)
Supervisor:
Madsen, Kristoffer Hougaard (Intern)
Schmidt, Mikkel Nørgaard (Intern)
Main Supervisor:
Mørup, Morten (Intern)
Examiner:
Hansen, Lars Kai (Intern)
Penny, William D. (Ekstern)
Särkkä, Simo (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Samfinansieret - Andet

Relations
Publications:
Bayesian Modelling of Functional Whole Brain Connectivity
Project: PhD

Large Scale Computing for the Modelling of Whole Brain Connectivity
Department of Applied Mathematics and Computer Science
Period: 01/11/2013 → 22/09/2017
Number of participants: 6
Phd Student:
Albers, Kristoffer Jon (Intern)
Supervisor:
Mørup, Morten (Intern)
Main Supervisor:
Schmidt, Mikkel Nørgaard (Intern)
Examiner:
Larsen, Jan (Intern)
Igel, Christian (Ekstern)
Tresp, Volker (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: 1/3 FUU, 1/3 inst 1/3 Andet

Relations
Publications:
Large Scale Computing for the Modelling of Whole Brain Connectivity
Project: PhD

Modeling Structural Brain Connectivity
Department of Applied Mathematics and Computer Science
Period: 01/04/2013 → 19/04/2017
Number of participants: 7
Phd Student:
Ambrosen, Karen Marie Sandø (Intern)
Supervisor:
Dyrby, Tim Bjørn (Intern)
Schmidt, Mikkel Nørgaard (Intern)
Main Supervisor:
Mørup, Morten (Intern)
Examiner:
Hansen, Lars Kai (Intern)
Jbabdi, Saad (Ekstern)
Thiran, Jean-Philippe (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: 1/3 FUU, 1/3 inst 1/3 Andet

Relations
Publications:
Modeling Structural Brain Connectivity
Project: PhD

Generative temporal modeling of neuroimaging - decomposition and nonparametric testing
Department of Applied Mathematics and Computer Science
Period: 15/04/2012 → 26/10/2016
Number of participants: 5
Phd Student:
Hald, Ditte Havenhoff (Intern)
Main Supervisor:
Winther, Ole (Intern)
Examiner:
Schmidt, Mikkel Nørgaard (Intern)
Kaski, Samuel (Ekstern)
Wallentin, Mikkel (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)

Relations
Publications:
Generative Temporal Modelling of Neuroimaging - Decomposition and Nonparametric Testing
Project: PhD

**Personalized Music Organization Systems**
Department of Applied Mathematics and Computer Science
Period: 15/12/2011 → 23/10/2015
Number of participants: 6
Phd Student:
Madsen, Jens (Intern)
Supervisor:
Hansen, Lars Kai (Intern)
Main Supervisor:
Larsen, Jan (Intern)
Examiner:
Schmidt, Mikkel Nørgaard (Intern)
Pearce, Marcus Thomas (Ekstern)
Theodoridis, Sergios (Ekstern)

**Financing sources**
Source: Internal funding (public)
Name of research programme: 1/3 FUU, 1/3 inst 1/3 Andet

**Relations**
Publications:
Predicting the emotions expressed in music
Project: PhD

**Modelling the structure of complex networks**
Department of Applied Mathematics and Computer Science
Period: 01/06/2011 → 09/09/2014
Number of participants: 7
Phd Student:
Herlau, Tue (Intern)
Supervisor:
Hansen, Lars Kai (Intern)
Schmidt, Mikkel Nørgaard (Intern)
Main Supervisor:
Mørup, Morten (Intern)
Examiner:
Winther, Ole (Intern)
Girolami, Mark (Ekstern)
Tresp, Volker (Ekstern)

**Financing sources**
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)
Project: PhD

**Signal separation using independent component analysis with explicit source modelling**
Department of Informatics and Mathematical Modeling
Period: 01/02/2005 → 28/01/2009
Number of participants: 4
Phd Student:
Schmidt, Mikkel Nørgaard (Intern)
Main Supervisor:
Larsen, Jan (Intern)
Examiner:
Hansen, Lars Kai (Intern)
Jutten, Christian (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: DTU-lønnet stipendie
Project: PhD