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Publications:

Mimetic Divergence and the Speciation Continuum in the Mimic Poison Frog Ranitomeya imitator
While divergent ecological adaptation can drive speciation, understanding the factors that facilitate or constrain this process remains a major goal in speciation research. Here, we study two mimetic transition zones in the poison frog Ranitomeya imitator, a species that has undergone a Mullerian mimetic radiation to establish four morphs in Peru. We find that mimetic morphs are strongly phenotypically differentiated, producing geographic clines with varying widths. However, distinct morphs show little neutral genetic divergence, and landscape genetic analyses implicate isolation by distance as the primary determinant of among-population genetic differentiation. Mate choice experiments suggest random mating at the transition zones, although certain allopatric populations show a preference for their own morph. We present evidence that this preference may be mediated by color pattern specifically. These results contrast with an earlier study of a third transition zone, in which a mimetic shift was associated with reproductive isolation. Overall, our results suggest that the three known mimetic transition zones in R. imitator reflect a speciation continuum, which we have characterized at the geographic, phenotypic, behavioral, and genetic levels. We discuss possible explanations for variable progress toward speciation, suggesting that multifarious selection on both mimetic color pattern and body size may be responsible for generating reproductive isolation.

General information
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Organisations: Department of Applied Mathematics and Computer Science, Image Analysis & Computer Graphics, East Carolina University, Centro de Ornitologia y Biodiversidad
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Canonical analysis based on mutual information

Canonical correlation analysis (CCA) is an established multi-variate statistical method for finding similarities between linear combinations of (normally two) sets of multivariate observations. In this contribution we replace (linear) correlation as the measure of association between the linear combinations with the information theoretical measure mutual information (MI). We term this type of analysis canonical information analysis (CIA). MI allows for the actual joint distribution of the variables involved and not just second order statistics. While CCA is ideal for Gaussian data, CIA facilitates analysis of variables with different genesis and therefore different statistical distributions and different modalities. As a proof of concept we give a toy example. We also give an example with one (weather radar based) variable in the one
Canonical Information Analysis

Canonical correlation analysis is an established multivariate statistical method in which correlation between linear combinations of multivariate sets of variables is maximized. In canonical information analysis introduced here, linear correlation as a measure of association between variables is replaced by the information theoretical, entropy based measure mutual information, which is a much more general measure of association. We make canonical information analysis feasible for large sample problems, including for example multispectral images, due to the use of a fast kernel density estimator for entropy estimation. Canonical information analysis is applied successfully to (1) simple simulated data to illustrate the basic idea and evaluate performance, (2) fusion of weather radar and optical geostationary satellite data in a situation with heavy precipitation, and (3) change detection in optical airborne data. The simulation study shows that canonical information analysis is as accurate as and much faster than algorithms presented in previous work, especially for large sample sizes. URL: http://www.imm.dtu.dk/pubdb/p.php?6270
Change detection in bi-temporal data by canonical information analysis

Canonical correlation analysis (CCA) is an established multivariate statistical method for finding similarities between linear combinations of (normally two) sets of multivariate observations. In this contribution we replace (linear) correlation as the measure of association between the linear combinations with the information theoretical measure mutual information (MI). We term this type of analysis canonical information analysis (CIA). MI allows for the actual joint distribution of the variables involved and not just second order statistics. Where CCA is ideal for Gaussian data, CIA facilitates analysis of variables with different genesis and therefore different statistical distributions. As a proof of concept we give a toy example. We also give an example with DLR 3K camera data from two time points covering a motor way.

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Interpretation of images from intensity, texture and geometry
The goal of the thesis is to develop flexible mathematical methods for quantitative interpretation of image content. Problems from research areas as diverse as evolutionary biology, remote sensing and materials science have motivated the methodological development. The solutions are inspired by classical mathematical image analysis techniques, information theory, probabilistic graphical models and manifold learning.

Specifically, the thesis revolves around describing three major components of images, namely intensity, texture and geometry. Intensity distribution modelling is important for obtaining useful global representations of the raw image data. Texture description provides a local representation of the image content, useful for descriptive and discriminative scenarios. Geometrical knowledge of the image content is leveraged within the framework of Markov random fields. Mathematical models are developed around these three topics and constitute building blocks useful for engineering image-based solutions to a wide range of problems.

The contributions include automated quantification of frog patterning from field imagery, statistical methods for estimating the genetic basis of quantified mimicry phenotypes, estimation of the atomic structure of graphene from low-contrast transmission electron microscopy images and patch-based crop classification from synthetic aperture radar data. Further, an information theoretic approach to two-set image decomposition is presented, representing a purely methodological contribution.

This thesis makes statistical image analysis available to fellow researchers with domain specific problems, and provides new methodology relevant for the field itself.

Number of genes controlling a quantitative trait in a hybrid zone of the aposematic frog Ranitomeya imitator
The number of genes controlling mimetic traits has been a topic of much research and discussion. In this paper, we examine a mimetic, dendrobatid frog Ranitomeya imitator, which harbours extensive phenotypic variation with multiple mimetic morphs, not unlike the celebrated Heliconius system. However, the genetic basis for this polymorphism is unknown, and not easy to determine using standard experimental approaches, for this hard-to-breed species. To circumvent this problem, we first develop a new protocol for automatic quantification of complex colour pattern phenotypes from images. Using this method, which has the potential to be applied in many other systems, we define a phenotype associated with differences in colour pattern between different mimetic morphs. We then proceed to develop a maximum-likelihood method for estimating the number of genes affecting a quantitative trait segregating in a hybrid zone. This method takes advantage of estimates of admixture proportions obtained using genetic data, such as microsatellite markers, and is applicable to any other system where a phenotype has been quantified in an admixture/introgression zone. We evaluate the method using extensive simulations and apply it to the R. imitator system. We show that probably one or two, or at most three genes, control the mimetic phenotype segregating in a R. imitator hybrid zone identified using image analyses.
Assessment of algorithms for mitosis detection in breast cancer histopathology images

The proliferative activity of breast tumors, which is routinely estimated by counting of mitotic figures in hematoxylin and eosin stained histology sections, is considered to be one of the most important prognostic markers. However, mitosis counting is laborious, subjective and may suffer from low inter-observer agreement. With the wider acceptance of whole slide images in pathology labs, automatic image analysis has been proposed as a potential solution for these issues. In this paper, the results from the Assessment of Mitosis Detection Algorithms 2013 (AMIDA13) challenge are described. The challenge was based on a data set consisting of 12 training and 11 testing subjects, with more than one thousand annotated mitotic figures by multiple observers. Short descriptions and results from the evaluation of eleven methods are presented. The top performing method has an error rate that is comparable to the inter-observer agreement among pathologists.

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HEp-2 Cell Classification Using Shape Index Histograms With Donut-Shaped Spatial Pooling

We present a new method for automatic classification of indirect immunofluorescence images of HEp-2 cells into different staining pattern classes. Our method is based on a new texture measure called shape index histograms that captures second-order image structure at multiple scales. Moreover, we introduce a spatial decomposition scheme which is radially symmetric and suitable for cell images. The spatial decomposition is performed using donut-shaped pooling regions of varying sizes when gathering histogram contributions. We evaluate our method using both the ICIP 2013 and the ICPR 2012 competition datasets. Our results show that shape index histograms are superior to other popular texture descriptors for HEp-2 cell classification. Moreover, when comparing to other automated systems for HEp-2 cell classification we show that shape index histograms are very competitive; especially considering the relatively low complexity of the method.

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Pattern recognition approach to quantify the atomic structure of graphene

We report a pattern recognition approach to detect the atomic structure in high-resolution transmission electron microscopy images of graphene. The approach provides quantitative information such as carbon-carbon bond lengths and bond length variations on a global and local scale alike. © 2014 Elsevier Ltd. All rights reserved.
Reproductive isolation related to mimetic divergence in the poison frog Ranitomeya imitator

In a mimetic radiation—when a single species evolves to resemble different model species—mimicry can drive within-species morphological diversification, and, potentially, speciation. While mimetic radiations have occurred in a variety of taxa, their role in speciation remains poorly understood. We study the Peruvian poison frog Ranitomeya imitator, a species that has undergone a mimetic radiation into four distinct morphs. Using a combination of colour-pattern analysis, landscape genetics and mate-choice experiments, we show that a mimetic shift in R. imitator is associated with a narrow phenotypic transition zone, neutral genetic divergence and assortative mating, suggesting that divergent selection to resemble different model species has led to a breakdown in gene flow between these two populations. These results extend the effects of mimicry on speciation into a vertebrate system and characterize an early stage of speciation where reproductive isolation between mimetic morphs is incomplete but evident.
A connection between microscopic structure and macroscopic properties is expected for almost all material systems. High-resolution transmission electron microscopy is a technique offering insight into the atomic structure, but the analysis of large image series can be time consuming. The present work describes a method to automatically estimate the atomic structure in two-dimensional materials. As an example graphene is chosen, in which the positions of the carbon atoms are reconstructed. Lattice parameters are extracted in the frequency domain and an initial atom positioning is estimated. Next, a plausible neighborhood structure is estimated. Finally, atom positions are adjusted by simulation of a Markov random field model, integrating image evidence and the strong geometric prior. A pristine sample with high regularity and a sample with an induced hole are analyzed. False discovery rate-controlled large-scale simultaneous hypothesis testing is used as a statistical framework for interpretation of results. The first sample yields, as expected, a homogeneous distribution of carbon–carbon (C–C) bond lengths. The second sample exhibits regions of shorter C–C bond lengths with a preferred orientation, suggesting either strain in the structure or a buckling of the graphene sheet. The precision of the method is demonstrated on simulated model structures and by its application to multiple exposures of the two graphene samples.
A kernel version of multivariate alteration detection

Based on the established methods kernel canonical correlation analysis and multivariate alteration detection we introduce a kernel version of multivariate alteration detection. A case study with SPOT HRV data shows that the kMAD variates focus on extreme change observations.

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Canonical correlation analysis (CCA) maximizes correlation between two sets of multivariate data. We applied CCA to multivariate satellite data and univariate radar data in order to produce a subspace descriptive of heavily precipitating clouds. A misalignment, inherent to the nature of the two data sets, was observed, corrupting the subspace. A method for aligning the two data sets is proposed, in order to overcome this issue and render a useful subspace projection. The observed corruption of the subspace gives rise to the hypothesis that the optimal correspondence, between a heavily precipitating cloud in the radar data and the associated cloud top registered in the satellite data, is found by a scale, rotation and translation invariant transformation together with a temporal displacement. The method starts by determining a conformal transformation of the radar data at the time of maximum precipitation for optimal correspondence with the satellite data at the same time. This optimization is repeated for an increasing temporal lag until no further improvement can be found. The method is applied to three meteorological events having caused heavy precipitation in Denmark. The three cases are analyzed with and without using the proposed method. In all cases, the use of pre-alignment shows significant improvements in the descriptive capabilities of the subspaces, thus supporting the posed hypothesis.
Automated Structure Detection in HRTEM Images: An Example with Graphene

Graphene, as the forefather of 2D-materials, attracts much attention due to its extraordinary properties like transparency, flexibility and outstanding high conductivity, together with a thickness of only one atom. The properties seem to be dependent on the atomic structure of graphene and therefore characterizations on the atomic level are of interest. High-resolution transmission electron microscopy (HRTEM) is a state-of-the-art method to characterize the atomic structure of materials. Due to the inherently low mass-thickness of graphene, the contrast levels in the recorded images are often challenging to interpret. In order to increase the signal-to-noise ratio of the images two routes can be pursued: 1) the exposure time can be increased; or 2) acquiring series of images and summarize them after alignment. Both methods have the disadvantage of summing images acquired over a certain period of time making it difficult to resolve dynamic processes or unstable structures. Tools that assist to get the maximum of information out of recorded images are therefore greatly appreciated.

In order to get the most accurate results out of the structure detection, we have optimized the imaging conditions used for the FEI Titan ETM with a monochromator and an objective-lens Cs-corrector. To reduce the knock-on damage of the carbon atoms in the graphene structure, the microscope was operated at 80kV. As this strongly increases the influence of the chromatic aberration of the lenses, the energy spread of the electron gun was reduced. Using the monochromator an energy spread of <0.2eV can be achieved. This gives a resolution better then 1.2Å which allow us to resolve the second order reflection of graphene and to visualize the atomic structure in HRTEM (fig. 1).

These images serve as a basis for the image analysis. Single-layer graphene with its regular honeycomb lattice is a perfect model structure to apply automated structure detection. By utilizing Fourier analysis the initial perfect hexagonal structure can easily be recognized. The recorded hexagonal tessellation reflects the unperturbed structure in the image. The centers of the C-hexagons are displayed as nodes. To segment the image into "pure" and "impure" regions, like areas with residual amorphous contamination or defects e.g. holes, a sliding window approach is used. The magnitude of the Fourier transformation within a window is compared to that of a perfect hexagonal tessellation. Areas where this relation exceeds a threshold are recognized as "impure" and a mask is created. As a result, the hexagonal tessellation overlays only the "pure" graphene structure in the image.

As the real graphene structure is never perfect and undisturbed, at least at a length-scale of several nm, the model structure has to be adjusted to the real structure. At this point, the image quality plays a crucial role. The algorithm assumes that irregularities in the graphene can be explained by a deformation in the xy-plane. To model this, a set of tensor B-splines is employed, which is deformed by matching model grid points with the C-hexagon centers. Dependent on the Cs and defocus-settings during microscopy these centers appear either dark or bright. One ends up with a deformed hexagonal tessellation, which can easily be transformed into a honeycomb lattice with the C-atom positions included. As the microstructure is now available in the model, information like the C-C distance can be visualized as shown in fig. 2.

Applying this method, the perfect graphene structure in recorded HRTEM-images can be determined fast and accurate over a wide length scale, and at the same time lattice deformations can be visualized. The method will be refined to facilitate the detection of larger defects like holes and the determination of the edge terminations.
**Dynamically constrained pipeline for tracking neural progenitor cells**

Large scale in vitro cell growth experiments require automated segmentation and tracking methods to construct cell lineages in order to aid cell biologists in further analysis. Flexible segmentation algorithms that easily adapt to the specific type of problem at hand and directly applicable tracking methods are fundamental building blocks of setting up multi-purpose pipelines. Segmentation by discriminative dictionary learning and a graph formulated tracking method constraining the allowed topology changes are combined here to accommodate for highly irregular cell shapes and movement patterns. A mitosis detector constructed from empirical observations of cells in a pre-mitotic state interacts with the graph formulation to dynamically allow for cell mitosis when appropriate. Track consistency is ensured by introducing pragmatic constraints and the notion of blob states. We validate the proposed pipeline by tracking pig neural progenitor cells through a time lapse experiment consisting of 825 images collected over 69 hours. Each step of the tracking pipeline is validated separately by comparison with manual annotations. The number of tracked cells increase from approximately 350 to 650 during the time period.
Quantification of Tissue Trauma following Insulin Pen Needle Insertions in Skin

Objective:
Within the field of pen needle development, most research on needle design revolves around mechanical tensile testing and patient statements. Only little has been published on the actual biological skin response to needle insertions. The objective of this study was to develop a computational method to quantify tissue trauma based on skin bleeding and immune response.

Method:
Two common sized pen needles of 28G (0.36mm) and 32G (0.23mm) were inserted into skin of sedated LYD pigs prior to termination. Four pigs were included and a total of 32 randomized needle insertions were conducted. The affected tissue was removed and fixed in formalin following tissue preparation for histology. Standard immunohistochemical staining procedure was applied with CD-45 and anti-hemoglobin primary antibodies to stain immune cells and red blood cells, respectively. The stained tissue slides were subsequently digitized using 200X magnification. Based on thresholding, morphological masks and blob detection, segmentation of the histology was performed to locate tissue bleeding and immune response. Image-to-image registration was used on images originating from the same tissue, and a quantitative measure of tissue trauma was obtained for each needle insertion.

Result:
Bleeding and immune response were seen for all tested needles. Positive correlation was seen between the needle diameter and the size of the bleeding. The quantitative measure reveal a trend that tissue trauma decreases with decreasing needle diameter.

Conclusion:
A computational and quantitative method has been developed to assess tissue trauma following insulin pen needle insertions. Application of the method is tested by conduction of a needle diameter study. The obtained quantitative measures of tissue trauma correlate positively to needle diameter.
Classification of Polarimetric SAR Data Using Dictionary Learning

This contribution deals with classification of multilook fully polarimetric synthetic aperture radar (SAR) data by learning a dictionary of crop types present in the Foulum test site. The Foulum test site contains a large number of agricultural fields, as well as lakes, forests, natural vegetation, grasslands and urban areas, which make it ideally suited for evaluation of classification algorithms.

Dictionary learning centers around building a collection of image patches typical for the classification problem at hand. This requires initial manual labeling of the classes present in the data and is thus a method for supervised classification. Sparse coding of these image patches aims to maintain a proficient number of typical patches and associated labels. Data is consecutively classified by a nearest neighbor search of the dictionary elements and labeled with probabilities of each class.

Each dictionary element consists of one or more features, such as spectral measurements, in a neighborhood around each pixel. For polarimetric SAR data these features are the elements of the complex covariance matrix for each pixel. We quantitatively compare the effect of using different representations of the covariance matrix as the dictionary element features. Furthermore, we compare the method of dictionary learning, in the context of classifying polarimetric SAR data, with standard classification methods based on single-pixel measurements.

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Improved Nowcasting of Heavy Precipitation Using Satellite and Weather Radar Data

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Large scale tracking of stem cells using sparse coding and coupled graphs
Stem cell tracking is an inherently large scale problem. The challenge is to identify and track hundreds or thousands of cells over a time period of several weeks. This requires robust methods that can leverage the knowledge of specialists on the field. The tracking pipeline presented here consists of a dictionary learning method for segmentation of phase contrast microscopy images. Linking of the cells between two images is solved by a graph formulation of the tracking problem.

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Parameter optimization in the regularized kernel minimum noise fraction transformation

Based on the original, linear minimum noise fraction (MNF) transformation and kernel principal component analysis, a kernel version of the MNF transformation was recently introduced. Inspired by these methods, here we give a simple method for finding optimal parameters in a regularized version of kernel MNF analysis. We consider the model signal-to-noise ratio (SNR) as a function of the kernel parameters and the regularization parameter. In 2-4 steps of increasingly refined grid searches we find the parameters that maximize the model SNR. An example based on data from the DLR 3K camera system is given.

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Pipeline for Tracking Neural Progenitor Cells

Automated methods for neural stem cell lineage construction become increasingly important due to the large amount of data produced from time lapse imagery of in vitro cell growth experiments. Segmentation algorithms with the ability to adapt to the problem at hand and robust tracking methods play a key role in constructing these lineages. We present here a tracking pipeline based on learning a dictionary of discriminative image patches for segmentation and a graph formulation of the cell matching problem incorporating topology changes and acknowledging the fact that segmentation errors do occur. A matched filter for detection of mitotic candidates is constructed to ensure that cell division is only allowed in the model when relevant. Potentially the combination of these robust methods can simplify the initiation of cell lineage construction and extraction of statistics.

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Sparse principal component analysis in hyperspectral change detection
This contribution deals with change detection by means of sparse principal component analysis (PCA) of simple differences of calibrated, bi-temporal HyMap data. Results show that if we retain only 15 nonzero loadings (out of 126) in the sparse PCA the resulting change scores appear visually very similar although the loadings are very different from their usual non-sparse counterparts. The choice of three wavelength regions as being most important for change detection demonstrates the feature selection capability of sparse PCA.

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BFI (2008): BFI-level 1
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Bidrag til automatisering af ortofotomosaikfremstilling

General information
State: Published
Organisations: Department of Informatics and Mathematical Modeling, National Space Institute, Geodesy, Image Analysis and Computer Graphics, Technical University of Denmark
Authors: Vestergaard, J. S. (Intern), Andersen, S. G. (Ekstern), Nielsen, A. A. (Intern)
Number of pages: 1
Publication date: 2010
Event: Poster session presented at Kortdage, Århus, Denmark.
Main Research Area: Technical/natural sciences
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imm5960.pdf
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Normalization of orthophotos based on no-change pixels using Multivariate Alteration Detection (MAD)

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Seventeen years of global SSH anomalies analyzed by a maximum information based extension to EOF analysis

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Projects:

A Grand Challenge: Large Scale Event Recognition and Tracking
Department of Applied Mathematics and Computer Science
Period: 01/09/2011 → 21/11/2014
Number of participants: 6
Phd Student:
Vestergaard, Jacob Schack (Intern)
Supervisor:
Nielsen, Allan Aasbjerg (Intern)
Main Supervisor:
Larsen, Rasmus (Intern)
Examiner:
Carstensen, Jens Michael (Intern)
Benediktsson, Jón Ali (Ekstern)
Jenssen, Robert (Ekstern)

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