Als naam voor uw Vereniging is weloverwogen gekozen voor "De vereniging voor Patroon Herkennen en Beeld Verwerken". Oude leden zullen dat beamen. In 1970, in de tijd van de eerste digitale dataverwerking trad er al een scheiding op tussen de Artificial Intelligence en de Pattern Recognition. Het was bijna persoonlijk: de AI-mensen vonden de patroonherkenners fantasieloos want het doel was niet meer dan naar beste vermogen een patroon proberen te herkennen in data. De patroonherkenners vonden Kunstmatige Intelligentie megalomaan: hoe kon men intelligentie proberen na te bootsen? Dezelfde scheiding trad veel later en veel rustiger op tussen Image Processing en Computer Vision. Image processing beschrijft een proces en Computer Vision een ideaal. De eerste bestuursleden van onze vereniging waren nuchter en bescheiden. Daarom gaven ze de vereniging zijn huidige naam die ze, nu 25 jaar later, nog draagt.

In mijn visie op de voortgang van de wetenschap kunnen AI en PR beter opgaan in een begrip "Machine Leren". De technieken die beide vakgebieden gebruiken groeien immers steeds meer naar elkaar toe. Ook heeft men de hooggespannen verwachtingen niet meer nodig om aandacht en fondsen te verkrijgen en behoudt men toch een bescheiden ideaal van machines die kunnen leren. Om precies dezelfde redenen zouden dan Image Processing en Computer Vision op kunnen gaan in Machine Perceptie. Dus ik stel voor om de Vereniging voor de komende 25 jaar de ondertitel mee te geven van Nederlandse Vereniging voor Kijken en Leren door Machines. (De vraag blijft wat je dan moet met het redeneren dat de AI ook op haar repertoire heeft staan. Juist in de hedendaagse complexe systemen is redeneren een belangrijk punt. Maar goed, "voor Leren en Redeneren" kan dan een goede ondertitel zijn van de Nederlandse Vereniging voor Kunstmatige Intelligentie.)

De voordracht gaat over Machines die Leren Kijken. Aan de orde komen: figuur 1 beeldbewerking, elke AIO een eigen stoel, het lot van een promovendus, wat een hoofd te maken heeft met de kleren van de keizer, en hoe dit alles te vermijden.

Shaving Diffusion Tensor Images in Discriminant Analysis: a Study into Schizophrenia
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Magnetic Resonance Diffusion Tensor Imaging (MR-DTI) is a technique to in vivo obtain information about human brain structures. This is done by measuring the diffusion of water caused by Brownian motion. In white matter, containing nerve bundles, this diffusion is anisotropic in the direction of the fibers. Using DTI, it is possible to reconstruct the course of the nerve bundles, as well as to study the integrity of the white matter structures. A technique called 'shaving' is introduced to automatically extract the combination of relevant image regions in a comparative study. No hypothesis is needed, as in conventional pre-defined or expert selected Region Of Interest (ROI)-analysis. In contrast to traditional Voxel Based Analysis (VBA), correlations within the data can be modeled using Principal Component Analysis (PCA) and Linear Discriminant Analysis (LDA). A study into schizophrenia using Diffusion Tensor Imaging (DTI) serves as an application.

Conventional VBA found a decreased Fractional Anisotropy (FA) in a part of the genu of the corpus callosum and an increased FA in larger parts of white matter. The proposed method reproduced the decrease in FA in the corpus callosum and found an increase in the posterior limb of the internal capsule and uncinate fasciculus. A correlation between the decrease in the corpus callosum and the increase in the uncinate fasciculus was demonstrated. Incorporating correlation in analysis is a new step in pathological studies, opening the way to more knowledge of brain diseases in the future.
Medical Imaging in Utrecht: Pattern recognition and image analysis for medical research, diagnosis and intervention
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The Image Sciences Institute in Utrecht forms the core of the Research School for Biomedical Image Sciences, ImagO. The research programme comprises a broad spectrum of medical imaging topics ranging from system and method development to diagnostic and interventional clinical applications. In the talk, an overview of pattern recognition and image analysis research in Utrecht will be given, with an emphasis on recently completed and ongoing PhD student projects.

Contour detection by multiresolution surround inhibition
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We consider the contour detection problem of discriminating the edge stimuli originated by object contours from the stimuli due to texture and noise. This is a challenging task in computer vision, since in many natural images the gradient magnitude (or the response to any other edge-tuned filter, like e.g. the Gabor filter) can be much weaker on a point of a contour than on a textured or noisy area. We propose a multiresolution contour detector inspired on biological principles. It consists in detecting contours at different resolutions by a scale dependant contour detector with surround inhibition, and combining the different binary maps by a contour-oriented selection algorithm. At each scale, edges surrounded by other edges are inhibited. Compared with previous surround inhibition schemes, the proposed method avoids the self-inhibition phenomenon and gives a better preservation of the weak contours.
Robustness to noise is achieved by an accurate modelling of the a priori knowledge about the first order statistics of both the useful signal and the noise for the more general non-Gaussian case. According to recent statistical studies on natural images, parametric probabilistic models based on Gaussian Scale Mixtures (GSM) are adopted for both signal and noise edge features. This assumption leads to a closed form of the optimal MMSE estimator.
Unlike many other contour detectors, we do not use only local operators, but also global analysis is performed. This enhances the ability of rejecting local variations originated by texture and noise. The proposed approach mimicks very well the Human Visual System for a wide range of images with different content, contrast, and texture type (examples: http://www.cs.rug.nl/~papari/resICIP06.htm). Quantitative performance evaluation shows that our contour detector outperforms the existing techniques. The talk presents the results of an article that recently received the ICIP’2006 best student paper award.

Pattern recognition meets bioinformatics
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Genomics research generates large volumes of measured biomolecular data such as transcripts, aberrations in the DNA, protein binding and expression and metabolic data. Finding significant patterns in these data is not longer possible by visual inspection. Consequently, Pattern Recognition is becoming a dominating area within Bioinformatics research. It is however not straightforward to apply pattern recognition tools within this field. Some problems are: 1) the ever present small sample size problem; 2) the fact that the data is badly balanced over classes; or 3) that there is a lack of ground truth (i.e. data is badly labeled). In addition the wide variety of data that represents different aspects of the underlying biological phenomena need to be integrated. To deal with this flexible representations are necessary to such as mixed type data, similarity based representations, and graphs. The tools are used to gain biological insight or to improve clinical practice. This implies that the tools need to take into account all sources of uncertainty present in real problems. Today the more sophisticated pattern
recognition tools are outperformed by simple methods. The application of Pattern Recognition within Bioinformatics has revealed that still great advances need to be made in the analysis of complex data.

**Detection of Protrusions on Curved Folded Surfaces Applied to Automated Polyp Detection in CT Colonography**
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Over the past years many computer aided diagnosis (CAD) schemes have been presented for the detection of colonic polyps in CT Colonography. The vast majority of these methods (implicitly) model polyps as approximately spherical protrusions. Polyp shape and size varies greatly, however and is often far from spherical. We propose a shape and size invariant method to detect suspicious regions. The method works by locally deforming the colon surface until the second principal curvature is smaller than or equal to zero. The amount of deformation is a quantitative measure of the 'protrudeness'. The deformation field allows for the computation of various additional features to be used in supervised pattern recognition. It is shown how only a few features are needed to achieve 95% sensitivity at 8 false positives (FP) per dataset for polyps larger than 6 mm.

**Polyp segmentation and automatic measurement**
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The risk of a polyp in the colon being malignant increases with its size. Accurate measurement of these polyps during CT Colonography is important because the measured size determines if a patient should be referred for polyp removal. Radiologists make errors measuring polyps on 2D CT slices and on 3D surface reconstructions.

We present a way of automatically measuring polyps in CT data. First the polyp is separated from the colon wall using two segmentation steps. Certain areas that definitely not belong to a polyp (like flat areas or haustral folds) are detected using curvature and excluded from the segmentation process. The quality of the segmentation results is evaluated by visual inspection.

After the polyp segmentation is finished the polyp can be measured. The segmented polyp is projected on a plane and the largest diameter of this projection is determined. The measurement results are evaluated against measurements from clinical practice.

**Segmentation of MR prostate images by atlas matching**
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Prostate cancer treatment by radiation therapy requires an accurate localisation of the prostate. Computed tomography (CT) images are primarily used for the treatment planning, but increasingly magnetic resonance (MR) images are added, because of their soft-tissue contrast. In current clinical practice, the prostate is manually delineated on the MR image, which is a labour intensive task. We propose an automatic segmentation method, based on nonrigid registration of prelabeled atlas images. Multiple atlas images are used, instead of a single atlas, to account for the large anatomical variability between people, and the differences in bladder and rectum filling. The algorithm consists of three stages. First, the target image is nonrigidly registered with each atlas image, using mutual information as the similarity measure. After that, a selection of suitable atlas images is made by comparing the mutual information values after registration. Finally, the segmentation is obtained by averaging the selected deformed segmentations and thresholding. The method is evaluated on 30 images by calculating the overlap of the automatic and manual segmentations, which resulted in a median overlap of 81%.
The MediaMill Challenge: Five Experiments for Generic Concept Detection in Video
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In this talk we introduce the MediaMill Challenge for generic video indexing to gain insight in intermediate steps that affect performance of multimedia analysis methods, while at the same time fostering repeatability of experiments. We provide a general scheme for the systematic examination of automated concept detection methods, by decomposing the generic video indexing problem into 2 unimodal analysis experiments, 2 multimodal analysis experiments, and 1 combined analysis experiment. For each experiment, we evaluate generic video indexing performance on 85 hours of international broadcast news data, from the TRECVID 2005/2006 benchmark, using a lexicon of 101 semantic concepts. By establishing a minimum performance on each experiment, the MediaMill Challenge allows for component-based optimization of the generic indexing issue, while simultaneously offering other researchers a reference for comparison during indexing methodology development. To stimulate further investigations in intermediate analysis steps that influence video indexing performance, the MediaMill Challenge offers to the research community a manually annotated concept lexicon, pre-computed low-level multimedia features, trained classifier models, and five experiments together with baseline performance, which are all available at http://www.mediamill.nl/challenge/.