# Titles and abstracts

Smögen workshop 2006

**Clive Anderson**: Models for Particle Movement and Interaction in Steel Making

**Abstract**: Even high quality modern steels contain imperfections - small particles of extraneous material called inclusions - whose presence is an inevitable consequence of the production process. Inclusions influence fatigue properties; in fact the sizes of the largest inclusions in a piece of the steel determine the fatigue limit of the piece. Estimation of the upper tail of the inclusion size distribution is therefore important for assessment of steel quality.

Data on which this estimation can be based come from measurements of the sizes of the largest inclusions in the finished steel. However, since internal inclusions are mostly inaccessible, such measurements are often indirect, and - as is almost universal in extreme value problems - the analyst wishes for more to improve inference. In these circumstances it is natural to seek further information - data or relevant structural information - that might help to improve estimation. One possible source for such information lies in the mechanics of the production process.

The production process consists of several stages of heating, mixing and refining. Inclusions begin to form in the molten steel at an early stage, and subsequently, depending on size, position and movement, may be removed through flotation, agglomeration and other mechanisms. A simple marked Poisson process model for initial size and position, and simple representations of particle movement and interaction during refining, suggest a form for the upper tail of the size distribution of particles at the end of the production process.

The talk will describe the point process modelling of the production process undertaken to date, will pose some open problems in the area and will discuss how results from such modelling can be incorporated into the estimation problem for large inclusions.

**Jenny Andersson and Mats Rudemo**: Identification of the three-dimensional gel microstructure from transmission electron micrographs

**Abstract**: In FRAP experiments we study diffusion of fluorescently tagged probe molecules in a medium, which may be a solution or a gel, with applications to controlled release of medical drugs from matrices and flavours from food. At time 0 a strong laser pulse destroys fluorescence in a cylinder, but fluorescence is recovered due to diffusion into the cylinder from the surrounding volume. We register recovery of fluorescence in a 2D area orthogonal to the cylinder for a sequence of time points, see Fig. 1 for a sample of images.

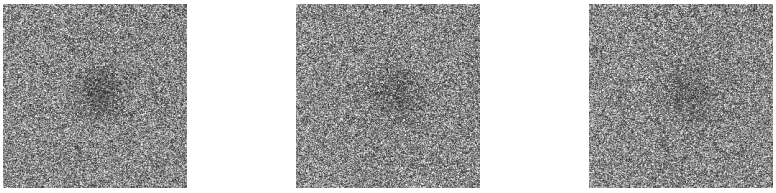

Figure 1: *Images at times 0, 4 and 8 from a FRAP experiment with FITC probe molecules diffusing in a solution of 90% glycerol and 10% water.*

The recovery of fluorescence intensity $C$ is described by the diffusion equation, which in cylindrical coordinates under the assumption of rotational symmetry takes the form

$$\frac{\partial C}{\partial t} = D\frac{1}{r}\frac{\partial}{\partial r}\left(r\frac{\partial C}{\partial r}\right). \tag{1}$$

Classical methods for analysing FRAP experiments (Axelrod et al. 1976 Biophysical J., Blonk et al. 1993 J. Microscopy) integrate the fluorescent intensity over a disk and fit a model for the intensity integral as a function of time. In our approach we use the use individual pixel values, which gives a better utilisation of data and possibilities to include features such intensity dependent pixel variance, compensation for some saturated pixel values and taking into account the precise timepoints when pixel values are sampled in the line-by-line scanning.

For independent pixel values the likelihood under a normality assumption becomes

$$\prod_{t\in T}\prod_{x}\frac{1}{\sqrt{2\pi\sigma^2}}\exp\left(-\frac{(p(x,t)-C(|x-c|,t))^2}{2\sigma^2}\right), \tag{2}$$

where $p(x,t)$ denotes the observed intensity at pixel $x$ at time $t$, $|x-c|$ is the distance from pixel $x$ to the center $c$ of the cylinder and $C(r,t)$ is the solution of (1).

This is joint work in progress together with Niklas Lorén and Paula Olofsson, Structure and material design, SIK, and Magnus Nydén, Materials and surface chemistry, Chalmers. In the talk in Smögen we will also review the history of estimation of diffusion coefficients (Brown, Einstein, Perrin and Smoluchovsky) and briefly describe other methods for diffusion coefficient estimation such as the use of NMR.

**Anastassia Baxevani**: Spatio-temporal modelling of significant wave height

**Abstract**: Significant wave height is defined as four times the standard deviation of the vertical displacement of the sea surface and is a measure of the sea variability. In this talk, we construct a homogeneous spatio-temporal model to describe the variability of the significant wave height over small regions of the sea and for short time-periods. Then, the model is extended to a non-homogeneous one that is valid over larger areas of the sea and for time periods up to ten hours, see Baxevani et al. (2006b).

The proposed model is parametric and the spatial parameters are estimated applying the methodology developed in Baxevani et al. (2006a), on the significant wave height estimates from the TOPEX-Poseidon satellite. The temporal dynamics are modelled using buoy measurements and the C-ERA-40 data.

The derived model is validated by reconstructing, under different scenarios, the significant wave height surface over a large area of the North atlantic and comparing it to the satellite measurements and the C-ERA-40 data.

**References**:

[1] Baxevani, A., Rychlik, I., Wilson, R.J., (2006a). A new method for modelling the space variability of significant wave height. To appear in *Extremes*.

[2] Baxevani, A., Caires, S., Rychlik, I., (2006b). Spatio-temporal modelling of significant wave height. *Department of Mathematical Sciences, Chalmers University of Technology* PREPRINT 2006:11

**Carles Comas**: Application of marked point processes to forest thinning strategies

**Abstract**: Although thinning strategies have a dramatic impact on both future stand development and the product yields, relatively little attention has been paid to the modelling of such highly inter-related operations. Forest modelling has been applied to predict resource availability in classical management contexts, though it has rarely been used as a tool to analyse how forest management can affect forest dynamics. The difficulty of obtaining experimental data to study the effects of distinct thinning strategies, due to trees generally having a long life span, has clearly limited the analysis of this key element in silviculture. Here, we apply a continuous space-time stochastic process to generate marked point patterns evolving through space-time (Renshaw and Särkkä, 2001) in order to study thinning strategies. The role of the thinning algorithm, based on the competitive status between trees, is to specify the trees to be harvested.

The effects of two distinct thinning regimes are analysed in terms of two distinct forest growth functions. First, we consider a single-thinning regime from below, and, second, a thinning from below followed by a thinning from above (i.e. a two-thinning regime). Tree growth is expressed in terms of the Von-Bertalanffy-Richards function for two particular cases: (1) a linear decay function, suggested by Särkkä and Renshaw (2006) to obtain genuine multi-tier structures; and, (2) a sigmoid curve used extensively to model tree and forest growth. A study analyses both the effect of considering these distinct growth functions, and the resulting forest dynamics generated though the chosen thinning strategies.

**References**:

Renshaw, E. and Särkkä, A. (2001) Gibbs point processes for studying the development of spatial-temporal stochastic processes. *Computational Statistics and Data Analysis* **36**, 85-105

Särkkä, A. and Renshaw, E. (2006) The analysis of marked point patterns evolving through space and time. Computational Statistics and Data Anal- ysis (submitted).

**Claus Ekstrøm**: Spatial correlation in peak detection of mass spectrometry data

**Abstract**: Mass spectrometry techniques have recently undergone important improvements, enabling the exploration of proteins along a wide range of molecular weights in biological samples. To compare spectra from different conditions, it is necessary to first align and normalise the different mass spectra and secondly to identify "peaks" that are present for one condition but not for the other.

The proteomic profiles generated by mass spectrometry contain noise from several sources and peaks may not be well defined. We present mass spectrometry data from an experiment with Arabidopsis and discuss how spatial correlation can help in peak identification by improving estimates of amplitude and peak width and reduce the influence of ghost peaks.

**Pavel Grabarnik**: Bayesian modelling of spatial and longitudinal structure of a forest stand

**Abstract**: We present a novel approach to modelling a forest spatio-temporal data. The approach has two ingredients: modelling the spatial structure of a forest stand by a Gibbs point process with hierarchical interactions (Högmander and Särkkä, 1999), and hierarchical Bayesian modelling for prediction of life spans of an individual trees. Rather than trying to find a full spatio-temporal model for the growth and mortality of trees, we model the tree pattern evolution into two stages.

At the first stage, we aim to quantify tension and direction of the competition process between the trees in terms of interaction between the trees within and between different tree size classes. Hogmander and Sarkka (1999) introduced multitype Gibbs point processes with hierarchical interactions. These processes consist of several type of points and allow nonsymmetric interaction between the different types and are therefore, appropriate for spatial structure of a forest stand since large trees affect small trees but not vice versa. We divide the trees into several size classes, which then form the hierarchical levels: The biggest trees are not influenced by any other trees than the trees in the same size class. Trees in the other size classes, however, are influenced by the other trees in the same class as well as all the bigger trees. Relationships between trees within a hierarchical level (size class) are described by symmetric interaction, while relationships between the levels (size classes) are described by nonsymmetric interaction.

At the second stage, we describe the tree pattern evolution, which in our case is due to the mortality process, by the hierarchical Bayesian model. The time dimension is included as a variable characterising the life span of a tree. Dependence of the life span on unobserved spatially structured covariates is modelled through a hidden Markov random field. In addition, the life span depends on size of the tree which can be regarded as fixed effect. We estimate the posterior distribution by Markov chain Monte Carlo simulations, obtaining as a result estimates of size-dependent mortality rates.

The approach is illustrated by the Temiryazevskaja dacha data set, collected on a pure, even aged, naturally established pine forest stand in Moscow region, consisting of locations and diameters of tree stems measured at 9 time points over 57 years.

**References**:

Högmander, H. and Särkkä, A. 1999. Multitype spatial point patterns with hierarchical interactions. *Biometrics* **55**, 1051-1058.

**Gilles Guillot**: Combining images and exact count data for weed mapping
**Abstract**: We combine estimates of weed content derived from pictures of small quadrats and exact count data to make spatial prediction of weeds in agricultural fields. We describe a Bayesian analysis under the transformed Gaussian model, and describe an MCMC sampling method involving data augmentation and reparameterisation. We discuss results from simulations and real data.

**Salme Kärkkäinen**: Orientational analysis of fibres

**Abstract**: Fibrous structures are common in human-made products such as building materials, textiles and paper fibres. They appear also in natural objects such as nerves, muscle fibres and wood fibres. The estimation of orientation of fibres observed through a greyscale image is, for example in paper production, one object of interests.

The underlying fibrous structure can be modelled by a fibre process and the orientation of fibres by the rose of directions. In the modelling of the grey level structure, three different image models, a binary model, a dead leaves model and a shot-noise model, have been considered.

Classically, the rose of directions is estimated observing the intersection points between fibres and sampling lines in a few directions. In the case of a greyscale image, the use of the scaled variograms of grey levels has been proposed. In the case of high resolution the relationship between point intensities and scaled variograms has been, under some regularity conditions, shown to be approximately proportional in the case of those image models mentioned above. An estimation method based on that proportional relation exists. In the case of low resolution, some refined versions of the method has been given for a binary model and, at latest, for a shot-noise model.

**Mats Kvarnström**: Yeast cell recognition using a dynamic programming algorithm for convex contour extraction

**Abstract**: We are concerned with automated quantification of green fluorescent protein (GFP)-tagged proteins in yeast cells using fluorescence microscopy. A key issue for quantitative cell studies is the cell recognition part, i.e. finding the cells in the images. Instead of using fluorescent staining of the cell membranes, we use bright field images for the cell recognition part and the fluorescence images are used for quantification of protein expression only.

In this talk, we will address various important issues for successful automated cell recognition and analysis. Specifically, we will present a method for extracting contours of yeast cells in light microscope images. The cell recognition part is complicated due to difference in appearance due different light conditions and out-of-focus effects, as well as differences in size. The shapes of the cells can however be well approximated by convex polygon. Low computational complexity is of importance in general for our problem and this rules out many methods. The basic steps in our method are first to find possible candidate cell centers using a modified circular Hough transform and then to find a suitable convex polygon surrounding these centers. We will show how this latter step can be performed in polygonal time using a dynamic programming scheme, while still enforcing the convex shape constraint of the resulting contour.

**Claudia Lautensack**: Anisotropy analysis of the system of air pores in polar ice (joint work with Katja Schladitz, Aila Särkkä and Johannes Freitag)

**Abstract**: Polar ice consists of compacted snow. The ice in deeper layers is compressed by the weight of newly fallen snow. The gain due to snowfall is balanced by a drift sidewards keeping the total height of the ice shield nearly constant. During this process, air pores are isolated within the ice. The question discussed in this talk is whether the spatial arrangement of the pores can tell us something about the interaction of the compaction and the drifting process.

We investigate the point pattern of centers of the air pores which are extracted from tomographic images of pieces of ice cores. Samples taken from four different depths are considered. Due to the compression in z-direction it seems to be reasonable to look for anisotropies in this direction. However, working with three-dimensional data makes the directional analysis as well as the illustration of results more challenging than in the planar case.

In order to detect anisotropies, the distribution of directions from a center to its nearest neighbour is investigated using methods from spherical statistics. Further, some approaches based on directional versions of the K-function and the nearest neighbour distance distribution are introduced.

**Finn Lindgren**: Gaussian Markov random fields on a globe

**Abstract**: Gaussian Markov random fields on planar lattices are commonly used to analyse spatial data, using both direct covariance constructions and Markov random field models. In this talk, I will discuss an approach for extending Markov random field models to the sphere, to take advantage of efficient computational techniques. The resulting methods have applications in environmental- and geo-statistics on a globe (modelling and Krigeing), as well as in medical shape analysis (deformable templates and point correspondences).

A popular method for constructing random fields on a sphere is to transform the sphere into polar coordinates, and then use ordinary planar random field techniques. Unfortunately, a random field that is stationary in polar coordinates is not stationary on the sphere itself, due to the non-linear change in distance measure, and the singularities at the poles can also be difficult to handle.

Just as for planar Gaussian random fields, one can work directly with stationary or non-stationary covariance functions on the sphere as well, with spherical harmonics taking over the role of spectral basis functions from the sine and cosine functions. Due to the lack of a spherical counterpart to the fast Fourier transform, this can unfortunately be computationally expensive even for stationary fields.

The approach that will be presented here is to construct Markov random field models directly on discrete triangulations of the sphere, that closely approximate continuous random fields, related to certain stochastic PDE:s. The Gaussian MRF structure lends itself to efficient computational methods.

A linear space for constructing warp functions from the sphere to itself will also be presented, using the spherical GMRF:s for practical computations, with the possible application of constructing non-stationary fields by warping stationary models.

**Johan Lindström**: Video Segmentation Using a Bayesian Online EM Algorithm

**Abstract**: A method for video segmentation using Bayesian models and an online EM algorithm is presented. The method models each layer as a Gaussian mixture, with local, per pixel, parameters for the background and global parameters for the foreground. The online EM algorithm also uses a progressive learning rate allowing the relative update speed of each Gaussian component to depend on how long that component has been observed and similar foreground components are merged using a Kullback-Leibler distance. Performance of the algorithm for gray-scale and RGB videos as well as on output from a Prewitt edge detector is compared to that of another algorithm. Especially for the edge detector, performance increases dramatically.

**Jacques de Maré**: Peak over threshold versus area maxima sampling in the steel quality control problem (joint work with Pär Johannesson and Sara Lorén)
**Abstract**: In design against high cycle fatigue the fatigue limit is a crucial quantity. The fatigue limit has the property that as long as no loads exceed the fatigue limit, the fatigue life is infinite. For hard clean steels, the fatigue limit is determined by the largest non-metallic inclusion in the steel. In fact there exists a functional relationship between the size of the largest inclusion and the fatigue limit. For steel producers and consumers it important to be able to estimate the size of the largest inclusion for fatigue assessment and as well as for steel quality classification.

In order to estimate the inclusion size, specimens are polished, a number of small control areas are inspected, and the maximal inclusion size on each control area is measured and analyzed using the Gumbel distribution. This procedure is in accordance with the ASTM standard. An alternative analysis is based on recording all inclusion sizes above a given threshold and assume that they follow the exponential distribution. The relative efficiency of the two methods is calculated when the aim is to estimate the extrapolated characteristic inclusion size on a much bigger area than the control area. It is shown that the rate of extrapolation determines which method is advantageous.

**Mari Myllymäki**: Modelling structures of marked point patterns with and without covariates I

**Abstract**: A marked point pattern $\{x_i, m_i\}$ is a collection of random locations $\{x_i\}$ of objects, each provided with a (vector of) measured quantity $m_i$ called "marks". The objectives are to construct models for such data and to suggest statistical procedures for model fitting. The main emphasis is in the case where the marks depend locally on the point intensity. External covariate information is allowed for heterogeneous data. The research is motivated by a study on tropical rainforest structures.

**Tommy Norberg**: Cost-effective Management of Remediation Projects

**Abstract**:Contaminated soil and groundwater is a problem of growing concern in our society and is today a major issue in land use planning and management, real estate assessment and property selling. Investigation and remediation of contaminated areas are often associated with hight costs. As an example the Swedish Environmental Protection Agency (Naturvårdsverket) estimates that there are about 40 000 contaminated sites in Sweden and provides annually 25–50 million Euro of governmental resources to the Swedish county authorities for investigation and remediation of contaminated areas where no responsible part can be found. The estimated cost for the 1 500 most contaminated sites is approximately 4.1 billion Euro. Similar, or even more severe, situations are present throughout Europe and North America.

The Polluter Pays Principle, which is the regulatory philosophy in the European Union, puts large financial pressure on responsible companies and authorities. The regulatory framework is therefore a strong incentive for both the public and private companies to apply cost-efficient investigation and remediation strategies. In addition, the environmental legislation in many countries, e.g in Sweden, state that the environmental value of remediation must be reasonable compared to the remediation costs in order to provide proper prioritization of resources and to achieve sustainable use of land and water.

This paper discusses a rather common situation in which the site is divided into Remediation Units of equal size. Typically all RUs are investigated (sampled) and the contaminated ones are completely remediated. It is shown that if one is willing to accept a specified small risk of leaving contaminated RUs unremediated, the budget for remediation can be used more cost-efficiently.for the same amount of money. The main idea is that risk is reduced by sampling and to sample sequentially until the risk is sufficiently low.

**Viktor Olsbo**: Modelling epidermal nerve fibre patterns

**Abstract**: We consider a set of two-stage marked Poisson process models describing the following scenario: Fibres represent branches and grow from "beginning" points to "ending" points under a process that encourages placement of "ending" points in current gaps in coverage. As a conceptual example, consider branch growth in trees where new branches tend to grow into open space which offer increased sunlight between existing trees and branches.

A more specific example motivating the current study involves the spatial growth and replacement patterns of epidermal nerve fibres (ENFs) in skin samples. ENFs are thin sinuous fibers branching from root ganglion cells in the dermis and terminating at all levels of the epidermis. The basic structure of ENFs is a tree-like structure with a "trunk" where the ENFs enter the epidermis from the dermis and "branches" spreading in different directions ending in terminal nodes that transmit sensations of heat and pain through the ENFs to the central nervous system. Kennedy et al. see (2), first imaged ENFs from skin biopsies. ENFs appear in the epidermis throughout the body. The number of ENFs per square unit of skin decreases as one moves to more peripheral sites in the body (i.e., the intensity of ENFs is smaller in the hands and feet than in the thigh), and several researchers have noted significant reduction in ENF intensity in patients experiencing diabetic neuropathy (nerve and sensory loss, often severe, in diabetic patients). In subsequent work, Kennedy et al. see (3), and Kennedy et al. see (2), noted that the spatial distribution of ENFs appears to change with disease progression and Leong, see (4), quantified increased clustering (as measured by the pair correlation function) in the distribution of ENF trunks in skin samples from patients suffering small fibre sensory neuropathy (SFSN), i.e., loss of feeling preceding quantifiable reduction in the number of ENFs.

We will consider features as *the number of branches connected to a typical base, the length of an individual branch, the total aggregated branch length connected to a typical base*. Further, we will discuss some modifications of the basic model by means of inducing different hierarchical constraints on the ending points.

# References

[1] Foss, S, Zuyev, S (1996) *On a Voronoi Aggregative Process Related to a Bivariate Poisson Process*, Adv. Appl. Prob., 28, pp. 965-981.

[2] Kennedy, W.R., Wendelschafer-Crabb, G., Johnson, T. (1996). *Quantitation of epidermal nerves in diabetic neuropathy*, Neurology, **47**, 1042-1448.

[3] Kennedy, W.R., and Wendelschafer-Crabb, G. (1993). *The innervation of human epidermis*, Journal of the Neurological Sciences **115**, 184-190.

[4] Leong, T. (2005) First- and Second-Order Properties of Spatial Point Processes in Biostatistics. Unpublished Ph.D. dissertation, Department of Biostatistics, Rollins School of Public Health, Emory University. Atlanta, GA.

**Antti Penttinen**: Modelling structures of marked point patterns with and without covariates II

**Abstract**: This talk has two subtopics. The first of these considers the application of first and second order statistics for extracting information from complex marked point patterns. The second subtopic deals with inference on random set generated Cox process where the underlying random set is a result of thresholding of a Gaussian random field.

**Eric Renshaw**: The Discrepancy Function: A New Way of Disentangling Mark/Point Interaction in Marked Point Processes

**Abstract**: In many spatial situations, not only do the point locations of mark variables (e.g. tree heights) play a key role in the underlying process generating mechanism, but there can be inter-dependence between the marks and points themselves. Although Monte Carlo frequency domain analyses can separate mark and point structure, theoretical advances for marks have so far related to the conditional mark spectrum based on a given point structure. A 'discrepancy function' is therefore developed which isolates the spatial structure of the marks alone, and involves a harmonic decomposition of the mark frequencies. The concept is introduced via various simulated examples based on mark cosine waves and thinned point processes, with particular attention given to the construction of sequential and simultaneous search procedures for developing parameter estimates. The procedure is then applied to Spanish daily ozone data with missing values, a spatial growth-interaction process, and a classic longleaf pine data set from the Wade Tract in Georgia, USA.

**Aila Särkkä**: Space-time growth-interaction models in modelling tree growth (joint work with Eric Renshaw)

**Abstract**: We suggest to use immigration-growth spatial interaction processes as models for growth of trees in a forest. New immigrants arrive randomly in time according to a Poisson process, have uniformly distributed locations on the study region and are assigned (small) marks. In the successive small time intervals, each tree either dies naturally with some probability, or else it undergoes a deterministic incremental size change, which depends on an individual growth function and a spatial interaction function. We discuss two growth functions (linear and logistic) and two interaction functions (symmetric and non-symmetric), and suggest to estimate the parameters of these models by the method of least squares. Finally, we apply the procedure to the analysis of a Swedish pine forest data set for which tree location and diameter at breast height were recorded in 1985, 1990 and 1996.

**Katja Schladitz**: Miles formulae for Boolean models observed on lattices (joint work with Joachim Ohser and Werner Nagel)

**Abstract**: The intrinsic volumes - in 3d up to constants volume, surface area, integral of mean curvature, and Euler number - are a very useful set of geometric characteristics. Combining integral and digital geometry allows efficient simultanous calculation of the intrinsic volumes of sets observed in binary images. In order to achieve consistency in the derived intrinsic volumes for both foreground and background, suitable pairs of discrete connectivities have to be used. To make this rigorous, the concepts discretisation w.r.t. an adjacency system and complementarity of adjacency systems are introduced. Four pairs of adjacency systems are considered: (14.1,14.1), (14.2,14.2), (6,26), and (26,6). The systematic error due to discretisation is investigated for Boolean models. Corrected Miles formulae are suggested.

**Martin Schlather**: Spatio-temporal covariance functions

**Abstract**: Spatio-temporal data are omnipresent in evolutionary spatial processes, especially in environmental modelling. Most approaches to modelling regionalised data are based on stationary Gaussian random fields which are characterised by their covariance function.

Recently, the search for space-time covariance models has gained high attractivity. Here, a survey over the classes of space-time covariance models is given. Some problems with estimating the parameters and the simulation of spatio-temporal random fields are discussed.

**Jürgen Schmiegel**: Self-scaling tumor growth

**Abstract**: We study the statistical properties of the star-shaped approximation of in vitro tumor profiles. The emphasis is on the two-point correlation structure of the radii of the tumor as a function of time and angle. In particular, we show that spatial two-point correlators follow a cosine law. Furthermore, we observe self-scaling behaviour of two-point correlators of different orders, i.e. correlators of a given order are a power law of the correlators of some other order. This power-law dependence is similar to what has been observed for the statistics of the energy-dissipation in a turbulent flow. Based on this similarity, we provide a Lévy based model that captures the correlation structure of the radii of the star-shaped tumor profiles.

**Lance Waller**: Spatial statistical analysis of viruses and hosts in geographic and genetic space

**Abstract**: The field of landscape genetics explores how landscape and environment features influence gene flow, population structure, and local adaptation. Two key elements in such studies involve the identification of spatial discontinuities in population structure and correlating such discontinuities with environmental features. Most popular methods for the first component ignore geographic structure, yet often reveal geographically patterned results. Recent methods incorporate spatial correlation to provide model-based assignment to genetically distinct subpopulations. In this presentation, we consider the landscape genetic structure of virus-host systems and illustrate the methodology on two zoonotic systems. In the first, we analyze feline immunodeficiency virus samples from cougars in the Rocky Mountain area, and, in the second, patterns of raccoon rabies in the eastern United States. We explore general tests for geographic genetic structure and move toward model-based inference providing preliminary results and directions for further research.

**Jun Yu**: Nonparametric and Probabilistic Classification of Agricultural Crops Using Multitemporal Images

**Abstract**: Accurate and quality assured detection of spatial and temporal variation in land use or landscape patterns is needed as direct or indirect input for the assessment of ecosystem health. For these purposes remote sensing methods have potential to be an efficient tool. Unfortunately, several of the existing remote sensing classification methods will not give satisfactory results. For example, the traditional maximum likelihood method will not work for classification of sparse and rarely occurring objects in the landscape. To overcome the problems with traditional methods we propose a new approach for classification of multitemporal satellite data sets, combining multispectral and change detection techniques. The algorithm is based on the nearest neighbor method and derived in order to optimize the average probability for correct classification, i.e. each class is equally important. The new algorithm was applied to a study area where satellite images (SPOT and Landsat TM) from different seasons were used. It showed that using five seasonal images can substantially improve the classification accuracy compared to using a single image. As a large scale application, the approach was applied to the River Dalälven drainage basin. As the distributions for different classes are highly overlapping it is not possible to get satisfactory accuracy at pixel level. Instead it is necessary to introduce a new concept, pixel-wise probabilistic classifiers. The pixel-wise vectors of probabilities can be used to judge how reliable a traditional classification is and to derive measures of the uncertainty (entropy) for the individual pixels. It is extremely important that proper probability distributions allowing frequency interpretation are derived; otherwise misleading results are obtained. The probabilistic classifier gives also unbiased area estimates over arbitrary areas. It has been tested on two test sites of arable land with different characteristics.