

INSTITUT NATIONAL DE RECHERCHE EN INFORMATIQUE ET EN AUTOMATIQUE

Project-Team mistis

Modelling and Inference of Complex and Structured Stochastic Systems

Grenoble - Rhône-Alpes



Theme : Optimization, Learning and Statistical Methods

Table of contents

1.	Team	1
2.	Overall Objectives	1
	2.1. Introduction	1
	2.2. Highlights	2
3.	Scientific Foundations	2
	3.1. Mixture models	2
	3.2. Markov models	2
	3.3. Functional Inference, semi and non-parametric methods	3
	3.3.1. Modelling extremal events	3
	3.3.2. Level sets estimation	5
	3.3.3. Dimension reduction	5
4.	Application Domains	5
	4.1. Image Analysis	5
	4.2. Biology, Environment and Medicine	5
	4.3. Reliability	6
5.	Software	6
	5.1. The HDDA and HDDC toolboxes	6
	5.2. The Extremes freeware	6
	5.3. The SpaCEM ³ program	6
	5.4. The FASTRUCT software	7
	5.5. The TESS software	7
6.	New Results	8
	6.1. Mixture models	8
	6.1.1. Taking into account the curse of dimensionality.	8
	6.1.2. Conjugate mixture model for clustering multimodal data	8
	6.1.3. Rigid and Articulated Point Registration with Expectation Conditional Maximization	9
	6.2. Markov models	10
	6.2.1. A Fully Bayesian Joint Model for coupling Atlas registration with robust brain tissue a	nd
	structure segmentation	10
	6.2.2. Bayesian Weighting of Multiple MR Sequences for Brain Lesion Segmentation	11
	6.2.3. Variational approach for the joint estimation-detection of Brain activity from function	ıal
	MRI data	12
	6.2.4. A Joint Framework for Disparity and Surface Normal Estimation	12
	6.2.5. Consistent detection, localization and tracking of Audio-Visual Objects with Variation	
	EM	15
	6.2.6. Hidden Markov random fields for disease risk mapping	15
	6.2.7. Optimization of the consumption of printers using Markov decision processes	16
	6.2.8. Validation of hidden Markov tree models by comparison of empirical and predict	
	distributions	16
	6.3. Semi and non-parametric methods	17
	6.3.1. Modelling extremal events	17
	6.3.2. Conditional extremal events	17
	6.3.3. Level sets estimation	17
	6.3.4. Dimension reduction	18
	6.3.5. Nuclear plants reliability	18
	6.3.6. Quantifying uncertainties on extreme rainfall estimations	18
	6.3.7. Retrieval of Mars surface physical properties from OMEGA hyperspectral images.	20
	6.3.8. Statistical analysis of hyperspectral multi-angular data from Mars	20
7.	Contracts and Grants with Industry	. 20

8.	Other Grants and Activities	
	8.1. National Actions	21
	8.2. National initiatives	21
	8.3. International initiatives	21
	8.3.1. North Africa	21
	8.3.2. North America	21
	8.3.3. Europe	22
9.	Dissemination	
	9.1. Leadership within scientific commu	nity 22
	9.2. Actions Funded by the EC	22
	9.3. Teaching	23
10.	Bibliography	

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2. Overall Objectives

2.1. Introduction

The team MISTIS aims at developing statistical methods for dealing with complex problems or data. Our applications consist mainly of image processing and spatial data problems with some applications in biology and medicine. Our approach is based on the statement that complexity can be handled by working up from simple local assumptions in a coherent way, defining a structured model, and that is the key to modelling, computation, inference and interpretation. The methods we focus on involve mixture models, Markov models, and more generally hidden structure models identified by stochastic algorithms on one hand, and semi and non-parametric methods on the other hand.

Hidden structure models are useful for taking into account heterogeneity in data. They concern many areas of statistical methodology (finite mixture analysis, hidden Markov models, random effect models, ...). Due to their missing data structure, they induce specific difficulties for both estimating the model parameters and assessing performance. The team focuses on research regarding both aspects. We design specific algorithms for estimating the parameters of missing structure models and we propose and study specific criteria for choosing the most relevant missing structure models in several contexts.

Semi and non-parametric methods are relevant and useful when no appropriate parametric model exists for the data under study either because of data complexity, or because information is missing. The focus is on functions describing curves or surfaces or more generally manifolds rather than real valued parameters. This can be interesting in image processing for instance where it can be difficult to introduce parametric models that are general enough (e.g. for contours).

2.2. Highlights

The work achieved in the European STREP project POP (2006-2008) was reviewed as successful and selected for publication in ICT-RESULT http://cordis.europa.eu/ictresults/index. cfm?section=news&tpl=article&BrowsingType=Features&ID=90953 The main scientific results of POP will be presented at CogSys 2010, the 4th International Conference on Cognitive Systems, January 27 & 28 2010, ETH Zurich, Switzerland. The Mistis contribution corresponds mainly to the work achieved in Vasil Khalidov's PhD thesis (see Sections 6.1.2 and 6.2.5) applied to the multiple speaker localization from audio-visual data.

3. Scientific Foundations

3.1. Mixture models

Participants: Lamiae Azizi, Senan James Doyle, Jean-Baptiste Durand, Florence Forbes, Gersende Fort, Stéphane Girard, Vasil Khalidov, Darren Wraith, Marie-José Martinez.

In a first approach, we consider statistical parametric models, θ being the parameter possibly multidimensional usually unknown and to be estimated. We consider cases where the data naturally divide into observed data $y = y_1, ..., y_n$ and unobserved or missing data $z = z_1, ..., z_n$. The missing data z_i represents for instance the memberships to one of a set of K alternative categories. The distribution of an observed y_i can be written as a finite mixture of distributions,

$$f(y_i \mid \theta) = \sum_{k=1}^{K} P(z_i = k \mid \theta) f(y_i \mid z_i, \theta) .$$
(1)

These models are interesting in that they may point out an hidden variable responsible for most of the observed variability and so that the observed variables are *conditionally* independent. Their estimation is often difficult due to the missing data. The Expectation-Maximization (EM) algorithm is a general and now standard approach to maximization of the likelihood in missing data problems. It provides parameters estimation but also values for missing data.

Mixture models correspond to independent z_i 's. They are more and more used in statistical pattern recognition. They allow a formal (model-based) approach to (unsupervised) clustering.

3.2. Markov models

Participants: Lamiae Azizi, Senan James Doyle, Jean-Baptiste Durand, Florence Forbes, Gersende Fort, Vasil Khalidov, Darren Wraith.

Graphical modelling provides a diagrammatic representation of the logical structure of a joint probability distribution, in the form of a network or graph depicting the local relations among variables. The graph can have directed or undirected links or edges between the nodes, which represent the individual variables. Associated with the graph are various Markov properties that specify how the graph encodes conditional independence assumptions.

It is the conditional independence assumptions that give the graphical models their fundamental modular structure, enabling computation of globally interesting quantities from local specifications. In this way graphical models form an essential basis for our methodologies based on structures.

The graphs can be either directed, e.g. Bayesian Networks, or undirected, e.g. Markov Random Fields. The specificity of Markovian models is that the dependencies between the nodes are limited to the nearest neighbor nodes. The neighborhood definition can vary and be adapted to the problem of interest. When parts of the variables (nodes) are not observed or missing, we refer to these models as Hidden Markov Models (HMM). Hidden Markov chains or hidden Markov fields correspond to cases where the z_i 's in (1) are distributed according to a Markov chain or a Markov field. They are natural extension of mixture models. They are widely used in signal processing (speech recognition, genome sequence analysis) and in image processing (remote sensing, MRI, etc.). Such models are very flexible in practice and can naturally account for the phenomena to be studied.

They are very useful in modelling spatial dependencies but these dependencies and the possible existence of hidden variables are also responsible for a typically large amount of computation. It follows that the statistical analysis may not be straightforward. Typical issues are related to the neighborhood structure to be chosen when not dictated by the context and the possible high dimensionality of the observations. This also requires a good understanding of the role of each parameter and methods to tune them depending on the goal in mind. As regards, estimation algorithms, they correspond to an energy minimization problem which is NP-hard and usually performed through approximation. We focus on a certain type of methods based on the mean field principle and propose effective algorithms which show good performance in practice and for which we also study theoretical properties. We also propose some tools for model selection. Eventually we investigate ways to extend the standard Hidden Markov Field model to increase its modelling power.

3.3. Functional Inference, semi and non-parametric methods

Participants: Julie Carreau, Laurent Gardes, Stéphane Girard, Alexandre Lekina, Mathieu Fauvel, Eugen Ursu.

We also consider methods which do not assume a parametric model. The approaches are non-parametric in the sense that they do not require the assumption of a prior model on the unknown quantities. This property is important since, for image applications for instance, it is very difficult to introduce sufficiently general parametric models because of the wide variety of image contents. Projection methods are then a way to decompose the unknown quantity on a set of functions (e.g. wavelets). Kernel methods which rely on smoothing the data using a set of kernels (usually probability distributions), are other examples. Relationships exist between these methods and learning techniques using Support Vector Machine (SVM) as this appears in the context of *level-sets estimation*, see section 3.3.2. Such non-parametric methods have become the cornerstone when dealing with functional data [51]. This is the case for instance when observations are curves. They allow to model the data without a discretization step. More generally, these techniques are of great use for *dimension reduction* purposes (section 3.3.3). They permit to reduce the dimension of the functional or multivariate data without assumptions on the observations distribution. Semi-parametric methods refer to methods that include both parametric and non-parametric aspects. Examples include the Sliced Inverse Regression (SIR) method [59] which combines non-parametric regression techniques with parametric dimension reduction aspects. This is also the case in *extreme value analysis* [50], which is based on the modelling of distribution tails, see section 3.3.1. It differs from traditional statistics which focus on the central part of distributions, *i.e.* on the most probable events. Extreme value theory shows that distributions tails can be modelled by both a functional part and a real parameter, the extreme value index.

3.3.1. Modelling extremal events

Extreme value theory is a branch of statistics dealing with the extreme deviations from the bulk of probability distributions. More specifically, it focuses on the limiting distributions for the minimum or the maximum of a large collection of random observations from the same arbitrary distribution. Let $X_{1,n} \leq ... \leq X_{n,n}$ denote n ordered observations from a random variable X representing some quantity of interest. A p_n -quantile of X is the value x_{p_n} such that the probability that X is greater than x_{p_n} is p_n , *i.e.* $P(X > x_{p_n}) = p_n$. When $p_n < 1/n$, such a quantile is said to be extreme since it is usually greater than the maximum observation $X_{n,n}$ (see Figure 1).

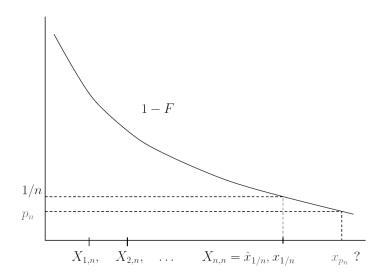


Figure 1. The curve represents the survival function $x \to P(X > x)$. The 1/n-quantile is estimated by the maximum observation so that $\hat{x}_{1/n} = X_{n,n}$. As illustrated in the figure, to estimate p_n -quantiles with $p_n < 1/n$, it is necessary to extrapolate beyond the maximum observation.

To estimate such quantiles requires therefore dedicated methods to extrapolate information beyond the observed values of X. Those methods are based on Extreme value theory. This kind of issues appeared in hydrology. One objective was to assess risk for highly unusual events, such as 100-year floods, starting from flows measured over 50 years. To this end, semi-parametric models of the tail are considered:

$$P(X > x) = x^{-1/\theta} \ell(x), \ x > x_0 > 0,$$
(2)

where both the extreme-value index $\theta > 0$ and the function $\ell(x)$ are unknown. The function $\ell(x)$ acts as a nuisance parameter which yields a bias in the classical extreme-value estimators developed so far. Such models are often referred to as heavy-tail models since the probability of extreme events decreases at a polynomial rate to zero. More generally, the problems that we address are part of the risk management theory. For instance, in reliability, the distributions of interest are included in a semi-parametric family whose tails are decreasing exponentially fast. These so-called Weibull-tail distributions [10] are defined by their survival distribution function:

$$P(X > x) = \exp\{-x^{\theta}\ell(x)\}, \ x > x_0 > 0.$$
(3)

Gaussian, gamma, exponential and Weibull distributions, among others, are included in this family. An important part of our work consists in establishing links between models (2) and (3) in order to propose new estimation methods. We also consider the case where the observations were recorded with a covariate information. In this case, the extreme-value index and the p_n -quantile are functions of the covariate. We propose estimators of these functions by using a moving window approach or a nearest neighbor method.

3.3.2. Level sets estimation

Level sets estimation is a recurrent problem in statistics which is linked to outlier detection. In biology, one is interested in estimating reference curves, that is to say curves which bound 90% (for example) of the population. Points outside this bound are considered as outliers compared to the reference population. Level sets estimation can be looked at as a conditional quantile estimation problem which permits to benefit from a non-parametric statistical framework. In particular, boundary estimation, arising in image segmentation as well as in supervised learning, is interpreted as an extreme level-set estimation problem. Level sets estimation can also be formulated as a linear programming problem. In this context, estimates are sparse since they involve only a small fraction of the dataset, called the set of support vectors.

3.3.3. Dimension reduction

Our work on high dimensional data imposes to face the curse of dimensionality phenomenon. Indeed, the modelling of high dimensional data requires complex models and thus the estimation of high number of parameters compared to the sample size. In this framework, dimension reduction methods aim at replacing the original variables by a small number of linear combinations with as small as possible loss of information. Principal Component Analysis (PCA) is the most widely used method to reduce dimension in data. However, standard linear PCA can be quite inefficient on image data where even simple image distorsions can lead to highly non linear data. Two directions are investigated. First, non-linear PCAs can be proposed, leading to semi-parametric dimension reduction methods [58]. Another field of investigation is to take into account the application goal in the dimensional data for parametric inference [46]. Such models can then be used in a Mixtures or Markov framework for classification purposes. Another approaches consists in combining dimension reduction, regularization techniques and regression techniques to improve the Sliced Inverse Regression method [59].

4. Application Domains

4.1. Image Analysis

Participants: Senan James Doyle, Mathieu Fauvel, Florence Forbes, Laurent Gardes, Stéphane Girard, Vasil Khalidov, Darren Wraith.

As regards applications, several areas of image analysis can be covered using the tools developed in the team. More specifically, in collaboration with team Perception, we address various issues in computer vision involving Bayesian modelling and probabilistic clustering techniques. Other applications in medical imaging are natural. We work more specifically on MRI data, in collaboration with the Grenoble Institute of Neuroscience (GIN) and team Magma from Laboratoire d'Informatique de Grenoble (LIG) (see Sections 6.2.1 and 6.2.2). We also consider other statistical 2D fields coming from other domains such as remote sensing, in collaboration with Laboratoire de Planétologie de Grenoble. Also, in the context of the ANR MDCO project Vahine, see section 8.2, we work on hyperspectral multi-angle images.

4.2. Biology, Environment and Medicine

Participants: Lamiae Azizi, Senan James Doyle, Florence Forbes, Laurent Gardes, Stéphane Girard, Vasil Khalidov, Eugen Ursu, Darren Wraith.

A second domain of applications concerns biology and medecine. We consider the use of missing data models in epidemiology. We also investigated statistical tools for the analysis of bacterial genomes beyond gene detection. Applications in population genetics and neurosiences (Sections 6.2.1 and 6.2.2) are also considered. Finally, in the context of the ANR VMC project Medup, see section 8.2, we study the uncertainties on the forecasting and climate projection for Mediterranean high-impact weather events.

4.3. Reliability

Participants: Laurent Donini, Jean-Baptiste Durand, Laurent Gardes, Stéphane Girard.

Reliability and industrial lifetime analysis are applications developed through collaborations with the EDF research department and the LCFR laboratory (Laboratoire de Conduite et Fiabilité des Réacteurs) of CEA / Cadarache. We also consider failure detection in print infrastructure through collaboration with Xerox, Meylan and the CIFRE PhD thesis of Laurent Donini, co-advised by Jean-Baptiste Durand and Stéphane Girard.

5. Software

5.1. The HDDA and HDDC toolboxes

Participant: Stéphane Girard.

Joint work with: Charles Bouveyron (Université Paris 1) and Gilles Celeux (Select, INRIA). The High-Dimensional Discriminant Analysis (HDDA) and the High-Dimensional Data Clustering (HDDC) toolboxes contain respectively efficient supervised and unsupervised classifiers for high-dimensional data. These classifiers are based on Gaussian models adapted for high-dimensional data [46]. The HDDA and HDDC toolboxes are available for Matlab and are included into the software MixMod [45].

5.2. The Extremes freeware

Participants: Sophie Chopart, Laurent Gardes, Stéphane Girard.

Joint work with: Diebolt, J. (CNRS) and Garrido, M. (INRA Clermont-Ferrand-Theix).

The EXTREMES software is a toolbox dedicated to the modelling of extremal events offering extreme quantile estimation procedures and model selection methods. This software results from a collaboration with EDF R&D. It is also a consequence of the PhD thesis work of Myriam Garrido [57]. The software is written in C++ with a Matlab graphical interface. It is now available both on Windows and Linux environments. It can be downloaded at the following URL: http://extremes.gforge.inria.fr/. Besides, Sophie Chopart has developed a new interface in C++. The software is now independent of Matlab.

5.3. The SpaCEM³ program

Participants: Lamiae Azizi, Sophie Chopart, Senan James Doyle, Florence Forbes.

SpaCEM³ (Spatial Clustering with EM and Markov Models) is a software that provides a wide range of supervised or unsupervised clustering algorithms. The main originality of the proposed algorithms is that clustered objects do not need to be assumed independent and can be associated with very high-dimensional measurements. Typical examples include image segmentation where the objects are the pixels on a regular grid and depend on neighbouring pixels on this grid. More generally, the software provides algorithms to cluster multimodal data with an underlying dependence structure accounting for some spatial localisation or some kind of interaction that can be encoded in a graph.

This software, developed by present and past members of the team, is the result of several research developments on the subject. The current version 2.09 of the software is CeCILLB licensed.

6

Main features. The approach is based on the EM algorithm for clustering and on Markov Random Fields (MRF) to account for dependencies. In addition to standard clustering tools based on independent gaussian mixture models, SpaCEM³ features include:

- The unsupervised clustering of dependent objects. Their dependencies is encoded via a graph not necessarily regular and data sets are modelled via Markov random fields and mixture models (eg. MRF and Hidden MRF). Available Markov models include extensions of the Potts model with the possibility to define more general interaction models.
- The supervised clustering of dependent objects when standard Hidden MRF (HMRF) assumptions do not hold (ie. in the case of non correlated and non unimodal noise models). The learning and test steps are based on recently introduced Triplet Markov models.
- Selection model criteria (BIC, ICL and their mean-field approximations) that select the "best" HMRF according to the data.
- The possibility of producing simulated data from:
 - general pairwise MRF with singleton and pair potentials (typically Potts models and extensions),
 - standard HMRF, ie. with independent noise model,
 - general Triplet Markov models with interaction up to order 2
- A specific setting to account for high-dimensional observations.
- An integrated framework to deal with missing observations, under Missing At Random (MAR) hypothesis, with prior imputation (KNN, mean, ...), online imputation (as a step in the algorithm) or without imputation.

The software is available at http://spacem3.gforge.inria.fr. A paper describing the software and its main functionalities has been recently published in French [22]. A user manual in English is available on the web site above together with example data sets.

5.4. The FASTRUCT software

Participant: Florence Forbes.

Joint work with: Francois, O. (TimB, TIMC) and Chen, C. (former Post-doctoral fellow in Mistis).

The FASTRUCT program is dedicated to the modelling and inference of population structure from genetic data. Bayesian model-based clustering programs have gained increased popularity in studies of population structure since the publication of the software STRUCTURE [63]. These programs are generally acknowledged as performing well, but their running-time may be prohibitive. FASTRUCT is a non-Bayesian implementation of the classical model with no-admixture uncorrelated allele frequencies. This new program relies on the Expectation-Maximization principle, and produces assignment rivaling other model-based clustering programs. In addition, it can be several-fold faster than Bayesian implementations. The software consists of a command-line engine, which is suitable for batch-analysis of data, and a MS Windows graphical interface, which is convenient for exploring data.

It is written for Windows OS and contains a detailed user's guide. It is available at http://mistis.inrialpes.fr/ realisations.html.

The functionalities are further described in the related publication:

• Molecular Ecology Notes 2006 [47].

5.5. The TESS software

Participant: Florence Forbes.

Joint work with: Francois, O. (TimB, TIMC) and Chen, C. (former post-doctoral fellow in Mistis).

TESS is a computer program that implements a Bayesian clustering algorithm for spatial population genetics. Is it particularly useful for seeking genetic barriers or genetic discontinuities in continuous populations. The method is based on a hierarchical mixture model where the prior distribution on cluster labels is defined as a Hidden Markov Random Field [52]. Given individual geographical locations, the program seeks population structure from multilocus genotypes without assuming predefined populations. TESS takes input data files in a format compatible to existing non-spatial Bayesian algorithms (e.g. STRUCTURE). It returns graphical displays of cluster membership probabilities and geographical cluster assignments from its Graphical User Interface.

The functionalities and the comparison with three other Bayesian Clustering programs are specified in the following publication:

Molecular Ecology Notes 2007

6. New Results

6.1. Mixture models

6.1.1. Taking into account the curse of dimensionality.

Participant: Stéphane Girard.

Joint work with: Bouveyron, C (Université Paris 1) and Celeux, G. (Select, INRIA).

In the PhD work of Charles Bouveyron (co-advised by Cordelia Schmid from the INRIA team LEAR) [46], we propose new Gaussian models of high dimensional data for classification purposes. We assume that the data live in several groups located in subspaces of lower dimensions. Two different strategies arise:

- the introduction in the model of a dimension reduction constraint for each group,
- the use of parsimonious models obtained by imposing to different groups to share the same values of some parameters.

This modelling yields a new supervised classification method called HDDA for High Dimensional Discriminant Analysis [4]. Some versions of this method have been tested on the supervised classification of objects in images. This approach has been adapted to the unsupervised classification framework, and the related method is named HDDC for High Dimensional Data Clustering [3]. An introductory paper to these classification methods [23] has be written in order to disseminate them into various application domains. Another part of the work of Charles Bouveyron and Stéphane Girard has consisted in extending these methods to the semisupervised context or to the presence of label noise [14]. In collaboration with Gilles Celeux and Charles Bouveyron we are currently working on the automatic selection of the discrete parameters of the model.

6.1.2. Conjugate mixture model for clustering multimodal data

Participants: Florence Forbes, Vasil Khalidov.

Joint work with: Radu Horaud from the INRIA team Perception.

This work was initiated in the European STREP POP (Perception On Purpose-2006-2008) coordinated by Radu Horaud. We addressed the issue of clustering observations that are gathered using multiple measuring instruments, *e.g.* using several physically different sensors. A typical such issue, that we addressed is audio-visual speaker detection.

When the data originates from a single speaker/object, finding the best estimates for the objects characteristics is usually referred to as a pure fusion task and it reduces to combining multisensor observations in some optimal way. The problem is much more complex when several objects are present and when the task implies their detection, identification, and localization. In this case one has to consider two processes simultaneously: (i) segregation which assigns each observation either to an object or to an outlier category and (ii) estimation which computes the parameters of each object based on the group of observations that were assigned to that object. In other words, in addition to fusing observations from different sensors, multimodal analysis requires the assignment of each observation to one of the objects.

This observation-to-object association problem can be cast into a probabilistic framework. In the case of unimodal data (possibly multidimensional), the problems of grouping observations and of associating groups with objects can be cast into the framework of standard data clustering. The problem of clustering multimodal data raises the difficult question of how to group together observations that belong to different physical spaces with different dimensionalities, e.g., how to group visual data with auditory data? When the observations from two different modalities can be aligned pairwise, a natural solution is to consider the Cartesian product of two unimodal spaces. Unfortunately, such an alignment is not possible in most practical cases. Different sensors operate at different frequency rates and hence the number of observations gathered with one sensor can be quite different from the number of observations gathered with another sensor. Consequently, there is no obvious way to align the observations pairwise. Considering all possible pairs would result in a combinatorial blow-up and typically create abundance of erroneous observations corresponding to inconsistent solutions. Alternatively, one may consider several unimodal clusterings, provided that the relationships between a common object space and several observation spaces can be explicitly specified. Multimodal clustering then results in a number of unimodal clusterings that are jointly governed by the same unknown parameters characterizing the object space.

In a recent submitted paper [42], we show how the problem of clustering multimodal data can be addressed within the framework of mixture models. The proposed model is composed of a number of modality-specific mixtures. These mixtures are jointly governed by a set of common object-space parameters (which are referred to as the tying parameters), thus insuring consistency between the sensory data and the object space being sensed. This is done using explicit transformations from the unobserved parameter space (object space) to each of the observed spaces (sensor spaces). Hence, the proposed model is able to deal with observations that live in spaces with different physical properties such as dimensionality, space metric, sensor sampling rate, etc. We believe that linking the object space with the sensor spaces based on object-space-to-sensorspace transformations has more discriminative power than existing multisensor fusion techniques and hence performs better in terms of multiple object identification and localization. To the best of our knowledge, there has been no attempt to use a generative model, such as ours, for the task of multimodal data interpretation. The concept of conjugate mixture models is described in more details in our paper [42]. Standard Gaussian mixture models (GMM) are used to model the unimodal data. The parameters of these Gaussian mixtures are governed by the object parameters through a number of object-space-to-sensor-space transformations (one transformation for each sensing modality). A very general class of transformations, namely non-linear Lipschitz continuous functions is assumed. Figure 2 shows a graphical representation of our conjugate mixture models.

6.1.3. Rigid and Articulated Point Registration with Expectation Conditional Maximization Participant: Florence Forbes.

Joint work with: Radu Horaud from the INRIA team Perception and Manuel Iguel from team Emotion.

In image analysis and computer vision there is a long tradition of algorithms for finding an optimal alignment between two sets of points. This is referred to as the *point registration* (PR) problem, which is twofold: (i) Find point-to-point correspondences and (ii) estimate the transformation allowing the alignment of the two sets. Existing PR methods can be roughly divided into three categories: The Iterative Closest Point (ICP) algorithm and its numerous extensions, soft assignment methods and probabilistic methods to cite just a few. Probabilistic point registration uses, in general, Gaussian mixture models (GMM). Indeed, one may reasonably assume that

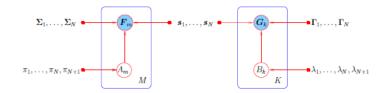


Figure 2. Graphical representation of the conjugate mixture model in the case of two modalities. The observed data consists of two sets of respectively M and K observations. Circles denote random variables, plates (rectangles) around them represent multiple similar nodes, their number being given in the plates. The representation inside each plate corresponds to a Gaussian mixture model (the observed data are in grey). The two modalities are then linked by the tying parameters $s_1, ...s_N$ shown in between the two plates.

points from the first set (the data) are normally distributed around points belonging to the second set (the model). Therefore, the point-to-point assignment problem can be recast into that of estimating the parameters of a mixture. This can be done within the framework of maximum likelihood with missing data because one has to estimate the mixture parameters as well as the point-to-cluster assignments, i.e., the missing data. In this case the algorithm of choice is the expectation-maximization (EM) algorithm. Formally, the latter replaces the maximization of the observed-data log-likelihood with the maximization of the expected complete-data loglikelihood conditioned by the observations. As explained in detail in [41], there are intrinsic difficulties when one wants to cast the PR problem in the EM framework. The main topic and contribution of our work [41] is to propose an elegant and efficient way to do that. We introduce an innovative EM-like algorithm, namely the Expectation Conditional Maximization for Point Registration (ECMPR) algorithm. The algorithm allows the use of general covariance matrices for the mixture model components and improves over the isotropic covariance case. We analyse in detail the associated consequences in terms of estimation of the registration parameters, and we propose an optimal method for estimating the rotational and translational parameters based on semi-definite positive relaxation. We extend rigid registration to articulated registration. Robustness is ensured by detecting and rejecting outliers through the addition of a uniform component to the Gaussian mixture model at hand. We provide an in-depth analysis of our method and we compare it both theoretically and experimentally with other robust methods for point registration.

6.2. Markov models

6.2.1. A Fully Bayesian Joint Model for coupling Atlas registration with robust brain tissue and structure segmentation

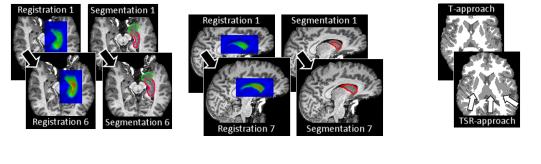
Participant: Florence Forbes.

Joint work with: Scherrer, B. and Dojat, M. (Grenoble Institute of Neuroscience).

The analysis of MR brain scans is a complex task that requires several sources of information to be taken into account and combined. The analysis is frequently based on segmentations of tissues and of subcortical structures performed by human experts. For automatic segmentation, difficulties arise from the presence of various artifacts such as noise or intensity non uniformities. For structures, the segmentation requires in addition the use of prior information usually encoded via a pre-registered atlas. Recently growing interest has been on tackling this complexity by combining different approaches. As an illustration, some authors propose to use a region based tissue classification approach followed by a watershed algorithm to label brain sulci while others combine a region-based bias field estimation and a level set method to segment the cortex. A step further the combinaison of methods is *coupling*, giving the possibility to introduce mutual interactions between

components of a model. Such a coupling can be naturally expressed in a statistical framework via the definition of joint distributions. In this vein, Ashburner and Friston [44] couple a global statistical tissue segmentation approach with the estimation of a bias field and a global registration of an atlas of tissue probability maps. Another growing feature in the literature is to locally estimate model parameters on the image to better fit local image properties. For instance, our previous work [64] couples a *local* tissue segmentation approach with a structure segmentation approach; Pohl et al., [62] couple structure segmentation with the local affine registration of an atlas.

In this work, we propose to go further towards coupling methods by constructing a *Conditional Random Field* (CRF) model that performs a number of essential tasks. We will focus on developing a statistical framework that allows 1) tissue segmentation using local Markov Random Field (MRF) models, 2) MRF segmentation of structures and 3) local affine registration of an atlas. All tasks are linked and completing each one of them can help in refining the others. The idea is to capture in a single model all the relationships that could be formalized between these tasks. Our basis toward a solution is similar to that in [64] with the major difference that therein a joint model was not explicitly given but defined through the specification of a number of compatible conditional MRF models. In this work, we specify directly a joint model from which the conditional models are derived. As a result, cooperation between tissues and structures is treated in a more symmetric way which results in new more consistent conditional models. In addition, interaction between the segmentation and registration steps is easily introduced. An explicit joint formulation has the advantage to provide a strategy to construct more consistent or complete models that are open to incorporation of new tasks. For estimation, we provide an appropriate variational EM framework allowing a Bayesian treatment of the parameters. The evaluation performed on both phantoms and real 3T brain scans shows good results and demonstrates the clear improvement provided by coupling the registration step to tissue and structure segmentation. See Figure 3 for an illustration and [32] for more details.



(a)

(b)

(c)

Figure 3. (a) Evolution of hippocampus local affine registration and segmentation; (b) Evolution of the caudate atlas registration and segmentation after an artificial perturbation of the initial registration; (c) Tissue segmentations with T (tissue segmentation only) and TSR (combined tissue, structure segmentations and registration) approaches.

6.2.2. Bayesian Weighting of Multiple MR Sequences for Brain Lesion Segmentation

Participants: Florence Forbes, Senan James Doyle, Darren Wraith.

Joint work with: Michel Dojat (Grenoble Institute of Neuroscience), Daniel Garcia-Lorenzo and Christian Barillot (INRIA Team Visages).

A healthy brain is generally segmented into three tissues: cephalo spinal fluid, grey matter and white matter. Statistical based approaches usually aim to model probability distributions of voxel intensities with the idea that such distributions are tissue-dependent. The delineation and quantification of brain lesions is critical to establishing patient prognosis, and for charting the development of pathology over time. Typically, this is performed manually by a medical expert, however automatic methods have been proposed (see [65] for review) to alleviate the tedious, time consuming and subjective nature of manual delineation. Automated or semi-automated brain lesion detection methods can be classified according to their use of multiple sequences, *a priori* knowledge about the structure of normal brain, tissue segmentation models, and whether or not specific lesion types are targeted. A common feature is that most methods are based on the initial identification of *candidate regions* for lesions. In most approaches, normal brain tissue *a priori* maps are used to help identify regions where the damaged brain differs, and the lesion is identified as an outlier. Existing methods frequently avail of complementary information from multiple sequences. For example, lesion voxels may appear atypical in one modality and normal in another. This is well known and implicitly used by neuroradiologists when examining data. Within a mathematical framework, multiple sequences enable the superior estimation of tissue classes in a higher dimensional space.

For multiple MRI volumes, intensity distributions are commonly modelled as multi-dimensional Gaussian distributions. This provides a way to combine the multiple sequences in a single segmentation task but with all the sequences having equal importance. However, given that the information content and discriminative power to detect lesions varies between different MR sequences, the question remains as to how to best combine the multiple channels. Depending on the task at hand, it might be beneficial to weight the various sequences differently.

In this work, rather than trying to detect lesion voxels as outliers from a normal tissue model, we adopt an incorporation strategy whose goal is to identify lesion voxels as an additional fourth component. Such an explicit modelling of the lesions is usually avoided. It is difficult for at least two reasons: 1) most lesions have a widely varying and inhomogeneous appearance (*eg.* tumors or stroke lesions) and 2) lesion sizes can be small (*eg.* multiple sclerosis lesions). In a standard tissue segmentation approach, both reasons usually prevent accurate model parameter estimation resulting in bad lesion delineation. Our approach aims to make this estimation possible by modifying the segmentation model with an additional weight field. We propose to modify the tissue segmentation model so that lesion voxels become inliers for the modified model and can be identified as a genuine model component. Compared to *robust estimation* approaches (*eg.* [66]) that consist of down-weighting the effect of outliers on the main model estimation, we aim to increase the weight of candidate lesion voxels to overcome the problem of under-representation of the lesion class.

We introduce weight parameters in the segmentation model and then solve the issue of prescribing values for these weights by developing a Bayesian framework. This has the advantage to avoid the specification of *adhoc* weight values and to allow the incorporation of expert knowledge through a weight prior distribution. We provide an estimation procedure based on a variational Expectation Maximization (EM) algorithm to produce the corresponding segmentation. Furthermore, in the absence of explicit expert knowledge, we show how the weight prior can be specified to guide the model toward lesion identification. Experiments on artificial (Table 1) and real lesions (Table 2, Figures 4, 5, 6) of various sizes are reported to demonstrate the good performance of our approach.

6.2.3. Variational approach for the joint estimation-detection of Brain activity from functional MRI data

Participants: Florence Forbes, Alexandre Janon.

Joint work with: Michel Dojat (Grenoble Institute of Neuroscience).

The goal is to investigate the possibility of using Variational approximation techniques as an alternative to MCMC based methods for the joint estimation-detection of brain activity in functional MRI data [60]. The 5-month internship of Alexandre Janon enabled us to initiate this activity which will be pursued in 2010 with a new collaboration with Philippe Ciuciu from Neurospin, CEA in Saclay.

6.2.4. A Joint Framework for Disparity and Surface Normal Estimation

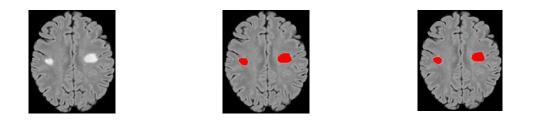
Participant: Florence Forbes.

Table 1. DSC results (%) on MS Brain Web simulated data, for various lesion sizes, noise and non-uniformity levels. Comparison of different methods: AWEM for our Adaptive Weighted EM, Garcia-Lorenzo & al's method [G], Van Leemput & al.'s method [EMS] and Rousseau & al.'s method [R]. The corresponding gain/loss over the best comparable results is given in parenthesis. NA means not available.

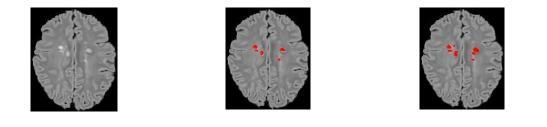
Method	3%	5%	7%	9%
	Mild lesion	s (0.02% of the voxels)		
AWEM	68 (+1)	49 (-21)	36 (+2)	12 (+8)
[G]	67	70	34	0
[EMS]	56	33	13	4
[R]	52	NA	NA	NA
	Moderate lesio	ons (0.18% of the voxels))	
AWEM	86 (+7)	80 (-1)	73 (+14)	64 (+27)
[G]	72	81	59	29
[EMS]	79	69	52	37
[R]	63	NA	NA	NA
	Severe lesion	ns (0.52% of the voxels)		*
AWEM	92 (+7)	86 (-2)	78 (+6)	68 (+27)
[G]	79	88	72	41
[EMS]	85	72	56	41
[R]	82	NA	NA	NA
	0% nc	on-uniformities		•
		-		
Method	3%	5%	7%	9%
	Mild lesion	s (0.02% of the voxels)		
AWEM	0 (-75)	0 (-65)	0 (-20)	0 (-30)
[G]	75	65	20	30
[EMS]	58	27	13	6
	Moderate lesio	ons (0.18% of the voxels))	
AWEM	52 (-24)	51 (-25)	52 (-15)	27 (-21)
[G]	75	76	67	48
[EMS]	76	64	47	31
	Severe lesion	ns (0.52% of the voxels)		
AWEM	87 (+1)	70 (-13)	61 (-13)	50 (-8)
[G]	75	83	74	58
[EMS]	86	74	62	45
	40% n	on-uniformities		•

Table 2. Lesion load or percentage of lesion voxels (LL), DSC results (%) for Van Leemput & al.'s method (EMS) and for our Adaptive Weighted EM (AWEM), for 5 patients with MS.

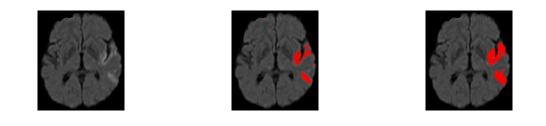
· · · · ·	1 0	· · · · · ·	
	LL	EMS	AWEM
Patient1	0.42	62	82 (+20)
Patient2	1.71	54	56 (+2)
Patient3	0.29	47	45 (-2)
Patient4	1.59	65	72 (+7)
Patient5	0.31	47	45 (-2)
Average		55 +/-8	60 +/-16



(a) (b) (c) Figure 4. Real MS data, patient 1. (a): Flair image. (b): identified lesions with our approach (DSC 82%). (c): ground truth.



(a) (b) (c) Figure 5. Real MS data, patient 3. (a): Flair image. (b): identified lesions with our approach (DSC 45%). (c): ground truth.



(a) (b) (c) Figure 6. Real stroke data. (a): DW image. (b): identified lesions with our approach (DSC 63%). (c): ground truth.

Joint work with: Elise Arnaud, Radu Horaud and Ramya Narasimha from team Perception.

This work deals with the stereo matching problem. Stereo matching has been one of the core challenges in computer vision for decades. The most recent algorithms show very good performance. However, most existing stereo algorithms have inherent fronto-parallel assumption in their modelling of the stereo correspondence problem. Such an assumption supposes that the scene under consideration can be approximated by a set of fronto-parallel planes (on which the disparity is constant) and thus biases the results towards staircase solutions. As described in our paper [43], we propose an novel algorithm that provides surface consistent solutions. To move away from the traditional fronto-parallel assumption, we propose an algorithm that provides disparities in accordance with the surface properties of the scene under consideration. To do so, we carry out cooperatively both disparity and surface normal estimations by setting the two tasks in a unified Markovian framework. We define a new joint probabilistic model based on the definition of two MRFs that are linked to encode consistency between disparities and surface properties. The consideration of normal and disparity maps as two separate random fields increases the model's flexibility. For both MRFs, we include geometric contextual information in the pair-wise regularizing term, thus favoring a disparity solution consistent with the scene surfaces - possibly slanted and/or curved. The respective MRFs data terms are designed to extract data information that specifically impact both the disparity and normal fields. In particular, for normals, we propose a data term favoring proximity to a set of observed normals derived from an oversegmentation of the image into small regions and a plane fitting procedure, thus including explicitly these steps within the model. The surface properties are then approximated using surface normals in disparity space. These normals provide a reasonable approximation of the true surface. The proposed joint model results in a posterior distribution, for both the disparity and normal fields, which is used for their estimation according to a Maximum A Posteriori (MAP) principle. The alternating maximization procedure used for the MAP search is based on belief propagation and leads to cooperative estimation and mutual improvement of disparity and normal accuracies. Moreover, our approach has the following advantages:

(i) it does not require the computation of high-order disparity derivatives, (ii) it embeds the estimation of surface properties in the Markovian model rather than refining the results using a post-processing step, and (iii) it does not require knowledge of the intrinsic camera calibration parameters.

We illustrate the performance of our approach on synthetic and real data. The results obtained are comparable to the state-of-the-art and show improvement in many cases.

6.2.5. Consistent detection, localization and tracking of Audio-Visual Objects with Variational EM

Participants: Florence Forbes, Vasil Khalidov.

Joint work with: Radu Horaud from team Perception.

This work addresses the issue of detecting, localizing and tracking objects in a scene that are both seen and heard. We give this problem an interpretation within an unsupervised clustering framework and propose a novel approach based on features consistency. This model is capable of resolving the observations that are due to detector errors, improving thus the estimation accuracy. We formulate the task as a maximum likelihood estimation problem and perform the inference by a version of the expectation-maximization algorithm, which is formally derived, and which provides cooperative estimates of observation errors, observation assignments and object tracks. We describe several experiments with single- and multiple person detection, localization and tracking.

6.2.6. Hidden Markov random fields for disease risk mapping

Participants: Lamiae Azizi, Florence Forbes, Stéphane Girard.

Joint work with: David Abrial, Christian Ducrot and Myriam Garrido from INRA Clermont-Ferrand-Theix.

Risk mapping in epidemiology enables to identify the location of areas with low or high risk of contamination. It provides also a measure of risk differences between these regions. Most risk mapping methods for pooled data used by epidemiologists are based on hierarchical Bayesian approaches designed for the estimation of risk at each geographical unit. They rely on a Gaussian auto-regressive spatial smoothing. The risk classification, i.e. grouping of geographical units with similar risk, is then necessary to easily draw interpretable maps, but it must be performed in a second step. By analogy with the methods used in image segmentation, we investigate, in the context of Lamiae Azizi' PhD thesis, alternative methods for risk mapping based on the introduction of an hidden discrete random field representing assignment of each spatial unit to a risk class (partition approaches). The most standard such case is the Hidden Markov Random Field (HMRF) model where the hidden field is defined as a Potts model. Other possibilities consist in modelling spatial dependencies at different levels in the hierarchy and in mixing auto-regressive modelling with partition approaches. In the hidden Potts model case, the risk value attached to a class is represented as a parameter of the model and is estimated during the classification procedure. The conditional distribution of the observed field given the class assignments is given by a product of Poisson distributions. To estimate the model parameters and determine the risk classes, we investigate the use of EM variants based on mean-field like approximations, as implemented in the Spacem³ software. Preliminary experiments on realistic synthetic data sets rise a number of questions. Difficulties arise from a number of sources including the presence of a lot of zeros in the data and the possible inappropriate use of the Poisson distribution in this case, the particularity of the data sets we consider that sometimes correspond to very small populations (rare disease case) and inhomogeneous population sizes and the high impact of the EM initialization on the final mapping result. More investigations are then necessary before addressing our second goal which is the addition of a time component in the analysis.

6.2.7. Optimization of the consumption of printers using Markov decision processes

Participants: Laurent Donini, Jean-Baptiste Durand, Stéphane Girard.

Joint work with: Ciriza, V. and Bouchard, G. (Xerox XRCE, Meylan)

In the context of the PhD thesis of Laurent Donini, we have proposed several approaches to optimize the consumption of printers. The first aim of this work is to determine an optimal value of the timeout of an isolated printer, so as to minimize its electrical consumption. This optimal timeout is obtained by modeling the stochastic process of the print requests, by computing the expected consumption under this model, according to the characteristics of the printers, and then by minimizing this expectation with respect to the timeout. Two models are considered for the request process: a renewal process, and a hidden Markov chain. In [48], explicit values of the optimal timeout are provided when possible. In other cases, we provide some simple equation satisfied by the optimal timeout. It is also shown that a model based on a renewal process offers as good results as an empirical minimization of the consumption based on exhaustive search of the timeout, for a largely lower computational cost. This work has been extended to take into account the users' discomfort resulting from numerous shutdowns of the printers, which yield increased waiting time. This has also been extended to printers with several states of sleep, or with separate reservoirs of solid ink.

As a second step, the case of a network of printers has been considered. The aim is to decide on which printer some print request must be processed, so as to minimize the total consumption of the network of printers, taking into account user discomfort. Our approach is based on Markov Decision Processes (MDPs), and explicit solutions for the optimal decision are not available anymore. Furthermore, to simplify the problem, the timeout values are considered are fixed. The state space is continuous, and its dimension increases linearly with the number of printers, which quickly turns the usual algorithms (*i.e.* value or policy iteration) intractable. This is why different variants have been considered, among which the Sarsa algorithm.

6.2.8. Validation of hidden Markov tree models by comparison of empirical and predicted distributions

Participants: Jean-Baptiste Durand, Inga Paukner-Stojkov.

This study consists in validating biological models of tree growth based on hidden Markov trees by comparing empirical characteristics of the trees, and their theoretical counterpart, as predicted by the model. In a first step, we focused on trees with discrete univariate variables associated with each vertex. In this case, the characteristics can consist of the size of homogeneous zones (connected vertices with the same value for the variable), their number, the tree depth before the first occurrence of a given value, or the path length separating homogeneous zones.

Since no explicit formula is available for the predicted distributions, these have been approximated by MC simulations. This work has been achieved by Inga Paukner-Stojkov, in the context of a 5-month internship.

6.3. Semi and non-parametric methods

6.3.1. Modelling extremal events

Participants: Stéphane Girard, Laurent Gardes.

Joint work with: Guillou, A. (Univ. Strasbourg)

We introduced of a new model of tail distributions depending on two parameters $\tau \in [0, 1]$ and $\theta > 0$ [55]. This model includes very different distribution tail behaviors from Fréchet et Gumbel maximum domains of attraction. In the particular cases of Pareto type tails ($\tau = 1$) or Weibull tails ($\tau = 0$), our estimators coincide with classical ones proposed in the literature, thus permitting to retrieve their asymptotic normality in an unified way.

6.3.2. Conditional extremal events

Participants: Stéphane Girard, Laurent Gardes, Alexandre Lekina, Eugen Ursu.

Joint work with: Amblard, C. (TimB in TIMC laboratory, Univ. Grenoble 1).

The goal of the PhD thesis of Alexandre Lekina is to contribute to the development of theoretical and algorithmic models to tackle conditional extreme value analysis, *ie* the situation where some covariate information X is recorded simultaneously with a quantity of interest Y. In such a case, the tail heaviness of Y depends on X, and thus the tail index as well as the extreme quantiles are also functions of the covariate. We combine nonparametric smoothing techniques [51] with extreme-value methods in order to obtain efficient estimators of the conditional tail index [9] and conditional extreme quantiles [56]. Conditional extremes are studied in climatology where one is interested in how climate change over years might affect extreme temperatures or rainfalls. In this case, the covariate is univariate (the time). Bivariate examples include the study of extreme rainfalls as a function of the geographical location. The application part of the study is joint work with the LTHE (Laboratoire d'étude des Transferts en Hydrologie et Environnement) located in Grenoble. The obtained results are submitted for publication [54].

More future work will include the study of multivariate and spatial extreme values. To this aim, a research on some particular copulas [1], [11] has been initiated with Cécile Amblard, since they are the key tool for building multivariate distributions [61].

6.3.3. Level sets estimation

Participants: Stéphane Girard, Laurent Gardes.

Joint work with: Daouia, A. (Univ. Toulouse I) and Jacob, P. (Univ. Montpellier II).

The boundary bounding the set of points is viewed as the larger level set of the points distribution. This is then an extreme quantile curve estimation problem. We propose estimators based on projection as well as on kernel regression methods applied on the extreme values set, for particular set of points. Our work is to define similar methods based on wavelets expansions in order to estimate non-smooth boundaries, and on local polynomials [17] estimators to get rid of boundary effects. Besides, we are also working on the extreme quantile to more general sets of points. To this end, we focus on the family of conditional heavy tails. An estimator of the conditional tail index has been proposed [9] and the corresponding conditional extreme quantile estimator has been derived [56] in a fixed design setting. The extension to the random design framework is investigated in [49]. This work has been initiated in the PhD work of Laurent Gardes [53], co-directed by Pierre Jacob and Stéphane Girard.

6.3.4. Dimension reduction

Participants: Stéphane Girard, Laurent Gardes, Mathieu Fauvel.

To overcome the curse of dimensionality arising in high-dimensional regression problems, one way consists in reducing the problem dimension. To this end, Sliced Inverse Regression (SIR) is an interesting solution. The original method, however, requires the inversion of the predictors covariance matrix. In case of collinearity between these predictors or small sample sizes compared to the dimension, the inversion is not possible and a regularization technique has to be used. We thus develop a new approach [13] based on a Fisher Lecture given by R.D. Cook where it is shown that SIR axes can be interpreted as solutions of an inverse regression problem. In this paper, a Gaussian prior distribution is introduced on the unknown parameters of the inverse regression problem in order to regularize their estimation. We show that some existing SIR regularizations can enter our framework, which permits a global understanding of these methods. Three new priors are proposed leading to new regularizations of the SIR method. Results are compared with the Support Vector Machine (SVM) approach on hyperspectral data [12].

6.3.5. Nuclear plants reliability

Participants: Laurent Gardes, Stéphane Girard.

Joint work with: Perot, N., Devictor, N. and Marquès, M. (CEA).

One of the main activities of the LCFR (Laboratoire de Conduite et Fiabilité des Réacteurs), CEA Cadarache, concerns the probabilistic analysis of some processes using reliability and statistical methods. In this context, probabilistic modelling of steels tenacity in nuclear plants tanks has been developed. The databases under consideration include hundreds of data indexed by temperature, so that, reliable probabilistic models have been obtained for the central part of the distribution. However, in this reliability problem, the key point is to investigate the behavior of the model in the distribution tail. In particular, we are mainly interested in studying the lowest tenacities when the temperature varies (Figure 7).

This work is supported by a research contract (from December 2008 to December 2010) involving MISTIS and the LCFR.

6.3.6. Quantifying uncertainties on extreme rainfall estimations

Participants: Eugen Ursu, Laurent Gardes, Stéphane Girard.

Joint work with: Molinié, G. from Laboratoire d'Etude des Transferts en Hydrologie et Environnement (LTHE), France.

Extreme rainfalls are generally associated with two different precipitation regimes. Extreme cumulated rainfall over 24 hours results from stratiform clouds on which the relief forcing is of primary importance. Extreme rainfall rates are defined as rainfall rates with low probability of occurrence, typically with higher mean return-levels than the maximum observed level. For example Figure 8 presents the return levels for the Cévennes-Vivarais region. It is then of primary importance to study the sensitivity of the extreme rainfall estimation to the estimation method considered. A preliminary work on this topic is available in [54]. MISTIS got a Ministry grant for a related ANR project (see Section 8.2).

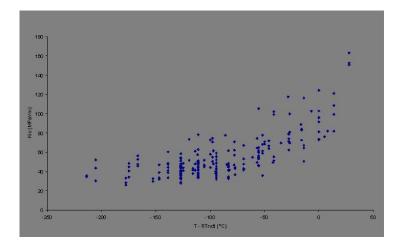


Figure 7. Tenacity as a function of the temperature.

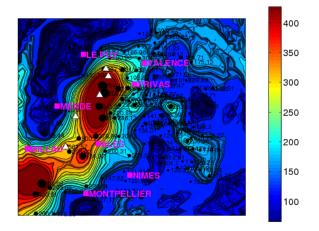


Figure 8. Map of the mean return-levels (in mm) for a period of 10 years.

6.3.7. Retrieval of Mars surface physical properties from OMEGA hyperspectral images.

Participants: Mathieu Fauvel, Laurent Gardes, Stéphane Girard.

Joint work with: Douté, S. from Laboratoire de Planétologie de Grenoble, France in the context of the VAHINE project (see Section 8.2).

Visible and near infrared imaging spectroscopy is one of the key techniques to detect, to map and to characterize mineral and volatile (eg. water-ice) species existing at the surface of the planets. Indeed the chemical composition, granularity, texture, physical state, etc. of the materials determine the existence and morphology of the absorption bands. The resulting spectra contain therefore very useful information. Current imaging spectrometers provide data organized as three dimensional hyperspectral images: two spatial dimensions and one spectral dimension. Our goal is to estimate the functional relationship F between some observed spectra and some physical parameters. To this end, a database of synthetic spectra is generated by a physical radiative transfer model and used to estimate F. The high dimension of spectra is reduced by Gaussian regularized sliced inverse regression (GRSIR) to overcome the curse of dimensionality and consequently the sensitivity of the inversion to noise (ill-conditioned problems). This method is compared with the more classical SVM approach. GRSIR has the advantage of being very fast, interpretable and accurate [12]. Recall that SVM approximates the functional F: y = F(x) using a solution of the form $F(x) = \sum_{i=1}^{n} \alpha_i K(x, x_i) + b$, where x_i are samples from the training set, K a kernel function and $((\alpha_i)_{i=1}^n, b)$ are the parameters of F which are estimated during the training process. The kernel K is used to produce a non-linear function. The SVM training entails minimization of $\left[\frac{1}{n}\sum_{i=1}^{\ell}l\left(F(x_{i}),y_{i}\right)+\lambda\|F\|^{2}\right]$ with respect to $((\alpha_i)_{i=1}^n, b)$, and with l(F(x), y) = 0 if $|F(x) - y| \le \epsilon$ and $|F(x) - y| - \epsilon$ otherwise. Prior to running the algorithm, the following parameters need to be fitted: ϵ which controls the resolution of the estimation, λ which controls the smoothness of the solution and the kernel parameters (γ for the Gaussian kernel).

6.3.8. Statistical analysis of hyperspectral multi-angular data from Mars

Participants: Mathieu Fauvel, Florence Forbes, Laurent Gardes, Stéphane Girard.

Joint work with: Douté, S. from Laboratoire de Planétologie de Grenoble, France in the context of the VAHINE project (see Section 8.2).

A new generation of imaging spectrometers is emerging with an additional angular dimension, in addition to the three usual dimensions, two spatial dimensions and one spectral dimension. The surface of the planets will now be observed from different view points on the satellite trajectory, corresponding to about ten different angles, instead of only one corresponding usually to the vertical (0 degree angle) view point. Multi-angle imaging spectrometers present several advantages: the influence of the atmosphere on the signal can be better identified and separated from the surface signal on focus, the shape and size of the surface components and the surfaces granularity can be better characterized. However, this new generation of spectrometers also results in a significant increase in the size (several tera-bits expected) and complexity of the generated data. To investigate the use of statistical techniques to deal with these generic sources of complexity, we made preliminary experiments using our HDDC technique on a first set of realistic synthetic 4D spectral data provided by our collaborators from LPG. It appeared that this data set was not relevant for our study due to the fact that the simulated angular information provided was not discriminant and could not allow us to draw useful conclusions. Further experiments on other data sets are then necessary.

7. Contracts and Grants with Industry

7.1. Contracts

We signed in December 2006 a three-year CIFRE contract with Xerox, Meylan, regarding the PhD work of Laurent Donini about statistical techniques for mining logs and usage data in a print infrastructure. The thesis is co-advised by Stéphane Girard and Jean-Baptiste Durand. The results are submitted for publication [48].

We signed in December 2008 a two-year contract with the LCFR (Laboratoire de Conduite et Fiabilité des Réacteurs), CEA Cadarache, see Subsection 6.3.5.

8. Other Grants and Activities

8.1. National Actions

MISTIS participates to the weekly statistical seminar of Grenoble, F. Forbes is one of the organizers and several lecturers have been invited in this context.

8.2. National initiatives

MISTIS got, for the period 2008-2010, Ministry grants for two projects supported by the French National Research Agency (ANR):

- MDCO (Masse de Données et Connaissances) program. This three-year project is called "Visualisation et analyse d'images hyperspectrales multidimensionnelles en Astrophysique" (VAHINE). It aims at developing physical as well as mathematical models, algorithms, and software able to deal efficiently with hyperspectral multi-angle data but also with any other kind of large hyperspectral dataset (astronomical or experimental). It involves the Observatoire de la Côte d'Azur (Nice), and several universities (Strasbourg I and Grenoble I). For more information please visit the associated web site: http://mistis.inrialpes.fr/vahine/dokuwiki/doku.php.
- VMC (Vulnérabilité : Milieux et climats) program. This three-year project is called "Forecast and projection in climate scenario of Mediterranean intense events: Uncertainties and Propagation on environment" (MEDUP) and deals with the quantification and identification of sources of uncertainties associated with the forecast and climate projection for Mediterranean high-impact weather events. The propagation of these uncertainties on the environment is also considered, as well as how they may combine with the intrinsic uncertainties of the vulnerability and risk analysis methods. It involves Météo-France and several universities (Paris VI, Grenoble I and Toulouse III). (http://www.cnrm.meteo.fr/medup/).

MISTIS is also a partner of a new three-year MINALOGIC project (I-VP for Intuitive Vision Programming) supported by the French Government. The project is led by VI Technology (http://www.vitechnology.com), a world leader in Automated Optical Inspection (AOI) of a broad range of electronic components. The other partners involved are the CMM (Centre de Morphologie Mathematiques) in Fontainebleau, and Pige Electronique in Bourg-Les-Valence. The NOESIS company, which is a leader in the field of image processing and analysis software, in Crolles, is also involved to provide help with software development. The overall goal is to exploit more intensively statistical and image processing techniques to improve defect detection capability and programming time based on existing AOI principle so as to reach eventually a reliable defect detection with virtually zero programming skills and efforts.

MISTIS is also involved in another 3three-year MINALOGIC project, called OPTYMIST-II, through the coadvising, with Dominique Morche from LETI, of Julie Carreau's Post-doctoral subject. The goal is to address variability issues when designing electronic components.

8.3. International initiatives

8.3.1. North Africa

S. Girard has joint work with M. El Aroui (ISG Tunis).

8.3.2. North America

F. Forbes has joint work with C. Fraley and A. Raftery (Univ. of Washington, USA).

8.3.3. Europe

S. Girard has also joint work with Prof. A. Nazin (Institute of Control Science, Moscow, Russia).

9. Dissemination

9.1. Leadership within scientific community

Since September 2009, F. Forbes is head of the committee in charge of examining post-doctoral candidates at INRIA Grenoble Rhône-Alpes ("Comité des Emplois Scientifiques").

Since September 2009, F. Forbes is also a member of the INRIA national committee, "Comité d'animation scientifique", in charge of analyzing and motivating innovative activities in Applied mathematics.

F. Forbes is part of an INRA (French National Institute for Agricultural Research) Network (MSTGA) on spatial statistics.

She is also part of an INRA committee (CSS MBIA) in charge of evaluating INRA researchers once a year.

S. Girard is member of the committees (Comité de Sélection) in charge of examining applications to Faculty member positions at University Lille I, University Pierre Mendes France (UPMF, Grenoble II) and University Montpellier II.

S. Girard was involved in the PhD commitee of Dmitri Novikov University Montpellier II (December 2009). He is also co-advisor (with Armelle Guillou) of Gilles Stupfler's PhD thesis "Estimation de la probabilité de ruine", University of Strasbourg, since september 2009.

F. Forbes was involved in the PhD committee of Eric Durand from TimB, Joseph Fourier university (September 2009).

S. Girard was elected in 2009 as a member of the bureau of the "Analyse d'images, quantification, et statistique" group in the Société Française de Statistique (SFdS).

S. Girard was selected as an expert for the Agence Nationale de la Recherche (ANR), programme Blanc.

S. Girard was a member of the scientific committee of the "Société Francophone de Classification" 16th conference.

M. Fauvel and F. Forbes were members of the organization committee for the IEEE WHISPERS-09 Conference (Grenoble, France). M. Fauvel was the chairman of the oral session "Hyperspectral data for planetary exploration".

F. Forbes was a member of the organisation committee for the IEEE Signal Processing Society conference: Machine Learning for Signal Processing (MLSP 2009) in Grenoble. She organized with W. Pieczynski from INT, a special session on "New trends in Markov models and related learning to restore data" [29].

9.2. Actions Funded by the EC

F. Forbes and S. Girard are members of the Pascal Network of Excellence.

S. Girard is a member of the European project (Interuniversity Attraction Pole network) "Statistical techniques and modelling for complex substantive questions with complex data", Web site : http://www.stat.ucl.ac.be/IAP/frameiap.html.

MISTIS is involved in a new three-year European project (STREP) starting from January 2010, named HU-MAVIPS (Humans ables with auditory and visual abilities in populated spaces) coordinated by Radu Horaud from INRIA team Perception. The other partners are the Czech Technical University CTU Czech Republic, Aldebaran Robotics ALD France, Idiap Research Institute Idiap Switzerland and Bielefeld University BIU Germany. The goal is to develop humanoid robots with integrated audio-visual perception systems and social skills, capable of handling multi-party conversations and interactions with people in realtime.

9.3. Teaching

F. Forbes lectured a graduate course on the EM algorithm at Univ. J. Fourier, Grenoble I.

- L. Gardes and M.-J. Martinez are faculty members at Univ. P. Mendes-France.
- L. Gardes and S. Girard lectured a graduate course on Extreme Value Analysis at Univ. J. Fourier, Grenoble I.
- J.-B. Durand is faculty member at Ensimag (Grenoble INP).
- M. Fauvel is a temporary teacher at ENSE3 (Grenoble INP).

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