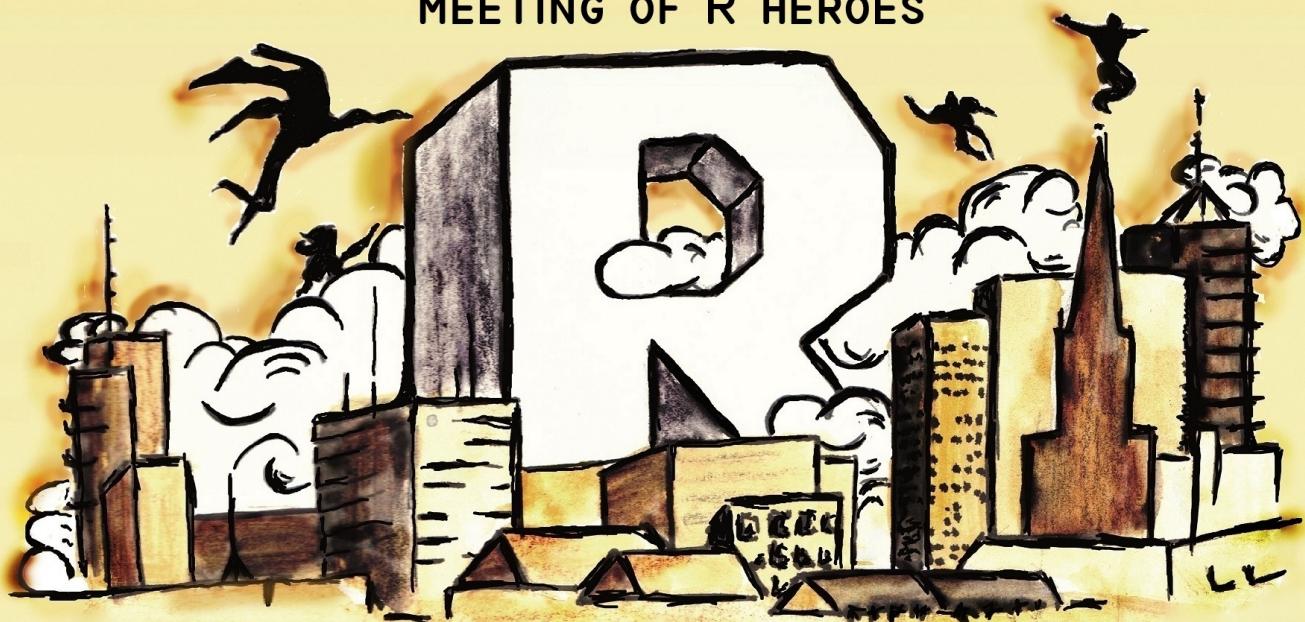


# EUROPEAN R USERS MEETING ERUM 2016

POZNAN | POLAND  
OCTOBER 12-14

MEETING OF R HEROES



Poznań University of Life Sciences



POZNAŃ UNIVERSITY  
OF ECONOMICS  
AND BUSINESS



**ESTYMATOR**  
STUDENCKIE KOŁO NAUKOWE



eRum 2016  
european R users meeting

October 12-14, 2016 in Poznan, Poland



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## The Organizing Committee

**Maciej Beręsewicz (Chair), Poznan University of Economics and Business**

Adolfo Alvarez, *Analyx*

Przemysław Biecek, *MIM University of Warsaw, MiNI Warsaw University of Technology*

Marcin Dyderski, *Institute of Dendrology of the Polish Academy of Sciences, Poznan University of Life Sciences*

Marcin Kosiński, *Warsaw R Enthusiasts*

Jakub Nowosad, *Adam Mickiewicz University in Poznan, University of Cincinnati*

Kamil Rotter, *SKN Estymator*

Alicja Szabelska-Beręsewicz, *Poznan University of Life Sciences*

Marcin Szymkowiak, *Poznan University of Economics and Business*

Łukasz Wawrowski, *Poznan University of Economics and Business*

Joanna Zyprych-Walczak, *Poznan University of Life Sciences*



# Welcome to eRum 2016

Dear participant,

Welcome to the European R users meeting *eRum 2016* which will be held at Poznan University of Economics and Business, Poland, 13-14 October 2016.

In addition, a series of short training courses will take place the day before the start of the Conference (12 October 2016).

Conferences succeed through the contributions of their participants. So we are happy to offer you an interesting and broad program. Owing to the overwhelming response to our call for papers, most sessions will run in parallel. The Conference aims to cover relevant and innovative topics including: Bayesian Statistics, Bioinformatics, Economics, Finance and Insurance, Industrial Applications, Spatial Statistics, and many more.

Besides the scientific program, the eRum Conference will be held in a familial atmosphere. There will be a poster session on Thursday evening with a Welcome paRty. The Saturday sightseeing tour will take us to the most famous places in Poznan. Your stay in Poznan will be an opportunity to enjoy other cultural activities in Poznan.

The Conference website provides information about the conference venue, accommodation, short courses, and leisure-time activities as well as deadlines for submission of papers.

Dr. Maciej Beresewicz

Chair of the Organising Committee  
Department of Statistics  
Poznan University of Economics and Business



## List of venues

12th of September:

- Poznan University of Life Sciences, Wojska Polskiego street 28;
- Statistical Office in Poznan, Wojska Polskiego street 27/29;
- **Registration:** Collegium Maximum, ground floor (Wojska Polskiego street 28)

13th - 14th of September:

- Poznan University of Economics and Business, Niepodleglosci avenue 10;
- **Registration:** Main Building, ground floor (Niepodleglosci avenue 10)

13th of September:

- INEA Stadium, Bułgarska street 17

14th of September:

- "Piwna Stopa" Pub, Szewska street 7



# Program at glance

Day 1 Workshops 12.10	8:00 - 9:00	Registration	
	9:00 - 12:30	Workshops at University of Life Sciences and Statistical Office	
	12:30 - 13:30	Registration and Lunch break ( <b>not included in fees</b> )	
	13:30 - 17:00	Workshops at University of Life Sciences and Statistical Office	
	Hours	Room AULA	Room 111A
Day 2 Conference 13.10	8.00 - 8:40	Registration + Coffee - sponsored by <i>Quantide</i>	
	8:40 - 9:00	Welcome session (AULA)	
	9:00 - 10:10	<b>Invited Talks I - Heather Turner + Katarzyna Stapor (AULA) - Chairman: Rasmus Bååth</b>	
	10:10 - 10:20	Group photo in front of the main entrance to the venue	
	10:20 - 10:45	Coffee Break - sponsored by <i>eoda</i>	
	10:45 - 12:15	Methodology 1	Business 1
	12:15 - 13:30	Lunch Break - sponsored by <i>McKinsey</i>	
	13:30 - 14:40	<b>Invited Talks II - Rasmus Bååth + Jakub Glinka (AULA) - Chairman: Katarzyna Kopczewska</b>	
	14:40 - 15:00	Fast coffee break - sponsored by <i>Analyx</i>	
	15:00 - 16:30	Methodology 2	Business 2
	16:30 - 17:00	Coffee Break - sponsored by <i>WLOG Solutions</i>	
	17:00 - 18:10	<b>Invited Talks III - Ulrike Grömping + Przemysław Biecek (AULA) - Chairman: Heather Turner</b>	
	18:20 - 19:45	Methodology 3	Data Workflow 1
	19:50	Buses to the Welcome paRty Venue	
Day 3 Conference 14.10	20:00+	Welcome paRty + poster session - sponsored by <i>McKinsey</i>	
	Hours	Room AULA	Room 407A
	8.00 - 8:30	Registration + coffee - sponsored by <i>Rstudio</i>	
	8:30 - 9:40	<b>Invited Talks IV - Romain François + Marek Gagolewski (AULA) - Chairman: Matthias Templ</b>	
	9:40 - 10:00	Fast coffee Break - sponsored by <i>DataCamp</i>	
	10:00 - 11:10	<b>Invited Talks V - Matthias Templ + Katarzyna Kopczewska (AULA) - Chairman: Katarzyna Stapor</b>	
	11:10 - 12:20	Sponsors session (AULA)	
	12:20 - 13:30	Lunch Break - sponsored by <i>Microsoft</i>	
	13:30 - 15:00	Lightning talks	Data Workflow 2
	15:00 - 15:20	Closing session (AULA)	
Day 4 Facultative tour 15.10	19:00+	A closing get-together with the organisers over beer in the City Center (facultative, not included in fee)	
	10:00 - 14:00	Sightseeing tour (facultative, extra fee)	





# Full Program

Session	Name	Surname	Title	Chairman
Invited Talks I	Heather	Turner	Addressing the Gender Gap in the R Project	Rasmus Bååth  Katarzyna Kopczewska  Heather Turner  Matthias Templ  Katarzyna Stapor
Invited Talks I	Katarzyna	Stapor	Heteroscedastic Discriminant Analysis and its integration into “mlr” package for uniform machine learning	
Invited Talks II	Rasmus	Bååth	A survey of tools for Bayesian data analysis in R	
Invited Talks II	Jakub	Glinka	Browse Till You Die: Scalable Hierarchical Bayesian Modeling of cookie deletion	
Invited Talks III	Ulrike	Grömping	Design of Experiments in R	
Invited Talks III	Przemysław	Biecek	How to use R to hack the publicly available data about skills of 2M+ worldwide students?	
Invited Talks IV	Romain	François	R and C++	
Invited Talks IV	Marek	Gagolewski	Genie: A new, fast, and outlier-resistant hierarchical clustering algorithm and its R interface	
Invited Talks V	Matthias	Templ	Simulation of complex synthetic data with the R package simPop	
Invited Talks V	Katarzyna	Kopczewska	Geo-located point data: measurement of agglomeration and concentration	
Business 1	Michał	Zylinski	Turning R into production – make your models reality	Adolfo Alvarez  Łukasz Wawrowski
Business 1	Łukasz	Grala	RevoScaleR - performance and scalability R	
Business 1	Wit	Jakuczun	Bringing R to Enterprise	
Business 1	Erik	Barzagari-Nazari	Data science outside the box: Developing a generic scoring algorithm for customer acquisition	
Business 1	Andreas	Wygrabek	Embedding R in business processes	
Business 2	David	Kun	Enterprise R Platform – the what, the why and the how	
Business 2	Oliver	Bracht	R in the Mittelstand: Bringing Data Science to small and mid-size companies	
Business 2	Paweł	Ładyżyński	R tools and tricks for marketing inference in a big internet company	
Business 2	Michał	Bryś	Using Google Analytics with R	
Business 2	Piotr	Wójcik	Using R for backtesting algorithmic trading strategies on high-frequency data	

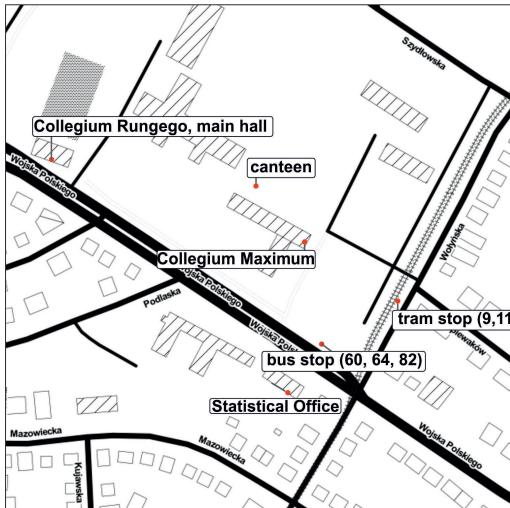
Data Workflow 1	Olgun	Aydin	Dynamic Inflation Rate Calculation of Fast-Moving Consumer Goods: Shiny-SparkR App	Marcin Kosiński
Data Workflow 1 Data Workflow 1	Michał Anna	Maj Wróblewska	Introduction to RDruid Search phrases in e-commerce platform allegro.pl - big data analysis using SparkR	
Data Workflow 1	Natalia	Potocka	The full process of creating an R application in recommendation systems: from Dockerfile to Zabbix monitoring	
Data Workflow 2	Pawel	Cejrowski	Power of Java's RSession and rKafka in the data science team collaboration	Marcin Dyderski
Data Workflow 2	Ming	Shan	R Shiny for Real-time Analytics and Insight Delivery – A Solution for Complex Data in Agriculture	
Data Workflow 2	Adam	Ryczkowski	Seamless external R server integration with Excel with step-by-step debugging of the R code	
Data Workflow 2	Filip	Stachura	Workflow around modelling in Data Science / R	
Methodology 1	Maren	Eckhoff	Predicting machine failures	Marcin Szymkowiak
Methodology 1	Mateusz	Filarowski	Ensemble learning - idea and applications	
Methodology 1	Tomasz	Smolarczyk	Ensemble learning - implementation with mlr	
Methodology 2	Emilio L.	Cano	Unattended SVM parameters fitting for monitoring nonlinear profiles	Maciej Beręsewicz
Methodology 2	Philipp	Thomann	SimonsSVM: A Fast and Scalable Support Vector Machine Implementation for R	
Methodology 2	Daniel Tomasz	Guhl Górecki	Discrete Choice Models in R	
Methodology 2	Christoph Adolfo	Hoffmann Alvarez	Multivariate analysis of variance for functional data using R	
Methodology 3	Maciej Marcin	Beręsewicz Dyderski	Text Mining in R	Tomasz Klimanek
Methodology 3	Gero	Szepannek	Classic and network based cluster analysis: together we're better	
Methodology 3			M-quantile regression in R	
Methodology 3			Is forest a pharmacy? - problems with data analyses	
Packages 1	Rob	Hyndman	k Prototypes Clustering of Mixed Type Data	
Packages 1	Robin	Lovelace	Reconciling forecasts: the hts package	Tomasz Górecki
Packages 1	Paul- Christian	Buerkner	splanr: an R package for transport planning	
Packages 1	Sebastian	Warnholz	brms: An R Package for Bayesian Multilevel Models using Stan	
			Modules in R	

Packages 1	Massimiliano	Pastore	influence.SEM 2.0: An R Package for Sensitivity Analysis in Structural Equation Models	
Packages 2	Rebecca	Killick	EnvCpt: An R package for changepoint identification in Environmental data	Marek Gałkowski
Packages 2	Marcin	Kosiński	archivist 2.0: News from Managing Data Analysis Results Toolkit	
Packages 2	Kamil	Wais	LimeRick: Bridge between LimeSurvey and R	
Packages 2	Rebhi	Ibtihel	An R package for consumer and sensory mapping: comparison of preference mapping stability	
BioR	Pawel	Łabaj	Are we ready for Personalized Medicine?	Przemysław Biecek
BioR	Michał	Burdukiewicz	N-gram analysis of biological sequences in R	
BioR	Stefan	Rödiger	R as an Environment for the Reproducible Analysis of DNA Amplification Experiments	
BioR	Marek	Wiewiórka	Big data genomics data warehouses analyses with R	
BioR	Michał	Okoniewski	Using SparkR with distributed database in Parquet - a genomic example	
Education Learning	Filip	Schouwenaars	Revolutionize how you teach and blog: add interactivity	Alicja Szabelska-Beręsewicz
Education Learning	Martin	Schneider	Aargh I have to teach R (Experiences in the teaching of R)	
Education Learning	Päivi	Julin	Using R for artistic purposes	
Education Learning	Kamil	Krawczyk	Polish Diet Commissions - Text Analysis	
Lightning talks	Agnieszka	Borsuk	R as a tool for graphical diagnostics in population pharmacokinetic modeling	Joanna Zyprych-Walczak
Lightning talks	Bartosz	Czernecki	Machine learning modeling of phenological phases in Poland	
Lightning talks	Paweł	Kleka	Latent Class Analysis in Psychology	
Lightning talks	Bogumil	Konopka	Exploratory data analysis of a clinical study group - revealing patient subgroups.	
Lightning talks	Alexander	Kruse	Multidimensional Clustering of Web Analytics Data	
Lightning talks	Giovanni	Lotti	R shiny server as core of multiple technologies into Travel Industry.	
Lightning talks	George	Moroz	Turning Text Mining into Language Mining: Corpus Linguistics in R	
Lightning talks	Paweł	Piątkowski	Structural bioinformatician's notebooks with pdbeeR and knitr	
Lightning talks	Paul	Roback	Using R to incorporate data science into the undergraduate statistics curriculum	

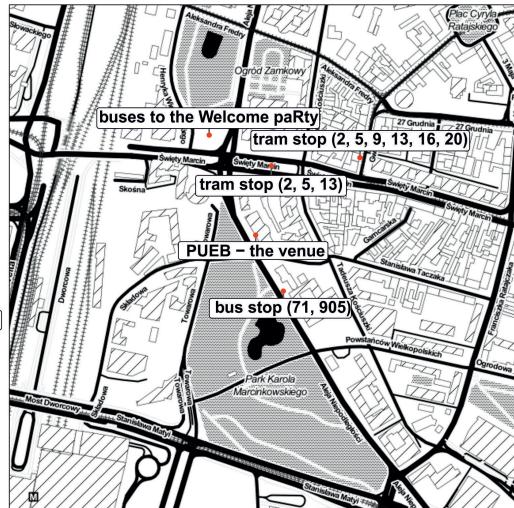
Lightning talks	Luigi	Lombardi	Analysing the statistical effects of manipulated data	
Lightning talks	Jeroen	Ooms	Cryptography in R	
Lightning talks	Piotr	Sobczyk	Visualizing changes in demographics with R	
Lightning talks	Zofia	Tylutki	R for pharmacokineticists - simulation of steady-state concentrations of amiodarone in heart compartmental model as an example.	
Poster session	Damian	Chmura	What are sampling errors in the vegetation studies using visual estimation of presence and cover of plants? R can help	
Poster session	Carolina	Correia	RNA-seq transcriptional profiling of PPD-b-stimulated peripheral blood from cattle infected with <i>Mycobacterium bovis</i>	
Poster session	Emilia	Daghir-Wojtkowiak	Pharmacokinetics-driven modeling of metabolomics data	
Poster session	Anna	Dmowska	R as a tool for geospatial modeling in large dataset - example of dasymetric modeling at a continental scale (United States)	
Poster session	Dimitri	Fichou	Application of Artificial Neural Network to Planar Chromatography Data	
Poster session	Jagoda	Jabłońska	cgmisc: enhanced genome-wide association analyses and visualization	
Poster session	Marta	Karas	Penalized regression inference regarding variable selection in regular and high dimensions: comparison of selected methods implemented in R	
Poster session	Wojciech	Kędziora	Wrestling with big data in forestry: use of R in Scots pine site index analysis.	
Poster session	Tomasz	Owczarek	An R implementation of Kauffman's NK model	
Poster session	Anna	Rybińska	R as an effective data mining tool in chemistry	
Poster session	Fabián	Santos	Applying genetic algorithms to calibrate a processing chain for a Landsat-based time series analysis of disturbance - regrowth dynamics in tropical forests	
Poster session	Sylwia	Wierzcholska	Modelling the distribution of the bryophytes in different spatial scales	
Poster session	Daniel	Rabczenko	Mortality mapping using R	

# Workshops

**Workshops venue**



**Conference venue**



**Morning workshops (9:00 - 12:30)**

	Location
Warsztaty wprowadzające do R (in Polish) - Adam Dąbrowski	Collegium Maximum, room 157
Predictive modeling with R - Artur Suchwałko	Collegium Rungeo, main hall
Data Visualization using R - Matthias Templ	Statistical Office
R for expression profiling by Next Generation Sequencing - Paweł Łabaj	Collegium Maximum, room 254
Time series forecasting with R - Adam Zagdański	Collegium Maximum, room 253

**Afternoon workshops (9:00 - 12:30)**

	Location
Introduction to Bayesian Statistics with R and Stan - Rasmus Bååth	Collegium Rungeo, main hall
Small Area Estimation with R - Virgilio Gómez-Rubio	Collegium Maximum, room 157
R for industry and business: Statistical tools for quality control and improvement - Emilio L. Cano	Collegium Maximum, room 253
An introduction to changepoint models using R - Rebecca Killick	Statistical Office
Visualising spatial data with R: from 'base' to 'shiny' - Robin Lovelace	Collegium Maximum, room 254





## Social Events

We would like to kindly invite you to participate in the following social events:

1. Thursday, 13.10 at 20:00 — Welcome paRty (only for the conference participants, included in the conference fee):

- The Welcome paRty will be held on 13th of October between 20:00 and 2:00;
- The venue is the INEA Stadium, the stadium of Lech Poznań football club (Bułgarska street 17);
- Buses will take conference participants to the Welcome paRty at 19:45 from Plac Mickiewicza (see maps);
- A poster session will be held during the welcome paRty;
- It will be possible to take a tour of the stadium for 10 PLN / person (not included in the fee, only Polish currency is accepted) during the welcome paRty. The tour takes about 1 hour and a maximum of 40 persons can take a part. During the tour you can see, among other things, the conference hall, the locker room for guest teams, the pitch, the Lodge of Presidents, the Hall of Fame, and the Press Tribune.

We've arranged buses to take you from the Venue to the City Center that will depart at 23:30, 00:00, 00:30, 01:00, 01:30, and 02:00. If you would like to return earlier, you should consider taking tram 13 or 15 that leaves from the stop "Inea Stadion".

2. Friday, 15.10 at 19:00 — A closing get-together with the organisers over a beer in the City Center (for all participants, facultative, not included in fees). We kindly invite you to "Piwna Stopa" Pub located in Szewska street 7.
3. Saturday, 16.10 at 9:50 — A sightseeing tour in the center of Poznań (for all participants, facultative, not included in the conference fee). The total cost of the tour and lunch is 50 PLN / 15 EUR, and should be paid in cash during the registration. The program is the following:
  - 09:50 – 12:50 Sightseeing tour, starting point at University of Economics (Niepodległości avenue 10);
  - 13.00 – 14.30 Lunch at Chłopskie Jadło restaurant (Fredry street 12).



## **Invited Talks**

### *Room AULA*

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## **Addressing the Gender Gap in the R Project**

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**Heather Turner<sup>1\*</sup>**

1. University of Warwick

\*Contact author: ht@heatherturner.net

**Keywords:** R community; package development

Despite **R**'s origins in the discipline of statistics and the strong uptake of **R** in fields such as ecology and genomics, where women are well represented in the workforce, the **R** developer community looks more like that of computer science generally, where women are in a distinct minority. If we consider contributions to the **R** project, the situation is even worse. How can we encourage more women to become developers and leaders in the **R** community?

Earlier this year the **R** Foundation, a not-for-profit organisation set up to support the **R** project (<https://www.r-project.org/foundation/>), established a task force to explore this question and to take actions to address the gender gap (<http://forwards.github.io/>; <https://twitter.com/RWomenTaskforce>). In this talk I will give an overview of the activities of the taskforce so far and our plans for the future. I will also share some tips for women looking to get more involved and ideas of ways everyone can help to make our community more inclusive.

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## Heteroscedastic Discriminant Analysis and its integration into ‘mlR’ package for uniform machine learning

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Katarzyna Stapor<sup>1\*</sup>

1. Institute of Computer Science, Silesian Technical University

\*Contact author: katarzyna.stapor@polsl.pl

**Keywords:** discriminant analysis; machine learning; heteroscedasticity

**R packages:** mlR

The *mlR* package (machine learning in **R**) offers a unified interface to access various machine learning algorithms from other packages in **R**. This framework provides supervised methods like classification, regression and survival analysis along with their corresponding evaluation and optimization methods, as well as unsupervised methods like clustering. It is written in a way that you can extend it yourself or deviate from the implemented convenience methods and construct your own complex experiments or algorithms. As an example, it will be shown how to integrate into the *mlr* package the new, proposed by us learner, the Heteroscedastic Discriminant Analysis (HDA), being the extension of the classical Fisher Linear Discriminant Analysis (FDA), implemented in the *base* package. HDA is the extension of FDA for dealing with the case of unequal covariance matrices in the populations, the situation that occurs very often in practice. The new implemented permutation test for testing the equality of covariance matrices will be also presented. Integration the new learner into *mlr* requires defining the learner itself with the name, description, parameters, and a few other things, then providing the function that calls the learner function and builds the model given the data, and finally, a prediction function that returns predicted values given new data. The example of usage the new HDA learner on the real world credit dataset will also be presented.

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## A survey of tools for Bayesian data analysis in R

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Rasmus Bååth<sup>1\*</sup>

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**Keywords:** Bayesian data analysis; MCMC

**R packages:** rjags; rstan; MCMCpack; R-INLA

Bayesian data analysis is an intuitive and straightforward framework for doing both inferential statistics and predictive analysis. Because of its popularity there is now a plethora of **R** packages for fitting Bayesian models. This talk will guide you through the jungle and survey some of the most useful tools for doing Bayesian data analysis in **R**. The talk will feature concrete code examples throughout and does not assume that you have much prior knowledge about Bayesian statistics.

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## Browse Till You Die: Scalable Hierarchical Bayesian Modeling of cookie deletion

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**Jakub Glinka<sup>1\*</sup>**

1. GfK SE, Nuremberg

\*Contact author: [Jakub.Glinka@gfk.com](mailto:Jakub.Glinka@gfk.com)

**Keywords:** hierarchical bayesian modeling; model based machine learning; consensus MCMC

**R packages:** rstan; parallelMCMCcombine; Rcpp

The common approach for tracking the device's on-line movement is through cookies - small portion of information stored within user Internet Browser. This enables Market Research companies to assign web browsing data to one specific browser. The main problem within cookie tracking framework is to assess whether on given day the lack of its activity is due to the real absence or deletion. In usual site-centric approach one can only observe cookie's digital footprint on limited number of media providers which leads to the highly skewed data, moreover the deletion moment is not directly observable. In order to deal with mentioned challenges we designed Hierarchical Bayes model of the cookie behavior that enables us to pose questions about the probability of the cookie deletion. We will present how it fits Model Based Machine Learning Paradigm and how one can efficiently estimate model coefficients using existing **R** packages.

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## Design of Experiments in R

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**Ulrike Grömping<sup>1\*</sup>**

1. Beuth University of Applied Sciences, Berlin

\*Contact author: groemping@bht-berlin.de

**Keywords:** design of experiments

**R packages:** agricolae; AlgDesign; conf.design; DiceDesign; DiceKriging; DoE.base; DoE.wrapper; ICAOD; lhs; OptimalDesign; planor; rsm; tgp

Starting with an example from the Obama electoral campaign, this talk initially introduces the main principles of experimental design and explains different types of designs suitable for different purposes. I then discuss the development of the landscape of packages on Design of Experiments in **R**, the current state of which is documented in the Experimental Design Task View (<http://cran.r-project.org/web/views/ExperimentalDesign.html>). That landscape is quite diverse, currently consisting of (at least) four larger areas and various specialized packages. Descendants and relatives of the pioneering packages *conf.design* (2001) and *AlgDesign* (2004) as well as the growing area of packages for computer experiments are considered in more detail, and recent additions based on modern optimization methods are discussed.

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## How to use R to hack the publicly available data about skills of 2M+ worldwide students?

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**Keywords:** visualisation; survey data; archivist; data mining

**R packages:** ggplot2; shiny; intsvy; archivist; knitr; BetaBit; PISA2012lite

During the talk I will introduce The Programme for International Student Assessment (PISA), an international survey that aims to evaluate education systems worldwide. It's a source of large data about educational performance and various other characteristics of over 2 000 000 students from 62 countries. The data from the last PISA assessment is available in the **R** package.

To play with it we will use packages and to explain the relation between parental occupation and student's performance. Then we will overview the package – the toolbox for statistical analyses of international surveys. Finally we will discuss applications of packages and the role of reproducibility and traceability of results. At the end I will introduce the project that aims to boost data science skills of students.

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## R and C++

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**Romain François<sup>1\*</sup>**

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**Keywords:** C++; high performance; Rcpp; dplyr

**R packages:** Rcpp; dplyr

*Rcpp* is now considered a major success in the **R** community. It allows easy connection between **R** and C++. I'll review some of its history and use cases (e.g. *dplyr*).

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## Genie: A new, fast, and outlier-resistant hierarchical clustering algorithm and its R interface

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**Keywords:** hierarchical clustering; single linkage; inequity measures; Gini-index

**R packages:** *genie*

The time needed to apply a hierarchical clustering algorithm is most often dominated by the number of computations of a pairwise dissimilarity measure. Such a constraint, for larger data sets, puts at a disadvantage the use of all the classical linkage criteria but the single linkage one. However, it is known that the single linkage clustering algorithm is very sensitive to outliers, produces highly skewed dendograms, and therefore usually does not reflect the true underlying data structure - unless the clusters are well-separated.

To overcome its limitations, we proposed a new hierarchical clustering linkage criterion called *genie*. Namely, our algorithm links two clusters in such a way that a chosen economic inequity measure (e.g., the Gini or Bonferroni index) of the cluster sizes does not increase drastically above a given threshold.

Benchmarks indicate a high practical usefulness of the introduced method: it most often outperforms the Ward or average linkage in terms of the clustering quality while retaining the single linkage speed. The algorithm is easily parallelizable and thus may be run on multiple threads to speed up its execution further on. Its memory overhead is small: there is no need to precompute the complete distance matrix to perform the computations in order to obtain a desired clustering. In this talk we will discuss its reference implementation, included in the *genie* package for **R**.

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## Simulation of complex synthetic data with the R package simPop

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**Matthias Templ<sup>1\*</sup>**

1. Vienna University of Technology

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**Keywords:** synthetic data; complex sample designs; population data; prediction

**R packages:** popSim

The production of synthetic datasets has been proposed as a statistical disclosure control solution to generate public use files out of protected data. This is also a tool to create “augmented datasets” to serve as input for micro-simulation models, and – more generally – the synthetic data sets can be used for design-based simulation studies in general. The performance and acceptability of such a tool relies heavily on the quality of the synthetic data, i.e. on the statistical similarity between the synthetic and the true population of interest. Multiple approaches and tools have been developed to generate synthetic data. These approaches can be categorized into three main groups: synthetic reconstruction, combinatorial optimization, and model-based generation. We introduce *simPop*, an open source data synthesizer. *simPop* is a user-friendly **R** package based on a modular object-oriented concept. It provides a highly optimized S4 class implementation of various methods, including calibration by iterative proportional fitting and simulated annealing, and modeling or data fusion by logistic regression, regression tree methods and many other methods.

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## Geo-located point data: measurement of agglomeration and concentration

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1. Faculty of Economic Sciences, Unievrsity of Warsaw

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**Keywords:** spatial location; agglomeration; specialization; SPAG; Ripley's K

**R packages:** rgeos; spdep; sp; rgdal; dbmss

Geo-located points, representing locations of business and other units can be analysed with regard to agglomeration and concentration patterns, which in fact indicate a density of region's coverage with the economic activity. There is plenty of measures on territorially aggregated data (so called cluster-based measures) and just few on geo-located individual data (so-called distance-based measures) as SPAG or Ripley's  $K$ . This is to present current possibilities of statistical analysis of geo-located data in **R**, as well its applications in regional science. It would consider the sensitivity of measures for different spatial patterns. Spatial package *rgeos* allows for treating points as geometries, what expands significantly the analytical capabilities. One can also see the neighbourhood relations between points, which can be applied further in econometric models.

## **Business 1**

*Room 111A - Chairman: Adolfo Alvarez*

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### **Turning R into production – make your models reality**

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**Michał Zylinski<sup>1\*</sup>**

1. Microsoft

\*Contact author: michałz@microsoft.com

**Keywords:** model deployment; Hadoop; scalability; interoperability; big data

Rapid popularity growth of **R** language among not only academic, but commercial communities poses also a few technical challenges. How to make **R** code interoperable and easily accessible to developer team? How to scale your models to sustain business needs? How to overcome initial hurdles, caused by introducing yet another technology stack? My talk will cover a few practical solutions that aim to resolve such difficulties in real-life scenarios.

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### **RevoScaleR - performance and scalability R**

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1. Poznań University of Technology

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**Keywords:** performance; scalability

**R packages:** RevoScaleR; RevoUtils; RevoUtilsMath; RevoMods; RevoTreeView; RevoPemaR

The Big Data scalability and performance are key issues. Microsoft Server **R** (HADOOP, Teradata, Spark) and **R** Services for SQL Server 2016 provides a set of libraries *RevoScaleR*.

During the session, we compare the performance and scalability CRAN **R** and *RevoScaleR* in typical applications.

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## Bringing R to Enterprise

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**Wit Jakuczun<sup>1\*</sup>**

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**Keywords:** enterprise; big scale solution; productivity; deployment

What does enterprise readiness mean? Is **R** enterprise ready? What are the components of efficient **R** architecture? How to manage development-test-deployment cycle? How to monitor and control **R** resources consumption? How to control safety in **R** based solutions?

In this short talk I will present summary of our 10+ years experience in delivering big scale solutions with **R**.

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## Data science outside the box: Developing a generic scoring algorithm for customer acquisition

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**Keywords:** data mining; customer acquisition; case study

One major task in virtually every predictive modelling project is to find the method best suited for the problem on hand. Luckily, most of the time data scientists can rely on one of the many already existing and well established methods such as Random Forests, Gradient Boosting Machines, Neural Networks or Support Vector Machines to solve a

variety of regression and classification problems. However, in some cases these standard approaches are not directly applicable to the problem on hand and data scientists need to become creative. In this talk, we will present a case study about a project we recently conducted for the databyte GmbH in Germany. As one of the leading business information providers, databyte maintains a vast database of several million companies, containing information such as revenue, size and many other properties. The aim of the project was to develop an application which, after provided with the customer base of a databyte client, would be able to score companies in the databyte database in order to identify the most promising contacts for direct marketing campaigns. While developing this application, we were facing two major requirements: first of all, each client has its own customer base, hence we could not just train one model; in fact, the algorithm must be able to ‘train itself’ in every run. Secondly, the customer base only contains ‘positive data’, that means we are dealing with a so-called positive-unlabelled-problem.

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## Embedding R in business processes

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**Andreas Wygrabek<sup>1\*</sup>**

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**Keywords:** business; process integration

There is no doubt about it: a variety of implemented statistical methods that are easy to access can make **R** a valuable tool for plenty application scenarios in business e.g. planning sales campaigns, monitoring machines, acceptance sampling on incoming goods or in-process control. All these scenarios are ruled by standardized business processes and tied with substantial financial risks. Beside the analytical capabilities of **R**, there are two main requirements on **R** that are important for companies: on the one hand **R** needs to be smoothly integrated into existing business processes. On the other hand, **R** needs to be a reliable part of the process chain: secure, easy to maintain, automatable and integrable into a right management system. Even though **R** reaches an incredible popularity many companies struggle to make **R** more than a proof of concept tool. The maturity level of **R** is reached when it has become crucial a part of business process chains. The talk will delight the main questions and critical issues of making **R** an essential link in a business process chain. Furthermore the talk will present some state of the art strategies to face the depicted issues regarding security, reliability and automatization in operating systems.



## Business 2

*Room 111A - Chairman: Łukasz Wawrowski*

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### Enterprise R Platform – the what, the why and the how

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**Keywords:** deployment; process; control; enterprise

**R packages:** base; roveR; shiny

In this talk we will introduce a concept for an Enterprise R Platform, starting with expectations towards such a platform, followed by the benefits and finally giving a reference implementation architecture and a case study. R users in enterprise settings are often building shadow IT, with no controls but also no access to efficient code sharing, automation, deployment, version control, etc. This also means that others in the enterprise cannot benefit from the R-based solutions. Our proposed architecture addresses all of these issues by introducing a playground for the R users and a deployment process supporting all the flexibility needed while subject to regular controls. Our solution also includes a way to separate the R projects within a single environment, so different versions of the same package can be installed for instance. Finally, by providing a REST API, we enable non-R users to embed the R-based tools in any other application in the enterprise, ranging from MS Excel via Java-based ETL tools like Informatica and MI/BI tools like Business Objects up to and including in-house solutions created in other languages.

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## R in the Mittelstand: Bringing Data Science to small and mid-size companies

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1. eoda GmbH

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**Keywords:** implementing R; R in business

Most success stories of **R** in business are told by either new economy companies or large international enterprises. However, there is another field where **R** can enable success. Small to midsize, mostly family owned, old economy companies: the Mittelstand. Besides its size, Mittelstand companies are characterized by their organisational culture, their value sets and their management philosophies. Hence, the introduction of Data Science in general and **R** in particular to Mittelstand companies needs to consider this specific characteristic in order to be successful. This talk will focus on patterns that Mittelstand companies typically follow when they implement **R**. Main challenges of the process as well as road blockers on the way will be pointed out. It will give practical advice with real world examples and finally propose strategies of how to achieve long term success.

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## R tools and tricks for marketing inference in a big internet company

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**Keywords:** marketing inference; clustering; big data; predictive modeling; feature engineering; feature selection

**R packages:** data.table; dplyr; ggplot2; h2o; rmarkdown; shiny

Data is becoming an integral part of digital marketing, as businesses realize the power of information to create successful campaigns and see real-time results. In 2016, big

data continues its growth as an important part of supporting business decisions. Armed with information on customer behaviors and purchases, we are now able to build profiles or user personas which ensure each marketing effort is geared toward a specific type of customer. However, the crucial part of business reasoning is to examine large data sets to uncover hidden patterns, unknown correlations, market trends, customer preferences and other useful business information. This step is usually connected with looking for new libraries or packages which performance is good enough to deal with large amounts of data. Fortunately, there are many **R** packages, like *data.table* or *h2o*, which enables **R** to be involved in the big data reasoning process.

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## Using Google Analytics with R

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**Michał Brys<sup>1\*</sup>**

1. Allegro

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**Keywords:** Google analytics; web analytics; Google Analytics API

**R packages:** plotly; ggplot2; RGoogleAnalytics

How to download data from Google Analytics to **R** via API and create more than standard analysis using data visualisation and machine learning.

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## Using R for backtesting algorithmic trading strategies on high-frequency data

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**Keywords:** algorithmic trading; high-frequency data; backtesting; efficient calculations

**R packages:** xts; chron; quantmod; Rbbg; IBrokers; TFX; tseries; PerformanceAnalytics; caTools; TTR; inline; Rccp; RcppArmadillo

Along with the advances in computer technology high-frequency trading developed in 1990s and became widely popular since then. Traders started to build algorithms that use highly developed quantitative models to automatically determine when and where to trade. The profitability of trading strategies based on such algorithms needs to be verified on historical data (backtested) prior to its application in real life. Intraday data in finance may have large volumes (up to 1440 minutes or 86400 seconds of quotations every day, i.e. 20 millions of observations for one year). In addition, developed algorithms are usually parametrized and their final version needs to be optimized with respect to these parameters. This introduces a possibly huge number of combinations that need to be compared with respect to selected performance measures. Large amounts of data and many variants of the algorithm require a computationally efficient tool that should also allow to relatively easily apply statistical models. And **R** together with C++ can provide such a tool. The presentation shows how **R** can be used to access intraday data and to develop and backtest different algorithmic trading strategies with the help of *Rcpp* family packages.

# Data Workflow 1

*Room 111A - Chairman: Marcin Kosiński*

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## **Dynamic Inflation Rate Calculation of Fast-Moving Consumer Goods: Shiny-SparkR App**

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**Keywords:** inflation rate; shiny; SparkR; shiny-SparkR; web scraping

**R packages:** SparkR; shiny; ggplot2; rvest

All official statistics centre or central banks of countries are calculating inflation rate in monthly period. Inflation is measured by the consumer price index includes the annual percentage change in the cost to the average consumer of acquiring a basket of goods and services for specific intervals, such as yearly. The central banks and the statistics centres serve these information publicly. Most of the institutes serve the information monthly. Its hard to track Inflation rates for “Fast-Moving Consumer Goods(FMCG)” daily. To monitor this, I created *SparkR-shiny* App. The application is scraping top FMCG related web sites in daily based and stored the data on Spark stand alone cluster on Amazon Web Services (AWS) Elastic Compute Cloud (EC2), calculating consumer price index and day on day, month on month or year on year changes based on FMCG categories, visualizing the results according to user defined criteria. With this application people could filter consumer price index for any time interval, any category also people could compare index changes of goods in different categories.

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## Introduction to RDruid

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**Keywords:** Druid

**R packages:** RDruid

This presentation will briefly describe *RDruid* package which is **R** connector for Druid data store.

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## Search phrases in e-commerce platform allegro.pl - big data analysis using SparkR

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Liliana Pięta<sup>1,2</sup>, Mariusz Strzelecki<sup>1</sup>, Anna Wróblewska<sup>1,3\*</sup>

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2. Cracow University of Economics  
3. Warsaw University of Technology

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**Keywords:** spark; big data; text analysis

**R packages:** SparkR; wordcloud; magrittr

**R** is a powerful tool for data visualization and analysis but it's speed is limited to only one CPU speed. It stays in the opposite with current Big Data trend that focuses on gathering and analysing huge, terabyte-scale datasets in clustered environment. Combining **R** and Spark technology we can synergize power of the both tools and we can efficiently work on huge datasets. During the presentation we will show you our approach to analyze search phrases in the biggest polish e-commerce marketplace platform Allegro.pl. We try text analysis methods on phrases that our users type into the search box. Moreover we analyse transactions and user search events and try to find out the associations between searching phrase and successful transactional event. We will focus on challenges we solved during adapting *SparkR* in Allegro and share difficulties we experienced.

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## The full process of creating an R application in recommendation systems: from Dockerfile to Zabbix monitoring

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**Keywords:** R application; docker; monitoring

**R packages:** rkafka; elastic; httr; RJDBC; RZabbix

The presentation covers the main steps of creating a reproducible **R** application. First of all, there is a need of collecting the data. We present how to receive it from various sources, including Kafka, Elasticsearch or Hadoop (with the help of suitable **R** packages). After transforming the data, doing the necessary calculations and obtaining the desired outcome we show how to push out the results. When the application is ready and running, it needs to be controlled. We present the process of creating reliable monitoring (with the help of Zabbix and Hipchat notifications). All of that can be wrapped up in a Docker to make the application reproducible in different environments and platforms.



## Data Workflow 2

*Room 111A - Chairman: Marcin Dyderski*

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### **Power of Java's RSession and rKafka in the data science team collaboration**

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**Keywords:** integration; microservices; rsession; kafka; team collaboration

**R packages:** rkafka

The times of single geniuses able to solve most advanced problems of the technical industry passed away. Nowadays, it is necessary to collaborate and support each other within teams. When it comes to Data Science teams, they are cross-functional and consist of people possessing different skills and having different duties. When working on a single product mathematicians, statisticians and engineers have to find right ways of exchanging and interfacing their piece of work. Unfortunately, not only they think differently, but they also use different platforms and languages. It implies in creating solutions for integration. One well known way of co-working is embedding code in different language in your own software. As an example, **R** code can be invoked from Java family languages using **RSession**. Another way of collaboration is passing messages throughout a middleware. Best known messaging system is Apache Kafka, originally developed by LinkedIn. It is distributed among cluster nodes and allows high-throughput in a publish-subscribe manner and what is more important can be accessed from **R** code using **rKafka** package. In my presentation, I am going to familiarize you with those subjects and prepare for using them in production. There are a few tricks that will make your life easier.

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## R Shiny for Real-time Analytics and Insight Delivery – A Solution for Complex Data in Agriculture

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**Keywords:** Bayesian; big data; choice modeling; complex survey; real-time; risk; Shiny; simulation; small area estimation; spatial; statistical learning; supervised; unsupervised; visualization

**R packages:** bayesm; cluster; dplyr; fields; ggplot2; kohonen; leaflet; magrittr; maps; maptools; party; randomForest; rgdal; rgeos; sp; spatstat; shiny

One of the key challenges to successfully harness the value of big data is to uncover the critical insight through analytics and make it easily accessible to decision makers in an intuitive way. **R Shiny** offers a platform for developing an end-to-end solution completely within **R** from mining the data with many modeling choices to insight delivery via powerful and dynamic data visualization. Such solution is highly suitable for agricultural data which is vast and dynamic, and increasingly abundant due to the recent development and adoption of precision farming and the related technologies. We would like to illustrate *Shiny* applications that integrate a mixture of privately collected and governmental data across many key dimensions such as time, different geographic levels, crops and product types and usage. Analytics including both supervised and unsupervised modeling capabilities and other approaches such as small area estimation under complex survey design and water pesticide contamination risk model are included. We also include an application of discrete choice modeling using hierarchical Bayesian estimation to capture the preference of brand or product features and the price sensitivity by small geographic units and offer the capability for the users to conduct market simulation by changing product mixture and prices. All the analytics are made and delivered in real-time.

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## Seamless external R server integration with Excel with step-by-step debugging of the R code

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**Keywords:** Excelsi-R; Rstudio; Excel; VBA

**R packages:** Rserve; svSocket

Excel can be a great UI for repetitive, semi-interactive **R** procedures. I want to present (yet another) solution that allows using **R** commands in Excel. It features:

- ability to connect to external **R** server so you don't have to be limited by local RAM/CPU
- inspection of variables on external **R** server
- compatibility with RStudio with its awesome step-by-step debugging capabilities

This setup allowed me to create Excel front end for analysis of dataset with >4M cases and 400 variables.

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## Workflow around modelling in Data Science / R

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**Filip Stachura<sup>1\*</sup>, Olga Mierzwa<sup>1</sup>, Paweł Przytuła<sup>1</sup>**

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**Keywords:** workflow; process; data science

**R packages:** dplyr; caret; randomForest

Working as a data scientist usually means working with data, building models, evaluating the results, translating them into actionable insights, getting feedback from experts and repeating the process. Hardly ever one starts with the model that finally will be used in production. It is usually trial and error process of trying new things and experimenting. That's why data science project could get disorganized rapidly. Every test involves a new

script, each script requires a multiple arguments and produces one or more data files. Keeping track of all this implied structure is a pain.

The talk stresses the importance of having a process around data science related tasks, while keeping the main focus on creating a data product. We demonstrate the implementation of the light data science workflow – Dataflows. Dataflows allows **R** users to create pipelines, without writing extra code, is self documenting and easy to start working with.

During the talk we show the benefits of formalizing and structuring the process of model building in **R**. We mention the bottlenecks, propose solutions and biggest wins accomplished by introducing Dataflows. We strive to share our hands-on experience from various data science projects using **R**.

Target audience practitioners, data scientists and researchers interested in rising standards of their current data product creation process, with the stress on reproducibility, early error detection, easy of results evaluation, comparison and communication with less technical colleagues.

# **Methodology 1**

*Room AULA - Chairman: Marcin Szymkowiak*

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## **Predicting machine failures**

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**Maren Eckhoff<sup>1\*</sup>**

1. McKinsey

\*Contact author: Marta\_Swiniarska@mckinsey.com

**Keywords:** failure modelling, machine learning

With the advent of the Internet of Things, companies collect a wealth of data that can be used to monitor degradation of their assets. In this talk, we will discuss how statistical modelling and machine learning can be used to predict failures and derive an optimal maintenance strategy. We will explore different modelling approaches and some of the feature engineering challenges. Moreover, the high value of combining different data sources to enrich the model will be explained.

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## **Ensemble learning - idea and applications**

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**Mateusz Filarowski<sup>1\*</sup>**

1. McKinsey

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**Keywords:** machine learning; ensemble learning; data mining

**R packages:** mlr

In every winning Kaggle solution nowadays you will find an ensemble technique. Latest and greatest methods of combining results from multiple learning algorithms can lead to better predictive performance. This lecture will give you an overview of techniques and real-world business cases.

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## Ensemble learning - implementation with mlr

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Tomasz Smolarczyk<sup>1\*</sup>

1. McKinsey

\*Contact author: Marta\_Swiniarska@mckinsey.com

**Keywords:** machine learning, ensemble learning, data mining

**R packages:** mlr

How to build multiple models and combine their results into powerful ensemble learners in less than one week? We will present a predictive modeling framework that is taking advantage of ensemble learning techniques and is heavily based on *mlr* package.

## Methodology 2

*Room AULA - Chairman: Maciej Beręsewicz*

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### Unattended SVM parameters fitting for monitoring nonlinear profiles

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**Keywords:** quality control; SVMs; nonlinear profiles

**R packages:** SixSigma; e1071; qcc

The monitoring of nonlinear profiles is a recent quality control technique. It allows to apply Statistical Process Control (SPC) methods to processes in which, rather than having a quality characteristic, there is a sort of nonlinear function that characterises the process. This method has been implemented in the *SixSigma* R package. The underlying idea is to compute a prototype profile and confidence bands using a data set from an in-control process, monitoring subsequent profiles thereafter. Thus, the same methodology used in well-known Shewhart control charts can be applied to complex processes. To this aim, raw data can be used. Nevertheless, using regularisation theory nonlinear profiles can be smoothed in order to better represent and analyse the profiles. In this work, we use Support Vector Machines (SVMs) to smooth profiles throughout the control process. Consequently, SVM parameters must be selected in order to reach a good fit of the nonlinear function at hand. Such parameters, namely:  $C$  and  $\epsilon$ , can be explicitly assigned in the *smoothProfile()* function of the *SixSigma* package. However, a quality control practitioner seldom knows about SVMs, needless to say that they have no time to spend modelling functions. Hence, we rely on Cherkassky, V and Ma, Y (2004)<sup>1</sup> to automatically fit the SVM parameters using the process data, thereby achieving unattended SVM fitting. Furthermore, noise is previously estimated by means of a loess fit.

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<sup>1</sup>Practical selection of SVM parameters and noise estimation for SVM regression. Neural Networks, 17(1), 113-126

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# SimonsSVM: A Fast and Scalable Support Vector Machine Implementation for R

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**Keywords:** support vector machine; machine learning; non-parametric classification; non-parametric regression

**R packages:** SimonsSVM

Support vector machines (SVMs) are non-parametric methods for various supervised learning scenarios like classification and regression. They have been studied extensively both theoretically and practically in the last 20 years. There are many well-known implementations also for **R**, for instance the package *e1071* provides bindings to *LIBSVM*. We present our recent package *Simons' SVM* for **R** with the following key features:

1. Unprecedented speed:

- Compared to, e.g. *LIBSVM*, training that includes 5-fold cross validation on a 10x10 hyper-parameter grid is about 300 times faster on, e.g. a 1000 samples containing subset of the binary version of the classical covtype data set.
- Partitioning strategies further decrease training (and testing) time without sacrificing generalization. For example, the full covtype data set (about 523.000 samples) takes less than 9 min.
- Partitioning even allows to attack huge problems. For instance the higgs data set (10 million samples) could be trained and tested in five hours.

2. Inclusion of some standard learning scenarios:

- (weighted) binary classification
- multiclass classification (both AvA and OvA)
- Neyman-Pearson-type classification
- Least squares / quantile / expectile regression

3. Flexible user interface:

- Fully integrated cross validation let's the user focus on parameters he/she can understand.
- The underlying implementation have more than twenty independent options leading to an enormous flexibility for the power user.
- Meaningful default values, which in many cases makes a fine-adjustment unnecessary.

- Comprehensive documentation.

Quick demo:

```
install.packages("SimonsSVM", repos="http://www.isa.uni-stuttgart.de")
library(SimonsSVM)
d <- ttspplit(iris)
model <- svm(Species ~ ., d$train)
test(model, d$test)
```

More information:

<http://www.isa.uni-stuttgart.de/software/R/demo.html>

<http://www.isa.uni-stuttgart.de/software/R/documentation.html>

## Discrete Choice Models in R

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**Keywords:** discrete choice models; econometrics; Bayesian statistics; Stan

**R packages:** rstan; mlogit; gmnl; bayesm; ChoiceModelR

Discrete choice models (DCM) are a widely used class of models in economics, marketing, and transportation science. These models are rooted in random utility theory and can be applied if a decision maker picks one alternative out of multiple options. The most commonly used variations of DCM are the multinomial logit model (MNL), the mixed logit model (MXL), and multinomial probit (MNP). Many R packages (e.g., *mlogit*, *gmnl*, *bayesm*) are available for frequentist and Bayesian inference of DCM. However, the different packages lack a unified data interface, common structure of functions and methods, and comparable output. Therefore, the analyst is faced with a typical dilemma: to test several models and follow established research processes (and maybe fulfill reviewer requests) one has to deal with data transformations, model translations, and output formatting, which is tedious, time consuming, and error-prone. In addition, the established R packages lack flexibility and transparency. To this end, we propose to use Stan, a general purpose modeling language for Bayesian inference written in C++ with interfaces to R, python, Matlab, Julia and Stata. We compare Stan-implementations of MXL models using simulated and real data. We show how Stan can be used for estimating more sophisticated models (e.g., models in willingness-to-pay space). We also provide a quick

reference over our **R** package *dcm* that aims at closing the gap for existing packages regarding a unified data API and comparable model output.

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## Multivariate analysis of variance for functional data using **R**

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**Keywords:** functional data; multivariate analysis of variance

**R packages:** fda

We develop two testing procedures for multivariate analysis of variance problem for functional data. Similarly as the one-way analysis of variance for such data, this problem seems to be of practical interest. The first method approximates the functional data from each observational unit with of linear combination of orthonormal basis. Then time is integrated out from the usual MANOVA sum-of-squares and cross-products matrices. The null distribution of the standard MANOVA statistics are determined by permutation. In the second test, the functional data from each observational unit are projected on  $\mathbb{R}^p$ . Then, standard or permutation MANOVA tests are applied to the projected data. The main rationale for this test is that equality of the mean-functions vectors does not hold if equality of mean vectors does not hold for any random projection of the mean-function vectors. The performance of these methods is examined in comprehensive simulation studies. The results suggest that the tests can detect small differences between vectors of curves even with small sample sizes. We demonstrate how these methods can be performed efficiently in **R** by applying them to real world data. We implement these methods for **R** in our forthcoming package.

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## Text Mining in R

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**Keywords:** text mining; classification; sentiment analysis

**R packages:** tm; e1071; twitteR

I would like to present the Text Mining cababilities of **R**. In particular the framework for Text Analysis with **R** provided by the *tm* package. Furthermore, I will show the publicly available API for Twitter. Then I will continue with a case study of Sentiment Analysis of Twitter Data/Feedback Data. This has been done with Naive Bayes Classification and/or Logistic Regression. The Case Study involves all the steps from obtaining raw text data to manipulating the data to running the actual algoritms adapted for text data. A bit of theory has been provided to motivate the use of the Bayesian classifier and if time allows I will run model comparisons.



## **Methodology 3**

*Room AULA - Chairman: Tomasz Klimanek*

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### **Classic and network based cluster analysis: together we're better**

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**Keywords:** cluster analysis; networks; data visualization

This talk will present how to use traditional and network based clustering techniques to identify groups in the data. Advantages of complementing both methodologies are better performance and visualization of results.

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### **M-quantile regression in R**

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**Keywords:** m-quantile regression, small area estimation, robust estimation

In the presentation we will discuss M-quantile regression as an alternative for robust linear mixed models and quantile mixed models. First, we discuss theory and current research on M-quantile models. We give examples of its application, in particular for small area estimation. Second, we provide a brief review of available R routines which

were prepared mainly for research projects (e.g. SAMPLE) or scientific papers. Finally, we give an overview of on-going work on an R package for M-quantile regression.

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## Is forest a pharmacy? - problems with data analyses

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**Keywords:** forest ecology; data mining; visualisation; linear models

**R packages:** caret; randomForest; ggplot2; hglm; sp; rgeos

**Scientific supervisor:** Dr. Andrzej M. Jagodzinski

Forest ecology is a specific branch of ecology, where due to extent spatial scale and large dimensions of individual objects we often need a special approaches. The aim of this presentation is to show a few case studies representing frequent analytical problems in forest ecology and its sources. I will present problem with unknown variability of studied phenomena on the example of individual biomass of herbaceous forest understory plant species. Although minimal sample size was unknown, the biggest analytical problem was discontinuity of species occurrences, connected with their specific biology. Thus, instead of two-factor analyses we performed simple ANOVA and exploratory data analysis to find specific patterns. In case of the study on alien species natural regeneration, due to high amount of zero values and lack of good explanatory variables, we were forced to simplify our densities data into presence-absence and use logistic model to find interactions between type of tree stand and distance from the seed source. However, this interaction is hard to find without graphical data exploration. I also will present the study in coarser spatial scale, based mainly on published data on ancient woodland indicator species. This study is a simple analyses of species richness and use of random forest model to analyze highly-collinear variables – land-use types within grid square. Here I will show that simple (ANOVA) and more sophisticated (Poisson Hierarchical GLM with SAR) statistical approach lead into the same conclusions. I will also discuss potential sources of outliers and artifacts, which may be important threat for results interpretation.

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## k Prototypes Clustering of Mixed Type Data

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**Keywords:** clustering; data mining; classification; k prototypes; multivariate statistics

**R packages:** *clustMixType*; *klaR*; *cluster*; *fpc*

Most literature in multivariate statistics deals with numeric data, same for clustering. In practical applications the analyst is often confronted with mixed type data of both numeric and factor variables. Hierarchical clustering can easily be extended to categorical data by specification of an appropriate (dis)similarity measure (e.g. Gower distance). The k means algorithm relies on euclidean distance. The *klaR* package offers an R implementation of the k modes extension to the k means algorithm for categorical data. Further, the recent *clustMixType* package also makes the k prototypes generalization to mixed type data accessible to R users. Both algorithms are presented together with their usage in R.



# Packages 1

Room 308A - Chairman: Tomasz Górecki

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## Reconciling forecasts: the hts package

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**Keywords:** forecast; time series

**R packages:** hts

Hierarchical time series occur when there are multiple time series that are hierarchically organized and can be aggregated at several different levels based on dimensions such as product, geography, or some other features. A common application occurs in manufacturing where forecasts of sales need to be made for a range of different products in different locations. The forecasts need to add up appropriately across the levels of the hierarchy. I will describe some new features in the *hts* package for R which provides several methods for analysing and forecasting hierarchical and grouped time series.

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## stplanr: an R package for transport planning

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**Keywords:** transport; GIS; modelling; visualisation

**R packages:** stplanr; leaflet; shiny

*stplanr* was developed to solve a real world problem: how to convert official data on travel patterns into geographic objects that could be plotted on a map and analysed using

GIS? Over time the package has evolved to include a number of other functions. Analysis of road traffic casualty data, various routing algorithms, ‘travel watershed’ analysis and access to Google’s Travel Matrix are all possible. This paper traces the development of these capabilities with a focus on applied case studies and reproducible examples.

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## brms: An R Package for Bayesian Multilevel Models using Stan

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**Keywords:** Bayesian inference; multilevel model; MCMC, Stan

**R packages:** brms

The *brm* package implements Bayesian multilevel models in **R** using the probabilistic programming language Stan. A wide range of distributions and link functions are supported, allowing to fit – among others – linear, robust linear, binomial, Poisson, survival, ordinal, zero-inflated, hurdle, and even non-linear models all in a multilevel context. Further modeling options include autocorrelation of the response variable, user defined covariance structures, censored data, as well as meta-analytic standard errors. Prior specifications are flexible and explicitly encourage users to apply prior distributions that actually reflect their beliefs. In addition, model fit can easily be assessed and compared with the Watanabe-Akaike Information Criterion and leave-one-out cross-validation.

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## Modules in R

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**Keywords:** programming; functional-programming

**R packages:** modules; import; parallel

In this talk I present the idea of modules inside the **R** language. Modules are an orga-

nizational unit for source code. The key idea of this package is to provide a unit which is self contained, i.e. has its own scope. The main and most reliable infrastructure for such organizational units of source code in the **R** ecosystem is a package. Compared to a package modules can be considered ad hoc, but – in the sense of an **R** package – self contained. Furthermore modules typically consist of one file; in contrast to a package which can wrap an arbitrary number of files. Inside of packages modules act more like objects, as in object-oriented-programming. In this talk I cover basic use cases in parallel computing and good coding practices.

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## **influenceSEM 2.0: An R Package for Sensitivity Analysis in Structural Equation Models**

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**Keywords:** sensitivity analysis; influential cases; structural equation models

**R packages:** lavaan; influenceSEM

The **R** package *influenceSEM* 2.0 provides tools to perform sensitivity analysis in Structural Equation Models (SEM). Despite SEM are widely used by researchers in the social and behavioral sciences, the application of associated case-diagnostic tools (i.e. sensitivity analysis) have received limited attention and understanding in practice. Sensitivity analysis provides information regarding the impact of single cases on parameter estimates and goodness of fit of the model, thus supporting the researcher in the interpretation of results. In this paper, we present an easy-to-use **R** package yielding several measures of case influence for SEM via two applications to real data. We discuss the utility of detecting influential cases in SEM, provide recommendations for the use of measures of case influence, and give suggestions on how this analysis can be usefully employed in combination with other statistical techniques.



## Packages 2

*Room 308A - Chairman: Marek Gagolewski*

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### **EnvCpt: An R package for changepoint identification in environmental data**

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**Keywords:** model selection; changepoints; nonstationary time series; environment; oceanography; climate science

**R packages:** EnvCpt; changepoint

Man-made pressure on the Earth's climate and ecosystems is increasing vulnerability to abrupt changes, which can be especially socio-economically challenging given the rapidity at which an ecosystem switches from one state to another relative to the time spent in the different states (e.g. a shift from one year to the next that persists on decadal or longer time scales). The ecosystem shift can be a response to change in external forcing (e.g. climate shift) or a random reorganization of the system, which can often be characterized by a simple autoregressive process. The distinction between stochastic and deterministic regime shifts is fundamental to gain a better understanding of the underlying mechanisms. In the climate and oceanography literature, the detection of regime shifts is commonly made using a sequential algorithm to test for shifts in the mean. However, this methodology can lead to spurious regime shift detection in the presence of autocorrelation, which is typically present in climate and environmental time series. Furthermore, a trend (e.g. long-term climate change) may be falsely interpreted as a series of regime shifts using this methodology. The *EnvCpt* R package presents a flexible methodology able to discern between the presence of mean, trend and autocorrelation and any combination of multiple shifts therein. The benefit of the package is that an automatic choice is made between whether trend, autocorrelation or changepoint models best fit the data using model selection. Thus no visual inspection of the data is required unlike current methods.

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## archivist 2.0: News from Managing Data Analysis Results Toolkit

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**Keywords:** reproducible research; sharing objects; archiving

**R packages:** archivist; archivist.github

Open science needs not only reproducible research but also accessible final and partial results. During the speech I will present the most valuable applications of the *archivist* package. The *archivist* is an **R** package for data analysis results management, which helps in managing, sharing, storing, linking and searching for **R** objects. The *archivist* package automatically retrieves the object's meta-data and creates a rich structure that allows for easy management of calculated **R** objects. The *archivist* package extends the reproducible research paradigm by creating new ways to retrieve and validate previously calculated objects. These functionalities also result in a variety of opportunities such as: sharing **R** objects within reports/articles by adding hooks to **R** objects in table/figure captions; interactive exploration of object repositories; caching function calls; retrieving object's pedigree along with information on how the object was created; automated tracking of performance of models.

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## LimeRick: Bridge between LimeSurvey and R

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**Keywords:** LimeSurvey, on-line survey, CAWI, survey meta data

**R packages:** LimeRick (not publicly available yet)

The first public presentation of the prototype of a new **R** package that provides useful connection between **R** and the most popular open-source web scripts for on-line surveys (<http://www.LimeSurvey.org>).

The package aims to enable and simplify the work flow of reproducible CAWI research in Social Science; preparing templates for ad hoc and real-time analysis, performing detailed meta-analysis, archiving and monitoring responses directly from **R**.

With the *LimeRick* package one can import pre-processed data from an on-line survey with an **R** script (with the use of RemoteConrol2 API or with non-API solution). Then, the data can be processed analytically by an **R** script and automatically reported with the use of *shiny* package. The whole process can be pre-programmed and performed without the researcher interference. This enables to build data products based on declarative data from on-line surveys, which are processed, analyzed, and visualized on-line and in real-time. It can be of use for performing automatic tracking studies with real-time KPIs monitoring (e.g. for a customer satisfaction survey). The package will be also linked to a tool for unique, advanced analysis of meta-data from an on-line survey, which has already been alpha tested during large CAWI research project. As the early prototype of the package is presented, the presentation will end with a call for collaboration for developing and testing the package in different usage cases.

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## An R package for consumer and sensory data mapping: Comparison of Preference Mapping stability

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**Keywords:** sensory analysis; external preference mapping; comparison of maps stability; assessment of predictions performance; functions for denoising; shiny application functions

We propose a new package for analyzing consumer and sensory data dedicated to both academic and industrial sensory analysts. This package implemented in R programming environement, is an easy solution that deals with the following problems: panel performance evaluation, characterizing products from both sensory and consumer data, mapping of instrumental (sensory or physico-chemical) and consumer data via mapping technics (Internal and External PrefMap), and much emphasis on comparisons of maps stability especially when denoising hedonic data. This variation on PrefMap is also implemented through assessing the performance of different predictions models such as GAM, LM ... and various multivariate analysis methods.

External Preference Mapping functions and Comparison of Maps Stability functions are provided. The shiny application for the functionalities forms part of the package.

This package produces also graphical displays of data that are simple to interpret and it also provides syntheses of results issuing from various ANOVA analysis or various factor analysis methods.

*Room 308A - Chairman: Przemysław Biecek*

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## **Are we ready for Personalized Medicine?**

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**Keywords:** medicine; exposome; biomedical data, Bioconductor

In the era of fast-paced development of technology and services, there are limitless opportunities for customization to meet specific user needs. Over the next decade, as much as half of the proportion of health care will shift from the hospital and clinic to the home and community. With Personalized Medicine understood as prevention and treatment strategies that take individual variability into account we need to identify this individual variability via characterizing each person's individual baseline health state instead of resorting to population-based variable distributions. This health state baseline cannot be, however, determined with use of just the classical medical records. Recent technological advances have created opportunities to harness additional sources of biomedical data on a real time basis, for instance through the use of: (1) mobile medical devices for monitoring dedicated health parameters (insulin, heart rate, etc), and (2) wearables. The synergy of these two streams should provide a good estimate of the health state baseline. In order to model estimated data of health state baseline and future scenarios, it is imperative to include an important, yet largely missing third component - the exposome. This term covers all the exposures of an individual in a lifetime. So far it was mostly connected with air quality, light, climatic variations, ozone and volatile organic compounds. But we cannot forget about the 'living' component of exposome. As dense human environments such as cities account for over a half of the world population (in EU 80%) there is a need to build a molecular portrait of cities in order to study what lives around us and how it affects our health and wellbeing. There are, however, no dedicated tools, frameworks or standards how to store, share, integrate these streams of data. There is a lot to do as there are many open questions and challenges which need to be addressed in order to provide valuable input. Fortunately, there is a very lively community around **R** Bioconductor project, which provides tools for the analysis and comprehension of high-throughput genomic and other

biomedical data. This community should take a leading role in the future development of solutions for Personalized Medicine.

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## N-gram analysis of biological sequences in R

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**Keywords:** n-gram; k-mer; feature selection; proteomics

**R packages:** biogram; ranger; slam

N-grams (k-mers) are vectors of  $n$  characters derived from input sequences, widely used in genomics, transcriptomics and proteomics. Despite the continuous interest in the sequence analysis, there are only a few tools tailored for comparative n-gram studies. Furthermore, the volume of n-gram data is usually very large, making its analysis in **R** especially challenging.

The CRAN package *biogram* facilitates incorporating n-gram data in the **R** workflows. Aside from the efficient extraction and storage of n-grams, the package offers also a feature selection method designed specifically for this type of data. QuiPT (Quick Permutation Test) uses several filtering criteria such as information gain (mutual information) to choose significant n-grams. To speed up the computation and allow precise estimation of small  $p$ -values, QuiPT uses analytically derived distributions instead of a large number of permutations. In addition to this, *biogram* contains tools designed for reducing the dimensionality of the amino acid alphabet, further scaling down the feature space.

To illustrate the usage of n-gram data in the analysis of biological sequences, we present two case studies performed solely in **R**. The first, prediction of amyloids, short proteins associated with the number of clinical disorders as Alzheimer's or Creutzfeldt-Jakob's diseases, employs random forests trained on n-grams. The second, detection of signal peptides orchestrating an extracellular transport of proteins, utilizes more complicated probabilistic framework (hidden semi-Markov model) but still uses n-gram data for training.

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## R as an Environment for the Reproducible Analysis of DNA Amplification Experiments

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**Keywords:** bioinformatics; qPCR; digital PCR; reproducible research; non-linear regression; smoothing; pre-processing

**R packages:** chipPCR; dpcR; MBmca; RDML; rkwarddev; qpcR

Quantitative PCR (qPCR), digital PCR (dPCR), quantitative isothermal amplification (qIA) and melting curve analysis (MCA) are key technologies in molecular diagnostics, forensics and life sciences. However, software for the biostatistical data analysis of such technologies is either tied to a specific task or part of a monolithic closed source software. This limits the reproducibility of computations and gives no control over the analysis algorithms.

We contributed bioinformatics software tools for reproducible and transparent data analysis. Analysis pipelines consisting of statistical procedures, raw data preprocessing, analysis, charts and report generation are implemented for increasingly demanded reproducible research. This is achieved with our packages *MBmca*, *chipPCR*, *dpcR* and *RDML*. We implemented selected findings for the **R** GUI/IDE RKWard and as *shiny* web browser applications. For rapid prototyping of RKWard plugins we used the *rkwarddev* package.

In our exemplary workflows we show analyzers for qPCR, qIA, MCA and dPCR experiments, which can be built in short development cycles. Our software is targeted at users who develop novel devices or users who wish to analyze raw and unprocessed data.

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## **Big data genomic data warehouses analyses with R**

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**Marek Wiewiórka<sup>1\*</sup>, Tomasz Gamin<sup>1</sup>, Michał Okoniewski<sup>2</sup>**

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**Keywords:** big data; next-generation sequencing; data warehousing

Genomic population studies incorporates storing, analyzing and interpretation of various kinds of genomic variants as its central issue. When thousands of patients sequenced exomes and genomes are being sequenced, there is a growing need for efficient database storage systems, querying engines and powerful tools for statistical analyses. Combination of **R** and scalable big data solutions such as Apache Impala, Apache Kudu, Apache Phoenix or Apache Kylin can address many of the challenges in large scale genomic analyses.

Proof-of-concept of a big data solution for running analyses with R/RStudio will be presented during the talk. Overview of some benchmark results, hints for designing and implementing scalable genomic data warehouse will be also covered during the talk.

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## **Using SparkR with distributed database in Parquet - a genomic example**

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**Keywords:** SparkR; next-generation sequencing; ADAM

*SparkR* is the **R** interface to Apache Spark map-reduce framework. It does not have the full capabilities the three main languages of Spark: scala, java and python, still can be used as an interface between scalable processing of distributed data frames and the vast galaxy of *R* data analytics.

A good example of a system where *SparkR* can be used to provide data to **R** analytical front-end is ADAM. It is a set of formats and Spark operations to process large next-generation sequencing datasets. ADAM keeps the data in Parquet columnar storage, which can be queried using SQL. This provides **R** analytics with a fully scalable data back-end. Overall, the presentation is a proof that it is possible to process real big data with it - not only in genomics, but in various other data science applications. It will include practical hints on using *SparkR* in Jupyter notebooks with Spark data frames and Parquet storage.



## **Education Learning**

*Room 308A - Chairman: Alicja Szabelska-Bereśewicz*

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### **Revolutionize how you teach and blog: add interactivity**

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**Filip Schouwenaars<sup>1\*</sup>**

1. DataCamp

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**Keywords:** education; web technology; reporting; interactivity

**R packages:** tutorial; knitr; rmarkdown

**R** vignettes, blog posts and teaching materials are typically standard web pages generated with *rmarkdown*. DataCamp has developed a framework to make this static content interactive: **R** code chunks are converted into an **R**-session backed editor so readers can experiment. This talk will explain the inner workings of the technology, as well as a the tutorial **R** package that makes the transition to interactive web pages seamless. Some hands-on examples will showcase the remarkable ease with which you can convert **R** Markdown documents, vignettes and Jekyll-powered blogs into interactive **R** playgrounds.

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### **Aargh I have to teach R (Experiences in the teaching of R)**

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**Keywords:** teaching; training

**R packages:** shiny

As **R** is gaining popularity, so there is the interest in **R** courses. **R**, generally considered as a programming language with a steep learning curve, has surely its own typical pit-

falls. The aim of this talk is to give an overview of the general do's and don'ts regarding the teaching of **R** and how a typical **R** course can be designed. Design and execution of a course depend on a variety of influences such as different types of course participants, content and context. Course participants usually differ regarding prior knowledge, interest in the material, ambitions as well as objectives to be reached. Generally, **R** courses focus either more on statistical or on programming topics. Another crucial aspect is whether the participants come from an academic or an industrial background, in other words, the context in which the course takes place. The talk is based on the experiences of an **R** trainer teaching **R** to academics, as well as in companies, with a topic area ranging from teaching the fundamentals to specialised workshops (e.g. performing a Network Analysis in a *shiny* app).

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## Using R for artistic purposes

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**Päivi Julin<sup>1\*</sup>**

1. Aureolis

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**Keywords:** visualization; design; typography; alternative; Processing

**R packages:** ggplot2; grid; Rserve; RColorBrewer

**R** can be tamed for serious business usage and data analysis, but this tool also has abilities for a different kind of approach: creating data art. Even **R** might not be mainly marketed with its graphics; it does have competence in genuine creativeness for unusual visualizations. Thus, **R** is much more than just bar plots, charts and maps – it is only a matter of practice and adaptation.

Data art focuses using raw data to produce visualizations with both aesthetic and informative scope. Having a creative process with digital media, real-time data and **R**, may lead to producing alternative interpretations from traditional information. Playing with **R** graphics devices, one is able to adjust any kind of visual presentations inside **R** console. Another option is to handle data manipulation with **R** and print output with alternative graphic portals - such as Processing or D3.

The presentation involves graphical visualizations, technical solutions, and general ideas, how to use **R** in alternative ways. Telling a story from data is a fun journey, therefore playing with **R** can be rather an amusing **R**-experience. This program being my muse, the aim is to inspire others.

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## Polish Diet Commissions - Text Analyzing

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**Keywords:** data mining; data visualization; text analyzing

**R packages:** ggplot2; shiny

We would like to talk about our investigation of texts from the general meetings of Polish Diet Commissions from two cadencies: the last one and the present one. We do believe that no one has ever done that before. Who knows what it can bring? We will discuss how we gathered the data and show some information that we get from it.



## **Lightning Talks**

*Room AULA - Chairman: Joanna Zyprych-Walczak*

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### **R as a tool for graphical diagnostics in population pharmacokinetic modeling**

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**Keywords:** graphical model diagnostics; population pharmacokinetics

**R packages:** ggplot2; lattice

Population pharmacokinetic (PopPK) modeling aims at finding typical pharmacokinetic parameters and their variability within a target population of patients treated with a drug of interest. Population approach to pharmacokinetic modeling is gaining popularity as it can handle sparse data and estimate pharmacokinetic parameters of each individual. Large datasets and complexity of the models hinder assessing the quality of a model fit with a single numerical value. Graphical analysis plays a unique role in PopPK since it enables a better insight into the model structure. **R** is a powerful and versatile tool for graphical model diagnostics. It offers variety of visualizations, allows creating flexible scripts for quick model assessment and saving the results as a formal report. The produced graphics are publication-ready and meet the requirements for most non-standard and customized plots.

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## Machine learning modeling of phenological phases in Poland

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Bartosz Czernecki<sup>1\*</sup>, Jakub Nowosad<sup>2</sup>, Katarzyna Jabłońska<sup>3</sup>

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**Keywords:** phenology; machine learning; modeling; satellite; meteorology; climatology

**R packages:** caret; raster; Boruta; parallel

Changes in timing of phenological phases are important proxies in contemporary climate research. The aim of the study was to create and evaluate different statistical models for reconstructing and predicting the selected phenological phase within *caret* R package. Three types of data sources were applied as predictors:

1. satellite derived products,
2. preprocessed gridded meteorological data
3. spatial features (longitude, latitude, altitude) of the monitoring sites.

The obtained results has shown potential for coupling meteorological derived indices with remote sensing products in terms of phenological (late spring) modelling. It was also shown that choosing a specific set of predictors and applying a robust preprocessing procedures is more affecting final results than applying a statistical model.

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## Latent Class Analysis in Psychology

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**Keywords:** LCA; classification;

**R packages:** e1071

In my opinion, the methods of statistical analysis are not developing in psychology, it is happened just beyond. Then, methods are only used by psychologists on their home

ground. Such a method, useful for building typology, is latent classes analysis (LCA), which I had ‘discovered’ by accident. In my presentation, I would like to show how use LCA to typical psychological data, which rarely meet the requirements of parametric methods (quantitative measuring scale, distribution normality, no outliers).

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## Exploratory data analysis of a clinical study group - revealing patient subgroups.

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**Keywords:** clustering; outlier detection; PCA

**R packages:** clv; ggplot2; chemometrics

Thorough knowledge of the structure of analyzed data allows to form precise research questions. The data structure and basic associations between parameters in the data can be revealed with methods for exploratory data analysis. Currently a researcher has a whole plethora of exploratory tools to choose from. Selecting methods that will work together well and facilitate data interpretation is not an easy task. In this work we present a well fitted set of tools for a complete exploratory analysis of a clinical study dataset and perform a case study analysis on a set of 515 patients. The proposed procedure comprises several steps:

1. robust data normalization,
2. outlier detection with Mahalanobis (MD) and robust Mahalanobis distances (rMD)
3. hierarchical clustering with Ward’s algorithm,
4. Principal Component Analysis with biplot vectors.

Introductory analysis showed that the case-study dataset comprises two clusters separated along the axis of sex hormone attributes. Further analysis was carried out separately for male and female patients. The most optimal partitioning in the male set resulted in five subgroups. Two of them were related to diseased patients: diabetes and gonadotroph adenoma patients. Analysis of the female set suggested that it was more homogeneous than the male dataset. No evidence of pathological patient subgroups were found. In the study we showed that outlier detection with MD and rMD allows not only to identify outliers but can also assess the heterogeneity of a dataset. The case study proved that our

procedure is well suited for identification and visualization of biologically meaningful patient subgroups.

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## Multidimensional Clustering of Web Analytics Data

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**Keywords:** data mining; clustering; web analytics

**R packages:** amap; dplyr; ggplot2

Web Analytics is the collection of data and their analysis regarding the behavior of website visitors. This presentation demonstrates a walkthrough on how to use multidimensional cluster analysis to divide a heterogeneous group of website visitors into smaller homogeneous segments.

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## R shiny server as core of multiple technologies into Travel Industry

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**Giovanni Lotti<sup>1\*</sup>, Pierre Alexandre Chanteau<sup>1</sup>**

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**Keywords:** shiny; d3; visualization; javascript

**R packages:** rHubble

The travel industry is a natural fit for big data applications – not only through the large transaction volumes but also through the diversity of data sources (e.g. search, booking, air, hotel, rail, ground, credit card, expense reports). The challenge is to transform these data into meaningful information for our various types of audiences – from non-technical staff to business intelligence specialists.

One solution we would like to showcase is the use of **R shiny** server as the core of multiple technologies. The data flows from Hadoop via hive to **shiny** server, from which

we transform the data through several **R** packages, including the famous *dplyr*, *tidyr*, *data.table* and more peculiar ones like *data.tree* or ad hoc functions written in c++ to obtain the most reactive experience.

For this session we would like to present our newly created package *rHubble*. *rHubble* package ports d3.js via htmlwidgets to enrich our visualizations by increasing user exploration possibilities, linking our multiple widgets through pubsub architecture. As the authors of the package we would be delighted to show its potential.

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## Turning Text Mining into Language Mining: Corpus Linguistics in R

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**Keywords:** corpus linguistics; cross-linguistic linked databases; minority language analysis; text mining

**R packages:** shiny; rmarkdown; leaflet; stringr

Few books deal with both linguistics and R. Most of them are actually textbooks on statistics with examples of real-life linguistic problems solved. So it is about analyzing linguistic data in **R** (there is nothing special about it, statistically speaking), not about doing linguistics in **R**. Fortunately, there are some linguistic packages in **R**. Santiago Barreda created package *phonTools* for phonetics research and experiments. Aaron Albin made a package *PraatR*, which provides **R** with the functionality of the well known phonetic program Praat by Paul Boersma and David Weenink. There are some text mining technics implemented in **R** (e.g. *tm*) and a few packages which allows extracting data from social networks.

However, linguistic **R** packages are mostly focused on phonetics. Pure text mining is insufficient for the linguistic research. So we decided to create an extended package, which helps to solve problems in linguistic typology and minority language description. In this talk, I will show preliminary results dealing with creation of a language corpora using *shiny*, *rmarkdown*, *leaflet*, and *stringr*. Problems, that I will cover during the talk:

- storing and analyzing texts in minority language: transcription, translation and morphological analysis; all examples are based on Adyghe (Circassian language family) and Mehweb (Northeast Caucasian language family)

- standardization of language documentation in **R**: integration with Cross-Linguistic Linked Databases

Support from the Basic Research Program of the National Research University Higher School of Economics is gratefully acknowledged

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## Structural bioinformatician's notebooks with pdbeeR and knitr

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**Keywords:** bioinformatics; biomolecules; knitr; reproducible research

**R packages:** pdbeeR; knitr

Working with biological molecules often involves much work with .pdb files – analyzing, subsetting, transforming and visualizing structural data. Doing this by hand is tedious, hard to reproduce and prone to errors. A new **R** package – *pdbeeR* – can help you make these chores fun, create interactive 3D visualizations, and save your work as elegant knitr notebooks to be shared with your collaborators and easily reproduced.

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## Using R to incorporate data science into the undergraduate statistics curriculum

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**Keywords:** undergraduate curriculum; statistical computing; data science

**R packages:** ggplot2; dplyr; ISLR

The American Statistical Association recently endorsed an updated set of Curriculum Guidelines for Undergraduate Programs in Statistical Science, and the first key point is: ‘Increased importance of data science’. In addition to traditional topics in statistical

reasoning, modeling, and inference, today's future statisticians also need the ability to access and manipulate data and to engage in algorithmic problem-solving to maximize their contributions. In this talk, I will explore what the increased importance of data science means for undergraduate programs in statistics and describe what we have done using **R** at St. Olaf College, an undergraduate institution of 3000 students in the United States. For example, statisticians partnered with colleagues in computer science to develop a 'statistics-infused' version of introductory computer science (CS125). This new statistical computing course introduces students to key foundational ideas in computer science by using mostly **R** (and some Python) and motivating the ideas through a data analysis context. Students learn about functions, loops, matrices, text strings, data scraping, and SQL while also discovering data visualization and classification methods. In fact, this course is one of seven featured in The American Statistician article 'Data science in the statistics curricula: preparing students to 'think with data''. In addition to CS125, we have integrated more data wrangling and data visualization into our regression course, added a course on Algorithms for Decision Making which primarily explores classification methods using **R**, and developed an entire course on Data Visualization with **R** to pilot this fall.

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## Analysing the statistical effects of manipulated data

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**Keywords:** manipulated data; probabilistic models; generative models, sample generation by replacement

**R packages:** sgr

Many self-report measures collected in different research fields such as, for example, social and psychological studies, marketing and epidemiological studies may be affected by manipulated information by respondents. For example, an individual may deliberately attempt to manipulate or distort responses to simulate grossly exaggerated psychiatric symptoms in order to obtain financial compensation or avoiding being charged with a crime. However, in other situations data manipulation can arise without a clear intention or goal by the respondent, for example, when an answer to a question is given under time pressure, or in heavily stressing contexts (e.g. during a job interview). Despite the reasons and motivations that induce people to (voluntarily or involuntarily) manipulate data can be different across contexts and situations, we believe that these processes can be represented by a single but flexible probabilistic model. In this contribution, we intro-

duce an **R** package, called *sgr*, that can be used to perform data analysis on manipulated data according to a sample generation by replacement approach. The package includes functions for making simple inferences about discrete, ordinal as well as categorical data under one or more scenarios of data manipulation. The package also allows to quantify uncertainty in inferences based on possible manipulated data as well as to study the implications of manipulated data for empirical results.

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## Cryptography in R

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**Keywords:** encryption; signatures; openssl; elliptic curves

**R packages:** openssl; sodium

Introduce a few packages that implement cryptographic methods.

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## Visualizing changes in demographics with R

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**Keywords:** visualization, demographics

**R packages:** plotly; ggplot2; leaflet

How to show aging of society? What is a good way to visualize population projections? How to reveal inadequate public investments related to the process of suburbanization? Data visualization is a perfect tool to bring intuitions about those complex and massive problems closer to the people. In my lighting talk I explore several visualization challenges related to demographics. For each I propose a solution from my blog (<http://www.szychtawdanych.pl>). Examples I show are created

with **R** packages *ggplot2*, *plotly* and *leaflet*. Codes are publicly available on my github <http://www.github.com/psobczyk>.

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## **R for pharmacokineticists - simulation of steady-state concentrations of amiodarone in heart compartmental model as an example.**

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**Keywords:** pharmacokinetics; modelling; parameter optimization

**R packages:** deSolve; FME

Amiodarone poses a known risk of torsade de pointes arrhythmia induction, according to CredibleMeds classification. Thus, the data on its effective concentration at heart tissue are desired. Patients prescribed to amiodarone usually are on long-term treatment following the standard dosing regimen, i.e. 200 mg t.i.d. as a priming dose, and 100 mg q.d. as a sustaining dose. The aim of the study was to build a functional heart model in order to simulate the amiodarone cardiac concentration at steady state. Three compartments of physiological volumes of plasma (central compartment), cardiac tissue, and pericardial fluid linked via first-order rate constants represented model structure. The model was described by set of differential equations, and written in **R** v.3.1.3. Numerical solutions were computed using *deSolve* library. The model parameters were optimized using *FME* package. The fit was performed to mean amiodarone concentrations observed by Escoubet et al. in plasma and heart tissue, respectively, in 61 patients given amiodarone in a single dose. The optimized parameters ([h-1] ka: 0.038, kht\_in: 0.200, kht\_out: 0.149, kpf\_in: 0.680, kpf\_out: 9.700, ke: 5.000) were used to simulate amiodarone time-concentration profiles in two-months standard dosage schedule of amiodarone. An event function was describing multiple administrations. The simulated cardiac concentrations at steady-state were ca. 20 times higher than corresponding amiodarone levels in central compartment, which occurred to be in accordance with the ratios reported in literature that can be assumed to refer to steady state situation. Results support the feasibility of the model as well as the approach to simulate steady-state.



## **Poster Session**

### *Room AULA*

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## **What are sampling errors in the vegetation studies using visual estimation of presence and cover of plants? R can help**

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**Keywords:** repeatability; interrater reliability, agreement; intraclass correlation coefficient

**R packages:** nlme; multilevel; irr; betapart; vegan

In vegetation science (e.g. phytosociology), visual estimates of plant cover belong to the most frequently used descriptors. The main reason for their attractiveness lies in the very low cost of the data obtained in this way, both in terms of labour, time and equipment. However, they are a subjective methods which result in sampling error, difficult to control. It is emphasised that using the visible estimation of cover requires some attempt and experience. However, many studies showed that comparison between observers yielded differences in the cover of recorded species as well as between repeated estimates of the same observer. We conducted several experiments with visual measurements of tree canopy, i.e. cover of tree layer and cover of herb layer in forest habitats. The experiments were performed with various raters, differing in experience in fieldwork: from students to professional researchers. Several field methods were applied: canopyscope, Braun-Blanquet approach, different scales of estimates; point method and a few vegetation types were chosen. Contrary to similar studies, where usually descriptive statistics are shown, we employed different statistical methods e.g. intra-class correlations, analyses of species pseudoturnover and nestedness – associated with loss of information among observes. The selected in **R** statistical methods turned out to be sensitive and robust tools. They revealed that even between professional researchers distinct differences appear. Advantages and disadvantages of available field methods are discussed and some possible improvements are suggested.

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## RNA-seq transcriptional profiling of PPD-b-stimulated peripheral blood from cattle infected with *Mycobacterium bovis*

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**Keywords:** transcriptomics; differential gene expression; tuberculosis

**R packages:** AnnotationFuncs; magrittr; VennDiagram; MASS; RColorBrewer; svglite; org.Bt.eg.db; dplyr; edgeR; limma; extrafont; ggplot2; gridExtra

*Mycobacterium bovis* infection, the cause of bovine tuberculosis (BTB), costs an estimated \$3 billion to global agriculture annually. During the last decade, the maturation of high-throughput sequencing technologies coupled with well-annotated genome resources, has provided an unprecedented opportunity to gain a deeper understanding of host-pathogen interactions for many infectious diseases. Within this context, transcriptional profiling of the host immune response to *M. bovis* infection is a powerful approach for identifying host genes and cellular pathways important to disease pathology. For the present study, ten age-matched male Holstein-Friesian calves were infected endobronchially with *M. bovis* (~2,000 CFU – colony forming units). Peripheral blood samples were collected in duplicate at four time points (-1 week pre-infection, +1 week, +2 week, and +10 week post-infection) and used for:

- a. an overnight stimulation with purified protein derivative of bovine tuberculin (PPD-b) at 37°C
- b. a control overnight incubation at 37°C without PPD-b stimulation.

After isolation of total RNA, poly(A)+ purified RNA was used to generate strand-specific RNA-seq libraries for high-throughput sequencing. Transcripts were quality checked, adapter and quality filtered, and then aligned to the *Bos taurus* reference genome UMD3.1.1. Following summarisation of gene counts, lowly expressed transcripts were removed prior to subsequent gene annotation and differential expression analyses. Results showed 929 differentially expressed (DE) genes at -1 week pre-infection, 1,619 DE genes +1 week post-infection, 1,170 DE genes at +2 week, and 5,535 DE genes at +10 week (compared to non-PPD<sub>b</sub>-stimulated group at each time point; FDR correction threshold  $\leq 0.05$ ).

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## Pharmacokinetics-driven modeling of metabolomics data

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**Emilia Daghir-Wojtkowiak<sup>1\*</sup>, Paweł Wiczling<sup>1</sup>, Małgorzata Waszczuk-Jankowska<sup>1</sup>, Roman Kalisz<sup>1</sup>, Michał J. Markuszewski<sup>1</sup>**

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**Keywords:** pharmacokinetics; metabolomics; Bayesian analysis; ROC; cancer

**R packages:** runjags; coda; caTools; MCMCglmm; caret; Hmisc; lattice

Metabolomics is a dynamically developing research area utilizing high-throughput analytical techniques to detect spectrum of changes in metabolites' levels. However, technological improvements designed for analytical systems are not parallel with the development/application of computational methods which would allow for more efficient elucidation of knowledge from large datasets. In this study, we introduced the concept of pharmacokinetics-driven modelling of targeted metabolomics data comprising nucleoside and creatinine concentration measurements in urine of healthy and cancer patients. An approach using Bayesian analysis was used for the estimation of model parameters. The classification performance of the proposed model was summarized via area under the ROC (Receiver-Operator Curve), sensitivity and specificity using external validation. Cancer was associated with an increase in methylthioadenosine/creatinine excretion rate by a factor of 1.82 (1.33–2.47). Age influenced nucleosides/creatinine excretion rates for all nucleosides in the same direction with likely sex-related differences among several nucleosides' concentrations. The individual a posteriori prediction of patient classification as area under the ROC was 0.58 (0.5–0.68) with sensitivity and specificity of 0.63 (0.46–0.76) and 0.58 (0.45–0.68), respectively suggesting limited usefulness of 13 nucleosides/creatinine measurements in predicting the disease in this population. Pharmacokinetic-based approach in metabolomics may be useful in understanding the data when searching for potential disease indicators.

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## R as a tool for geospatial modeling in large dataset - example of dasymetric modeling at a continental scale (United States)

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**Keywords:** geospatial data; large dataset; dasymetric modeling

**R packages:** rgrass7; rgdal; RSQLite; sp

Geospatial raster datasets are usually large data structures. Thus its processing requires algorithms that are both efficient and fully automatic. The philosophy of development of GIS software offers many solutions to a user. These solutions are conceptually limited which means that they perform well in their native tasks but are difficult to extend if the problem goes beyond its foundations. In such situations computationally complex tasks require tailored software which is difficult to develop without programming experiences. **R** language offers extensive amount of tools designed to work with geospatial data like *sp* library, as well as bindings to external data sources like *rgrass7*, *rgdal*, *RSQLite*. Flexible nature of geospatial objects in **R** allows to create a fully automatic procedure that complements GIS software without long-term programing experiences.

Here we present an automatic procedure which was designed to work on high resolution datasets at a continental scale: 11 million of records in tabular data and over 8 billion of grid cells. To process such amount of data we automated our procedure by dividing it into few steps:

1. import and store Census data in SQLite database,
2. preprocessing of geospatial data performed in GRASS GIS software,
3. performing dasymetric modeling in **R**,
4. propagation model for geospatial data and export geospatial data from **R** to GIS format to map population distribution.

Our results show that:

1. **R** can perform such a calculation in a reasonable time (60 hours for the entire U.S.),
2. no additional intermediate layers or steps are required,
3. procedure is flexible: it can be reproduced regardless of the data scale.

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## Application of Artificial Neural Network to Planar Chromatography Data

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**Keywords:** chemometrics; neural network; planar chromatography

**R packages:** deepnet; jpeg; abind; EBImage

Planar chromatography has a unique specificity compared to other chromatographic techniques, i. e. the data format is a picture, in which each pixel has quantitative and qualitative properties that corresponds to the molecular reality in the physical world. This results in a greater amount of data points that allows the use of high-level machine learning algorithms like artificial neural network. Restricted Boltzmann Machine was used on planar chromatograms for denoising and classification. For both, no other preprocessing than a normalization between 0 and 1 was needed. The denoising task took as input patches of pixels; when crossing the network, the noise is removed and only the signal remains. For the classification task, several layers of this neural network were stacked together in order to analyze vertical bands of pixels. The last layer of this network discriminated the two classes of the dataset with an accuracy of 85 % when compared to human decisions.

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## cgmisc: enhanced genome-wide association analyses and visualization

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**Marcin Kierczak<sup>1</sup>, Jagoda Jabłońska<sup>1\*</sup>, Simon Forsberg<sup>2</sup>, Matteo Bianchi<sup>1</sup>, Katarina Tengvall<sup>1</sup>, Mats Pettersson<sup>1</sup>, Veronika Scholz<sup>1</sup>, Jennifer Meadows<sup>1</sup>, Patric Jern<sup>1</sup>, Örjan Carlborg<sup>2</sup>, Kerstin Lindblad-Toh<sup>1,3</sup>**

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**Keywords:** GWAS; bioinformatics; visualization; sequencing

**R packages:** cgmisc; GenABEL

High-throughput genotyping and sequencing technologies facilitate studies of complex genetic traits and provide new research opportunities. The increasing popularity of genome-wide association studies (GWAS) leads to the discovery of new associated loci and a better understanding of the genetic architecture underlying not only diseases, but also other monogenic and complex phenotypes. Several softwares are available for performing GWAS analyses, R environment being one of them. We present *cgmisc*, R package that enables enhanced data analysis and visualization of results from GWAS. The package contains several utilities and modules that complement and enhance the functionality of the existing software. It also provides several tools for advanced visualization of genomic data and utilizes the power of the R language to aid in preparation of publication-quality figures. Some of the package functions are specific for the domestic dog (*Canis familiaris*) data but are easy to adjust for analysing other species.

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## **Penalized regression inference regarding variable selection in regular and high dimensions: comparison of selected methods implemented in R**

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**Keywords:** penalized regression; inference; p-value

**R packages:** lassoscore; hdi; refund

In recent years, penalized regression techniques, such as lasso, have become commonly used for variable selection in linear regression modeling, but relatively little work has been done on quantifying the uncertainty in these procedures. Here, we perform comparison of four different approaches to this problem. With a score test method, penalized regression of an outcome on all but a single feature is performed, and test for correlation of the residuals with the held-out feature follows. PEER Ridge estimation procedure exploits the equivalence between penalized least squares estimation and a linear mixed model representation, and thus provides an automatic selection of tuning parameter alpha using REML criterion; then, the General SVD provides algebraic insight and a convenient way to derive the variance expressions of the estimates, which allows to perform inference regarding variable selection. With Multi sample-splitting method, the sample is split into two equal halves, where the first half is used for variable selection and the second half, with the reduced set of already pre-selected variables, is used for statistical inference in terms of *p*-values. In stability selection method, a stable subset of variables is selected in stochastic simulation where probability of a variable being selected into a model is approximated. We utilized **R** implementations of the methods listed above to compare variables selection inference in terms of FDR and power. We experimented with different covariance settings as well as dimensions of X design matrix in looking for situations when one method might be preferred.

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## **Wrestling with big data in forestry: use of R in Scots pine site index analysis.**

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**Keywords:** national forest inventory; permanent plots; site index

National Forest Inventory (NFI) supplies high resolution data on forests of all property forms located throughout the country. These data are collected from the circular sample plots uniformly distributed in grid of squares 4 by 4 km. In Poland, around ~27,900 sample plots were established. Recently, the second measuring cycle NFI was completed, which, in addition to a potentially wide range of spatial analysis, creates a unique opportunity to analyze the change in the pattern of tree growth through time, giving opportunity to describe the reaction of species to changes of environmental conditions. NFI data give a great opportunity to determine one of the most important forest habitat's productivity factors – site index. It is often expressed as the average height of the trees of the target species at a given age. Determination of the site index for the dominant species in the stand allows one to characterize its growth potential in examined habitat conditions. The project envisages the use of empirical data collected in NFI to determine the structure of pine stands site index in Poland. Relatively high number of sample plots and complicated computations as well as future need for geostatistical analyses were reasons to choose **R** environment to work successfully with forestry big data.

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## An R implementation of Kauffman's NK model

---

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**Keywords:** nk model; complexity; fitness landscape; agent-based modeling

**R packages:** dplyr; ggplot2; igraph

Stuart Kauffman's NK model is a simple but powerful model of complex system with many interactions between its elements. It generates so called fitness landscape, i.e. a space consisted of many points with different attractiveness (fitness). The great advantage of the model is that only two parameters ( $N$  and  $K$ ) are required to be controlled to generate environments with 'tunable complexity' – from very simple with one local and global optimum to completely random, with a large number of local optima. The NK

model is used in the studies of many phenomena in various fields e.g. biology, economics, organizational studies or engineering. In my presentation I would like to introduce an **R** package which implements the NK model and show how to use it to generate fitness landscapes and explore their properties for different influence matrices.

---

## R as an effective data mining tool in chemistry

---

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**Keywords:** data mining; predictive modeling; ionic liquids; chemometrics

**R packages:** ggplot2; stats; dendextend; matrixStats; Matrix; MASS; klaR; cluster; dplyr; FWDselect

The vast amount of digital information generated every day in social media, industry and academia necessitates the use of advanced techniques enabling the processing, analysis and interpretation of data. A significant amount of data is generated during various types of chemical experiments. In this work, we present a workflow for predictive modeling of physical-chemical properties of a diverse group of chemicals (ionic liquids). Using selected chemometric methods, available in the most popular **R** packages, we analyze the chemical data, model key physical-chemical properties and validate the results. Moreover, the presented approach enables the evaluation of the raw data quality. We choose two unsupervised methods for data exploration: hierarchical cluster analysis (HCA) and principal component analysis (PCA). Multiple linear regression technique (MLR) was chosen as the example of a modeling technique.

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## Applying genetic algorithms to calibrate a processing chain for a Landsat-based time series analysis of disturbance - regrowth dynamics in tropical forests

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**Keywords:** time-series analysis; genetic algorithms; Landsat; tropical forests monitoring

**R packages:** GA; changepoint; BreakoutDetection; ecp

We present an innovative approach to calibrate processing chains designed for a time-series analysis based on genetic algorithms (GA). Using a case study of disturbance-regrowth monitoring employing Landsat data in tropical forests located in the Amazonian region of Ecuador. This area is characterized by mountainous terrain, high topographic relief and extensive cloud cover. These conditions can cause noise in the time-series of Landsat data and require different corrections before its analysis. We describe here the use of GA to reduce calibration uncertainties, enhance the output accuracy, and avoid unnecessary processing caused by trial-and-error approaches in remote sensing.

---

## Modelling the distribution of the bryophytes in different spatial scales

---

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**Keywords:** species distribution model; biodiversity; plant ecology; predictive modelling; mosses; forest

**R packages:** dismo; rasterVis

Species distribution models (SDM) are mathematical models describing distribution of species within environmental (ecological) and geographical space. These models are used for biodiversity conservation in two ways: to find out threatened species requirements and to predict spread of invasive species. We aimed to model distribution of model bryophyte species – *Dicranum viride* – in Poland and in Europe and compare its ecological niches obtained by these two models. We chose *D. viride*, as this easily-recognizable species is a subject of Natura 2000 protection and an ancient forest species. Thus, it may be an umbrella species for numerous bryophyte species occurring on decaying wood and in old woodlands. We used data from Global Biodiversity Information Facility (<http://www.gbif.org>), published papers and herbarium collections to find out complete information about *D. viride* localities. As most of data about species distribution for large areas is presence-only data, we used MaxEnt model from *dismo* package,

which is developed to processing this type of input data. As the explanatory variables we used 19 bioclimatic statistics from WordlClim database, available in 2.5' grid and, in case of model for Poland only, data about share of old ( $>100$  years old) forests within grid square. We also analyzed data about phorophyte species and collection year. Model developed by MaxEnt is a probabilistic model, which due to Receiver-Operator Curve allow to manage the threshold of species occurrence, and thus – its restrictiveness. Our model has shown importance of particular bioclimatic variables and potential distribution of species. Obtained results allow us to conclude about climatic requirements of species studied and its potential habitats, where species may be found or may be protected ex situ. SDMs are very useful tool for plant geography, biodiversity conservation and ecology.

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## Mortality mapping using R

---

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**Keywords:** spatial epidemiology, disease cluster

**R packages:** R2WinBUGS; INLA; spdep; GWR

Analyses of spatial distribution of mortality are important tool for searching of risk factors and as a starting point for preventing actions. Several techniques used for more deep analysis of spatial disease pattern are presented. Due to small number of in poviats deaths mortality characteristics shows large variability. Bayesian Besag-York-Mollie model was used for general spatial trend modelling and producing smooth disease maps. Local Moran coefficient was used to detect clusters of increased mortality. Geographically weighted regression technique as used for inspecting dependence between mortality and deprivation index in different county regions. This work was financed by research grant PL13 Reducing Social Inequalities in Health.

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