

Conference chairs:

Professor Dr. Karl-Ernst Biebler (Greifswald)
Professor Dr. Dietmar Cieslik (Greifswald)
Professor Dr. Andreas Dress (Shanghai)
Professor Dr. Georg Füllen (Greifswald)
Dr. Martin Haase (Greifswald)

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Information and Registration:

Please apply for the autumn academy via the following url: www.wiko-greifswald.de/anmeldung

The autumn academy is open to applicants who are interested in applied mathematics. Participants are supposed to have basic knowledge in mathematics and informatics. The conference language is English. Registration is free of charge.

In order to take part in the academy, a registration is required. Application deadline is September 29, 2008.

An autumn academy organized by the Alfried Krupp Wissenschaftskolleg Greifswald, financially supported by the Alfried Krupp von Bohlen und Halbach-Stiftung, Essen.

Phylogenetics has attained a central role in evolutionary biology with relevance in both, basic and applied research. The reconstruction of evolutionary processes based on sequence data emerged as a crucial issue in molecular biology. The results play an important role in the classification of species and microbiological entities, in biodiversity research, in the development of drugs and vaccines, and in several other topics. Therefore, phylogenetic combinatorics is being pursued in various directions. Starting with well-known techniques, we will describe new approaches and discuss open questions.

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Alfried Krupp Wissenschaftskolleg
Greifswald

Phylogenetic Combinatorics

Autumn academy
October 6 – 10, 2008

Monday, October 6, 2008

9.00 – 10.30

Phylogenetic networks

Andreas Dress (Shanghai)

In the lecture, we will discuss how sequence- and distance data can be used to derive phylogenetic information.

10.30 – 11.00

Coffee break

11.00 – 12.30

Phylogenetics. Past, present and future

Martin Haase (Greifswald)

Phylogenetics has attained a central role in evolutionary biology with relevance in both basic and applied research. Based on a historical account of the development of formalized methodologies in systematics, currently established approaches, viz. maximum parsimony, distance methods, maximum likelihood, and Bayesian inference, will be introduced. Strengths and weakness of these tree-building methods will be discussed. Progress in our understanding of sequence evolution as well as the rapid development of laboratory techniques and data mining demonstrate limits of the standard methods routinely used in phylogeny reconstruction. Guidelines for the future will be presented.

12.30 – 14.00

Lunch break

14.00 – 15.30

Sequence data and models of inheritance

Karl-Ernst Biebler (Greifswald)

Associations and correlations of sequence data and phenomena (e.g. illness X) do not explain any causalities. Causalities are conceptualized as models of inheritance. It was this idea, first conceived by Gregor Mendel, that became fundamental to modern genetics. We will define ideal populations and Mendelian models of inheritance. How many Mendelian models do exist? The answer will be given for selected situations. Parameter estimations and their properties are derived. The problem of the model choice is treated. Some extensions of Mendelian models are outlined.

Tuesday, October 7, 2008

9.00 – 10.30

Phylogenetics. Past, present and future

Martin Haase

10.30 – 11.00

Coffee break

11.00 – 12.30

Phylogenetic networks

Andreas Dress

12.30 – 14.00

Lunch break

14.00 – 15.30

Phylogenetic networks

Andreas Dress

Wednesday, October 8, 2008

9.00 – 10.30

Sequence spaces

Dietmar Cieslik (Greifswald)

We introduce so-called sequence spaces. These are metric spaces which points are arbitrary words generated by letters from some (finite) alphabet, and the metric measuring "sameness" of the words which is generated by a cost measure on the alphabet. In this sense, our considerations will play an important role in the construction of phylogenetic trees, which typically represent the evolutionary history of a collection of extant species or the line of descent.

10.30 – 11.00

Coffee break

11.00 – 12.30

Phylogenetic networks

Andreas Dress

12.30 – 14.00

Lunch

14.00 – 15.30

Phylogenetic networks

Andreas Dress

Thursday, October 9, 2008

9.00 – 10.30

Sequence data and models of inheritance

Karl-Ernst Biebler

10.30 – 11.00

Coffee break

11.00 – 12.30

Homology and Phylogeny – Applications and Large-Scale Analyses

Georg Füllen (Greifswald)

Phylogenetics and the (underlying) concept of homology will be tested with respect to the applicability to large-scale data analysis in biology and biomedicine. We discuss gene/species trees, homology search in genomic data and protein databases, genome annotation using homology search and phylogenetics, and large-scale automation of phylogenetic analyses (by so-called phylogenomic pipelines).

12.30 – 14.00

Lunch break

14.00 – 15.30

Homology and Phylogeny – Applications and Large-Scale Analyses

Georg Füllen

Friday, October 10, 2008

9.00 – 10.30

Phylogenetic networks

Andreas Dress

10.30 – 11.00

Coffee break

11.00 – 12.30

Phylogenetic networks

Andreas Dress

12.30 – 14.00

Snacks

14.00

Examination