Île Rousse

Calvi

Cargèse

Ajaccio

Propriano

EMBO

EMBO Practical Course on Computational RNA Biology

April 26 – May 1, 2010
Institut d'Études Scientifiques de Cargèse, Corsica

C–G
A-U
G-C
U-A
G-C
U-G

EMBO

application and registration
http://www.zbit.uni-tuebingen.de/pas/EMBO-RNACourse/

deadline for registration
January 15, 2010

prices
academic participants: 250 Euro,
participants from industry: 500 Euro
Prices include all meals, accomodation, and lecture notes.

organization
Kay Nieselt, Tübingen
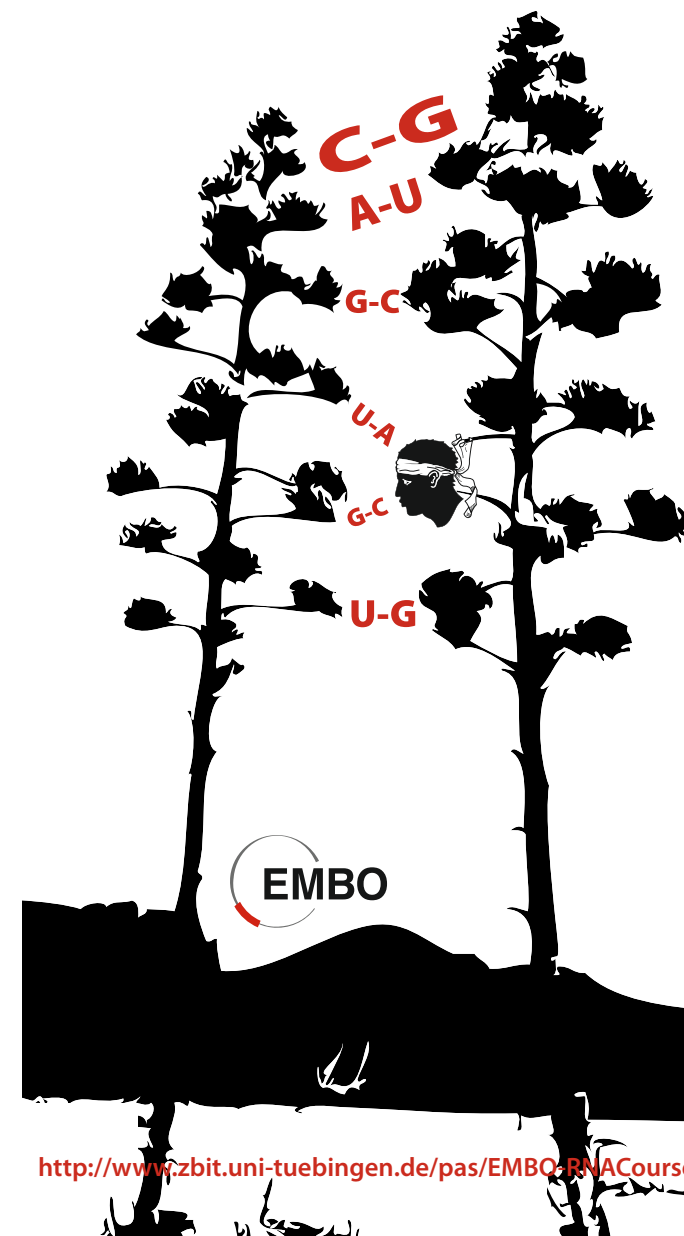Robert Giegerich, Bielefeld
Eric Westhof, Strasbourg

contact
Kay Nieselt, nieselt@informatik.uni-tuebingen.de

location
The Institute I.E.S.C. in Cargèse, Corsica, is widely known for its summerschools and workshops. It combines professional organization, and a pleasant, stimulating environment. The institute provides seminar rooms, library, computer rooms and modern IT infrastructure. Accomodation of participants and lecturers is partly on-site, and partly in the picturesque village of Cargèse.

http://www.zbit.uni-tuebingen.de/pas/EMBO-RNACourse

topics

thermodynamics and kinetics
minimum free energy, thermodynamic stability, kinetic folding

2D structure prediction
RNA folding, optimal and suboptimal structures, base pair probabilities, abstract shape analysis

structure comparison
structure alignment, consensus shapes

miRNAs and target prediction
genome-wide prediction, target prediction and characterization, expression

RNA databases
Rfam, miRBase, BRaliBase

modelling of RNA families
motif definition and motif search, structural clustering, covariance models

RNA gene prediction
from models, from 2D folding and comparison

RNA sequencing
deep sequencing of RNA transcripts

RNA 3D modelling
3D structure prediction, dynamics, simulations

computer tools
Vienna RNA package, RNAshapes, RNAz, RNAforester, Infernal, s2s, Assemble and more

motivation

Recent years have brought evidence of an unexpected wealth of functional roles of RNA – in programmed cell differentiation, disease, metabolic sensing, brain processes, and more. RNA deep sequencing and computational screens yield large numbers of candidate RNAs asking for functional analysis. Just in time with the increased interest in roles of RNA, computational tools dealing with RNA have been sharpened and extended. Skillful use of state-of-the-art computational methods is increasingly important for successful work in RNA biology.

audience

This EMBO Course addresses RNA biologists on the PhD-student or postdoctoral level. It teaches the effective use of computational tools for tasks such as comparative structure prediction, miRNA and target prediction, RNA family modelling and database searching based on structure. The course emphasizes the models behind the algorithms, whose understanding is essential for using the tools effectively, and provides practical, guided exercises in extensive computer labs.

lectures and courses

The course will provide lectures and hands-on, computer-based courses. There will be ample time to exchange experience and new ideas with other course participants and with the lecturers, who will be available on-site throughout the course.

prerequisites

The course requires good basic knowledge about RNA biology and its multi-facette functions in the organism. It also requires standard computer literacy. Participants should be prepared to start a program from the command line, while algorithmic skills or programming experience are not required. A first edition of this course was held at the same location in 2008.

lecturers

Rolf Backofen
Bioinformatics Group, University of Freiburg

Christoph Flamm
Theoretical Biochemistry Group, University of Vienna

Paul Gardner
Sanger Institute, Hinxton, Cambridge

Robert Giegerich
Practical Computer Science and Bioinformatics, Bielefeld University

Sam Griffiths-Jones
Faculty of Life Sciences, University of Manchester

Ivo Hofacker
Theoretical Biochemistry Group, University of Vienna

Debora Marks
Harvard Medical School, Boston

David Mathews
Department of Biochemistry & Biophysics, University of Rochester

Irmtraud Meyer
UBC Bioinformatics Centre, Vancouver

Kay Nieselt
Center for Bioinformatics, Tübingen, University of Tübingen

Cynthia Sharma
Max Planck Institute for Infection Biology, Berlin

Peter F. Stadler
Bioinformatics Group, Department of Computer Science, University of Leipzig

Gerhard Steger
Institute for Physical Biology, Heinrich-Heine-University of Düsseldorf

Eric Westhof
Institut de Biologie Moléculaire et Cellulaire du CNRS, Université Louis Pasteur, Strasbourg