## Schedule

### Tuesday, September 5
- 9:30 – 10:30 Robert Ghrist
- 10:30 – 11:00 Morning Break
- 11:00 – 12:00 Günter Ziegler
- 12:00 – 1:30 Lunch
- 1:30 – 2:30 Sergio Rajsbaum
- 2:30 – 3:30 Konstantin Mischaikow
- 3:30 – 4:00 Afternoon Break
- 4:00 – 5:00 Shmuel Weinberger
- 5:00 – 6:00 Reception

### Wednesday, September 6
- 9:30 – 10:30 Robert Ghrist
- 10:30 – 11:00 Morning Break
- 11:00 – 12:00 Rade Zivaljevic
- 12:00 – 2:30 Lunch
- 2:30 – 3:30 Konstantin Mischaikow
- 3:30 – 4:00 Afternoon Break
- 4:00 – 5:00 Susan Holmes

### Thursday, September 7
- 9:30 – 10:30 Gunnar Carlsson
- 10:30 – 11:00 Morning Break
- 11:00 – 12:00 Eric Babson
- 12:00 – 1:30 Lunch
- 1:30 – 2:30 Bob MacPherson
- 2:30 – 3:30 Persi Diaconis
- 3:30 – 4:00 Afternoon Break
- 4:00 – 5:00 Contributed Talk: Rima Izem

### Friday, September 8
- 9:30 – 10:30 Gunnar Carlsson
- 10:30 – 11:00 Morning Break
- 11:00 – 12:00 Yuliy Baryshnikov
- 12:00 – 1:30 Lunch
- 1:30 – 2:30 Persi Diaconis
- 2:30 – 3:15 Contributed Talk: Christian Laing
- 3:15 – 4:00 Contributed Talk: Steven Ellis
Contributed Talks

**Rima Izem**
**Christian Laing**

**Talk Title:** Writhe invariants as RNA shape descriptors  
**Keywords:** writhe, RNA, classification

**Abstract:** Given a polygonal curve (not necessarily closed or connected), geometric measures involving combinations of writhe and average crossing numbers of subcurves can be computed to obtain a set of features for the purpose of shape characterization. The function of nucleic acids and proteins are determined to a very large degree by the 3-dimensional shape of the biomolecule. We apply these writhe-based shape descriptors to RNA tertiary structures based on the polygonal carbon-phosphate backbone of the RNA. These geometric measures have been previously used by Peter Rogen and Boris Fain to correctly classify protein domains, by using the protein backbone of alpha-carbons, and producing a 98.5% success rate. In aims to find an optimal projection of the feature space into a plane that maximizes the variance among RNA classes, principal component analysis methods are applied. Also clustering techniques such as multiple discriminant and principal component analysis methods are used in the RNA shape classification. Among tRNA structures a differentiation between thermophilic and non-termophilic species is obtained, and also, a clear distinction between tRNA and diverse Ribozymes is produced.

**Steven Ellis**