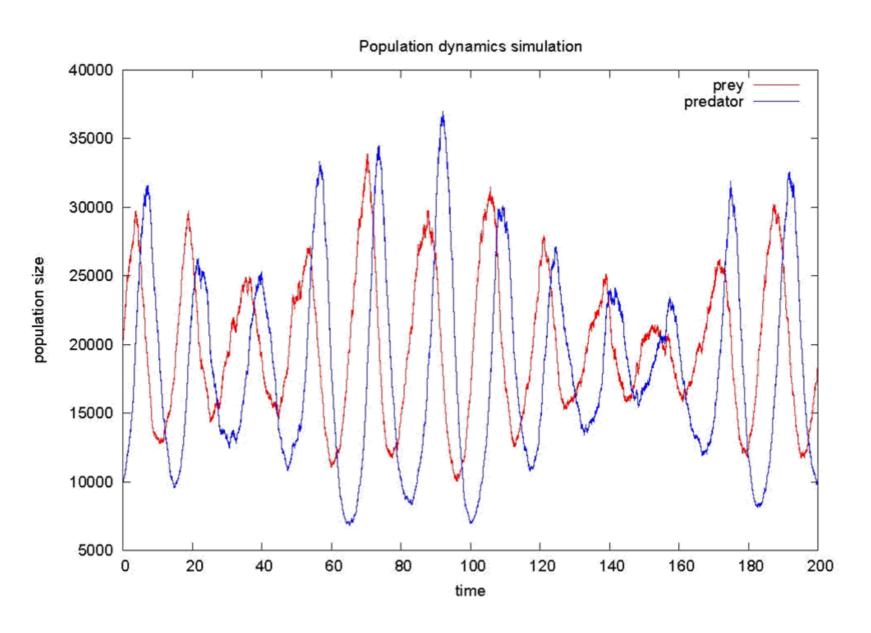
First floor topics

- Does it matter where you go?
 - one can change groups (in principle)
- what it means
 - seminar (small talk)
 - software project
 - masterarbeit
 - optional subjects (wahlpflicht)
- close contact with group members
- to do
 - talk to PhD students + students from last year

Names

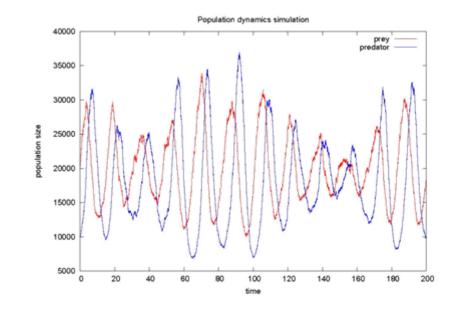
- students who are still around
 - Björn Hansen, Jacques Kühl (projects and seminars now)
 - Birute Karsten (now with Rarey group)
 - Marvin Mundry (worked as HiWi)
- Doktoranden
 - Paul Reuter
 - Nasir Mahmood
 - Stefan Bienert
 - Gundolf Schenk
 - Thomas Margraf

- Seminars
 - anything
- Software projects
 - small groups, technical projects
- Mastersarbeit
 - 1 semester serious project
 - in one of our research areas / external projects
- Broad areas
 - evolution
 - RNA
 - protein simulation / comparison / prediction

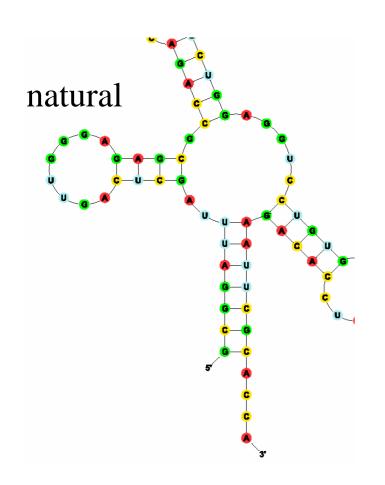


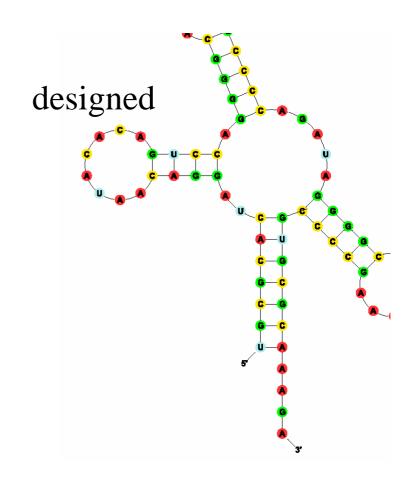
Evolution simulations

- Evolution applied to organisms? No
- what makes a whole system evolve?
- predator / prey, Hasen / Fuchs
 - do they evolve in isolation?
- what is evolving?
 - interaction parameters
- Paul's area
 - multi-level simulations
 - differential equations + high level search

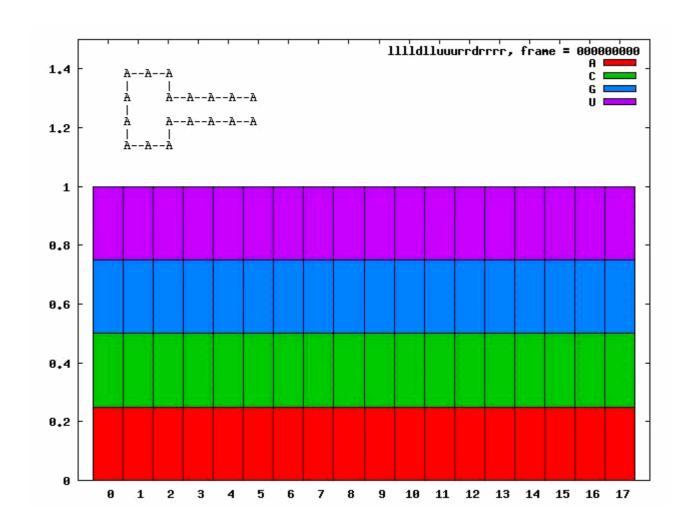


- Structure prediction
- Sequence design
- Work with biochemistry
 - finding riboswitches, sequence-based properties
- Side issues
 - drawing, pseudoknot removal
- Examples
 - structure prediction
 - sequence design





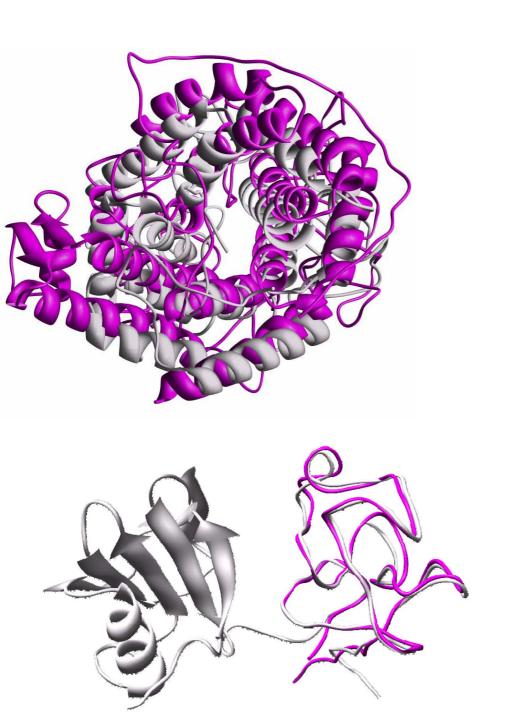
RNA

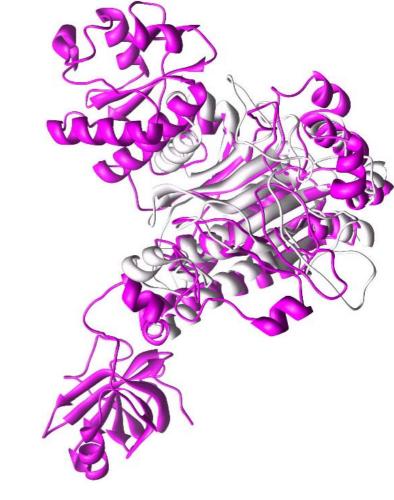


movie from Marco Matthies

Gundolf Schenk Nasir Mahmood Thomas Margraf





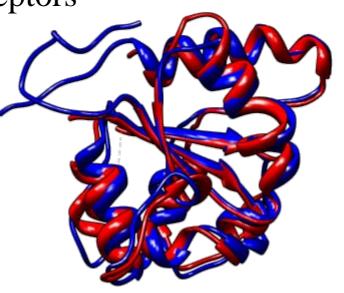


- very fast
- handles missing pieces..
- what is more interesting?

• TLR / toll-like receptors

48 % sequence id 1o77

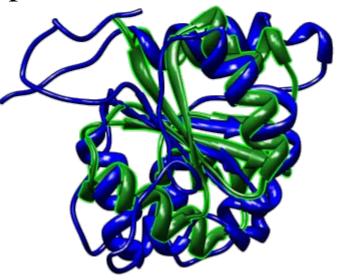
another TLR



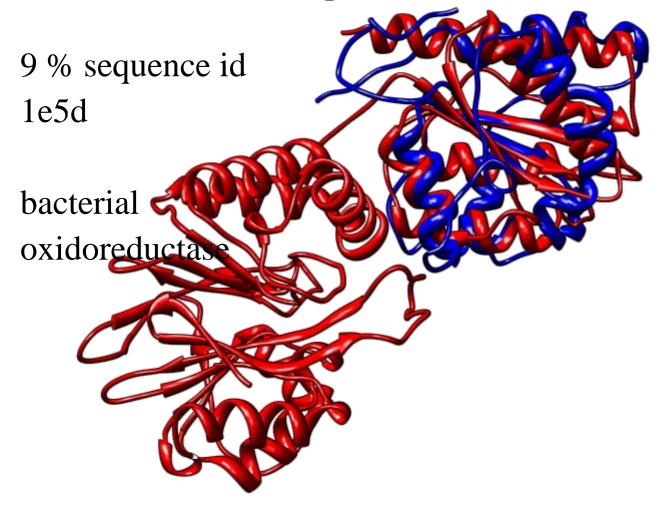
• TLR / toll-like receptors

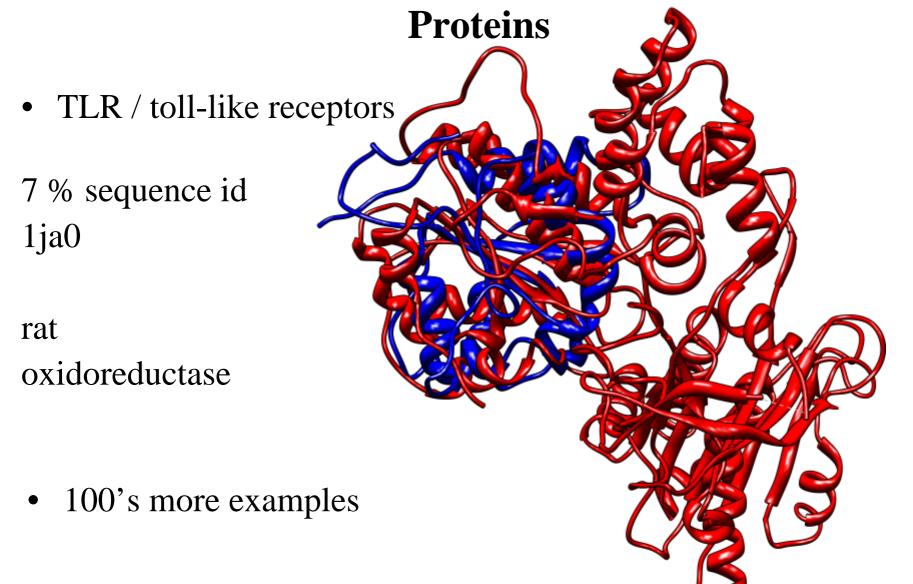
6 % sequence id 2qxy

response regulator T. Maritima



• TLR / toll-like receptors





how are they calculated?

Research themes

- structural phylogenies
- structure prediction
- sequence design

Typical projects

- phylogeny / distance embedding
- force fields for structure prediction

