# Translational Bioinformatics in Drug Discovery

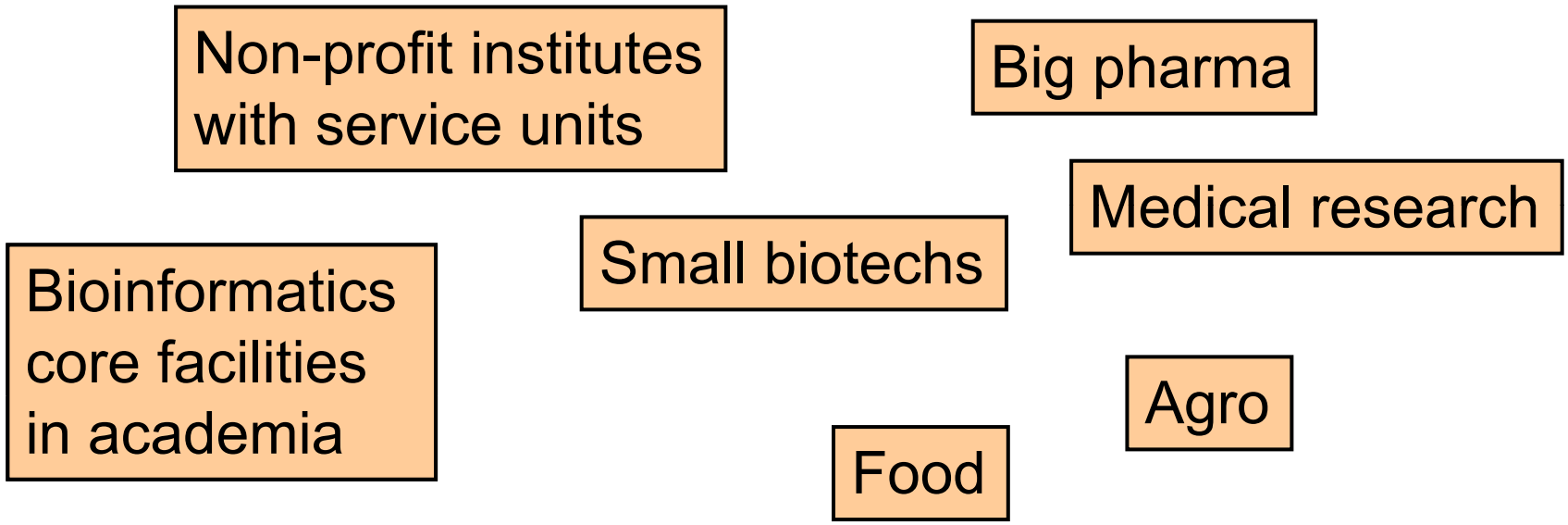
Michael Rebhan (Novartis Pharma AG, Basel, Switzerland)

ISMB July 2008, Toronto

BoF: Discussion on best practice for bioinformatics cores

NOVARTIS

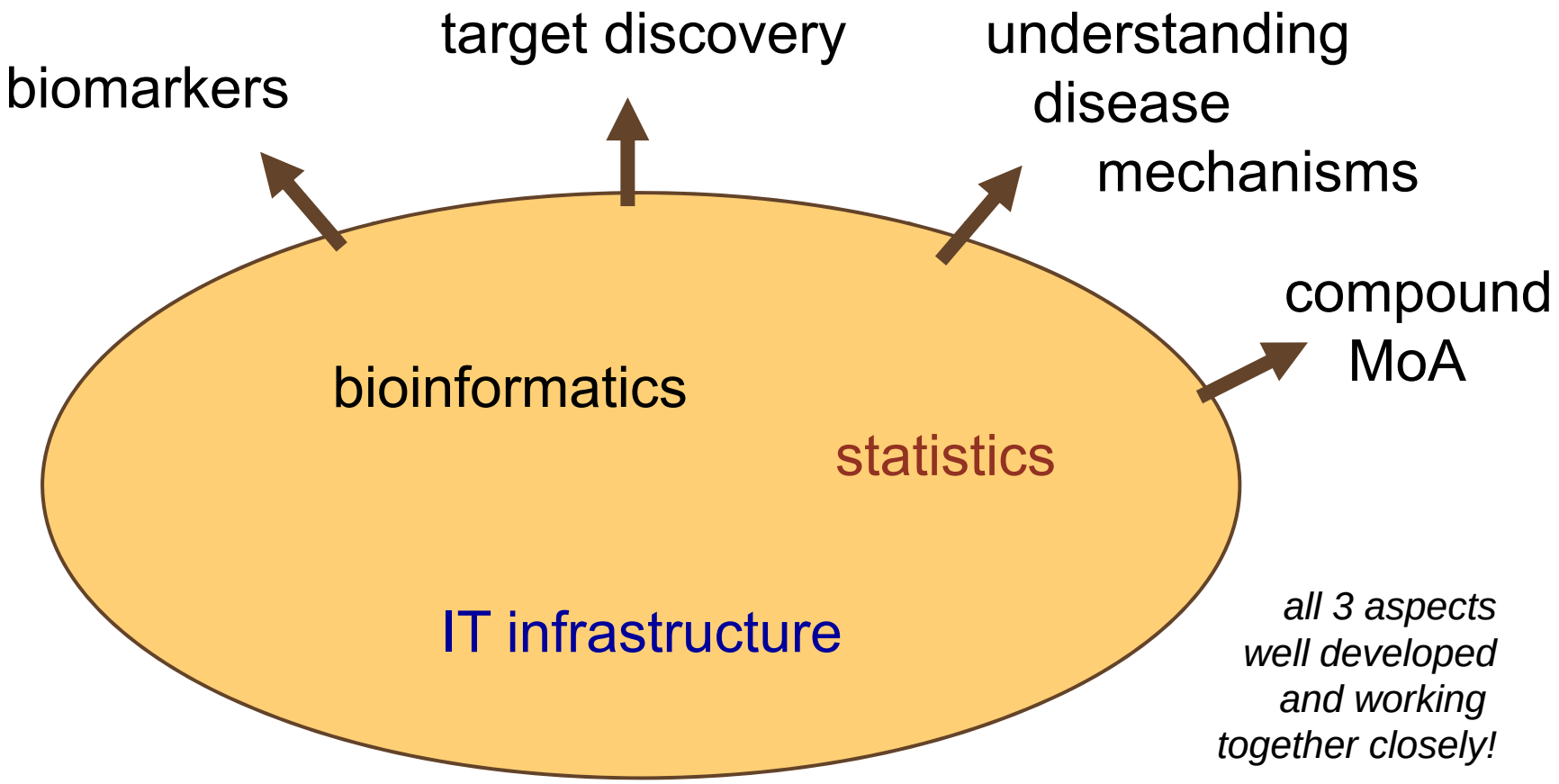
# What is best practice? How much does it vary?






NOVARTIS

# Bioinformatics in Biotech & Big Pharma

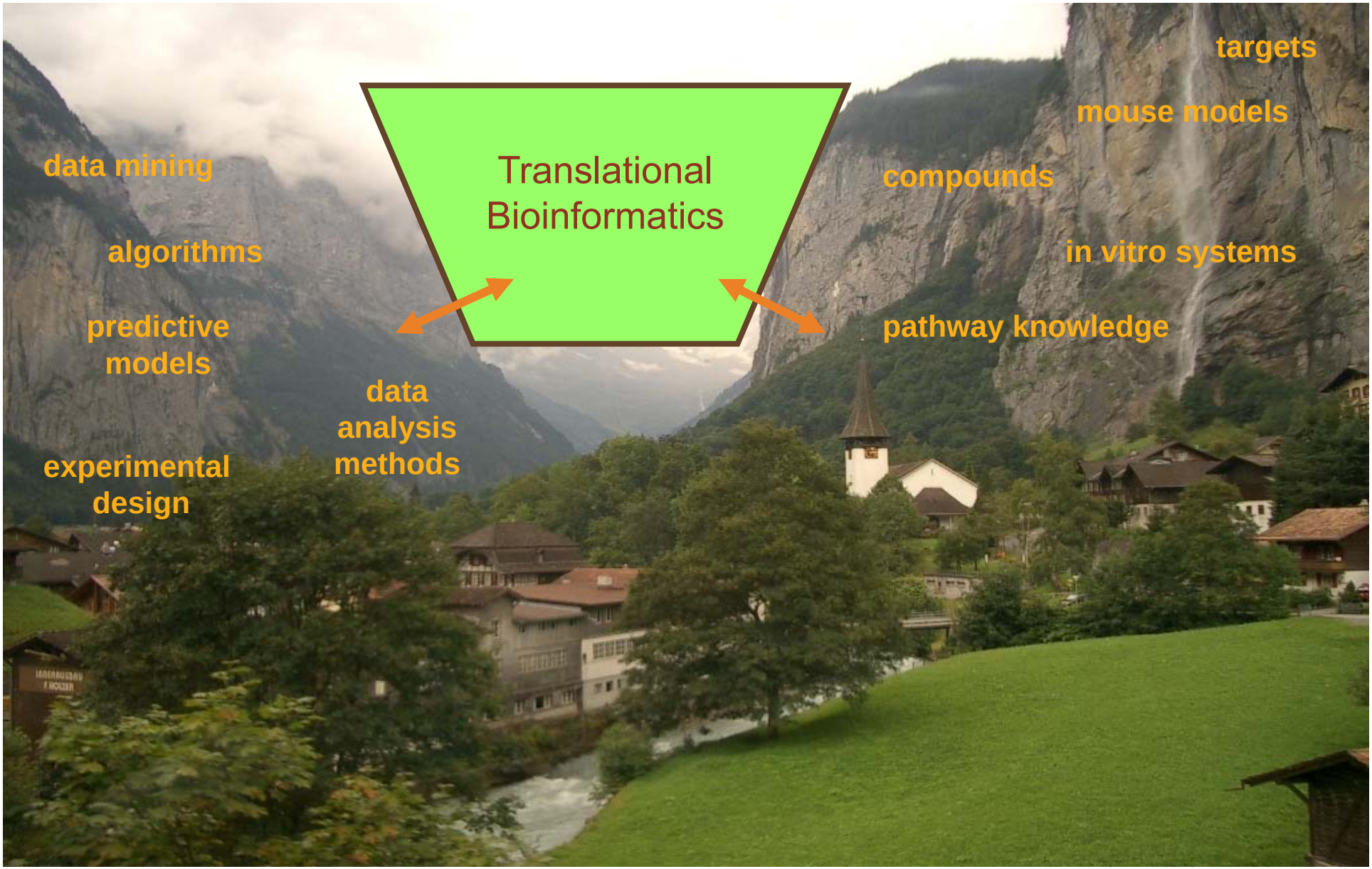



*all 3 aspects well developed and working together closely!*



NOVARTIS

# The Gap


targets
mouse models
data mining
Translational
Bioinformatics
compounds
algorithms
in vitro systems
predictive
models
pathway knowledge
data
analysis
methods
experimental
design

# Translational Bioinformatics

Transformation of genomic (and related biomedical) data into therapeutic (or diagnostic) concepts

- Staff with experience on both sides of the gap!
  - Relevant biology background plus several years of bioinformatics exposure (not afraid of scripting, careful usage of tools, curious!)
- Which datasets are most relevant? Which tools/methods?
  - Careful judgement of most relevant datasets, including public data for comparison
- Multiple lines of *in silico* evidence → justify costly experiments (e.g. using mouse models, patient samples)
- Less method development, more applied (using existing tools effectively)
- Expectation management within the organization
  - "Buy-in": key partners, showcases, informal and formal communication, presence at biology discussions, …

# Some Factors

- Ability to influence experimental design, early involvement
- Joint projects with wet lab units, finding key partners
  (benefits for those who are good partners)

  Service projects $\leftrightarrow$ True collaborations
  (basic analysis) (extensive analysis)
- Critical mass for the core:
  - Expertise (monitoring of external developments, their relevance)
  - Links into other groups/departments, sufficient focus!
  - Internal tool landscape: critical tools? is the tool mature enough?
- Testable hypotheses
  (incl. some aspects of experimental design, e.g. which primers or probes to use)

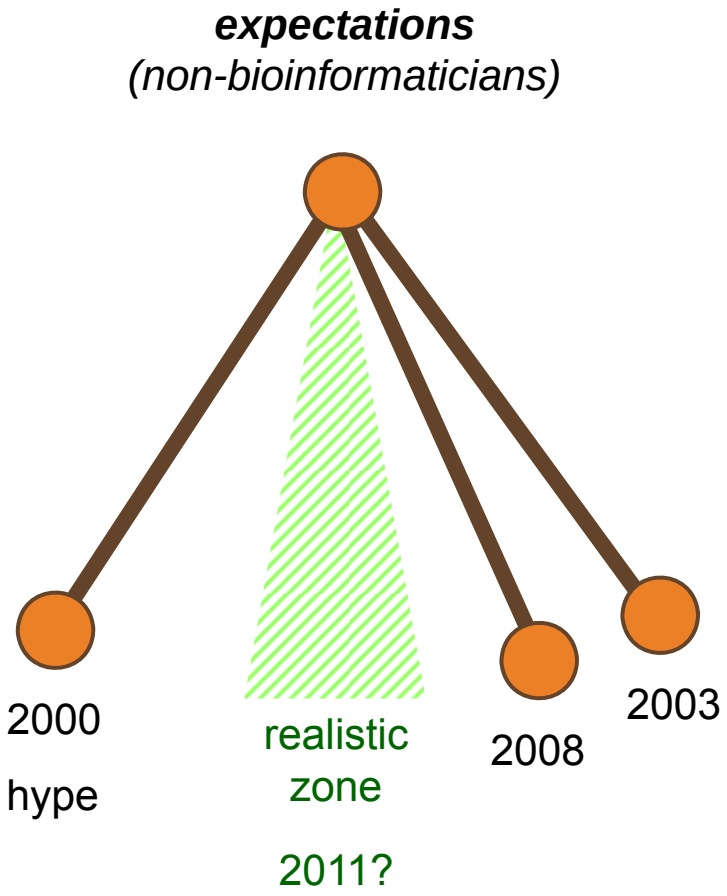
# Perspective

## Don't worry about:

1. *The amount of data produced by a single researcher will decrease*

2. *The data will become less heterogeneous*

3. *Communication will become easier*





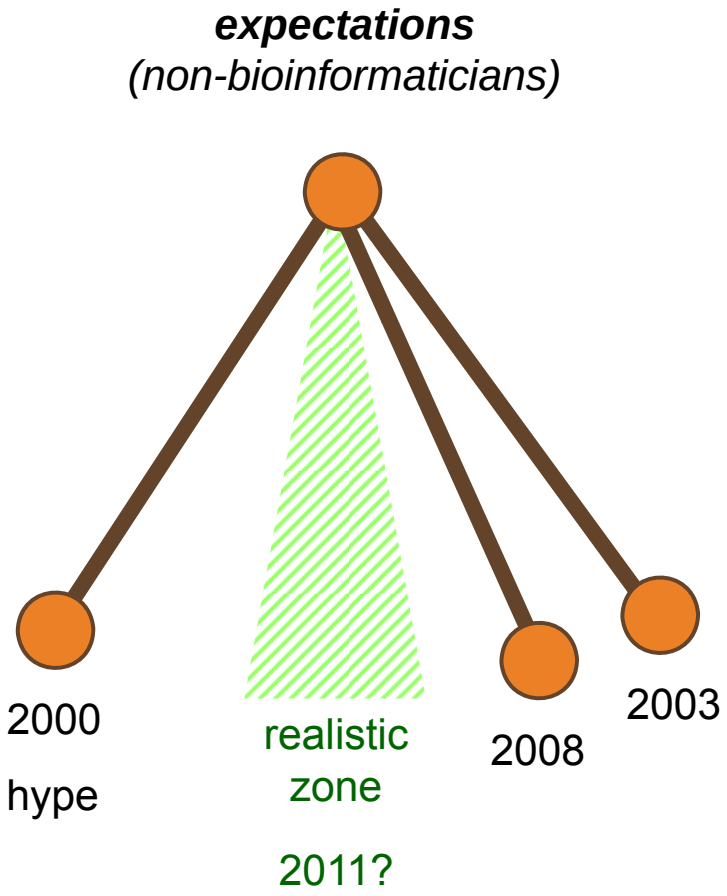

NOVARTIS

# Approaching the “realistic zone”

*Next gen sequencing*
*Epigenomics*
*Exon arrays*
*HT assays*
*etc. etc.*

How many “in silico biologists” do we need **per data-producing researcher** in 2011?

*Where will all those people come from??*






NOVARTIS