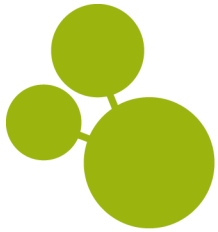

MAGNet

MULTISCALE ANALYSIS OF GENOMIC AND CELLULAR NETWORKS

Chris Wiggins

Associate Professor of Applied Mathematics

Columbia University

August 16 2006: Evening Panel Discussion

Mission

- ***Basic Science**: multiscale approach to biological networks (inference, organization, analysis)*
- ***Software Tools**: integrative framework (flexible, open source)*
- ***Driving Biological Projects:***
  - **structure / energetics of cadherin binding specificity**
  - **regulatory modules in normal and transformed b-cells**
  - **genomic / bioinformatics of determinants of complex, heritable disorders**

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MAGNet: Organization

MAGNet MULTISCALE ANALYSIS OF GENOMIC AND CELLULAR NETWORKS

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ADMINISTRATION

Andrea Califano
Principal Investigator
Department of Biomedical Informatics

Barry Honig
co-Principal Investigator
Department of Bibiochemistry and Molecular Biophysics

Aris Floratos
Executive Director
Joint Centers for Systems Biology

Jo-Ann Espaillat
Chief Administrator
Joint Centers for Systems Biology

(from magnet.c2b2.columbia.edu/people.php)

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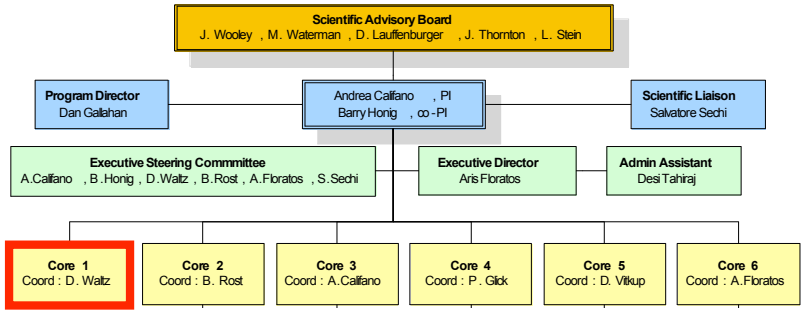
Core I: Computational Sciences

Coordinator: **Waltz**
Proj. Lead: **Leslie, Wiggins, Friedman, Califano, Yemini**
Invest.: **Servedio, Lussier, Kaiser, Ofran, Ross**

- **Machine Learning -** Classification, Network analysis, Functional analysis.
- **NLP -** Analysis of Literature for biomedical content (genotytic/phenotypic)
- **Software Design -** BISON, an ontology for bioinformatics interoperability
- **Biomedical Database Integration -** GeneTegrate a semantic layer for bioinformatics data integration



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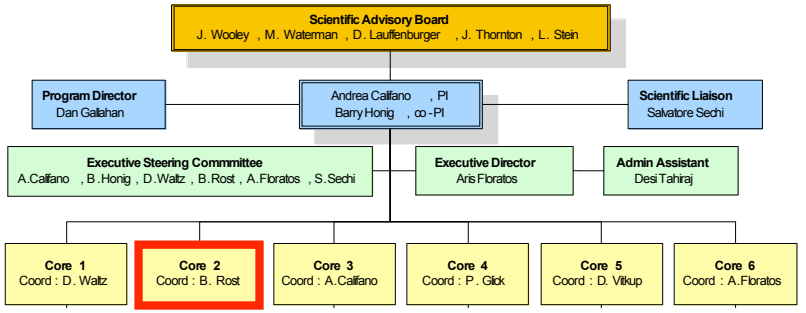
Core II: Bioinformatics

Coordinator: **Rost**
Leaders: **Honig, Bussemaker, Califano, Rzhetsky, Lussier**
Invest.: **Yemini, Ofran, Petrey, Long, Anastassiou, Leslie, Pavlidis, Wiggins, Friedman**

- ***Protein Structure and Function -*** Sequence and structure based annotation of protein function (specifically protein-protein interactions):
- **MAGNet Tools -** Software platform (geWorkbench)
- **Reverse Engineering of Cellular Networks**
- **Cellular and Molecular Context -** Using cellular and molecular phenotypes for context filtering



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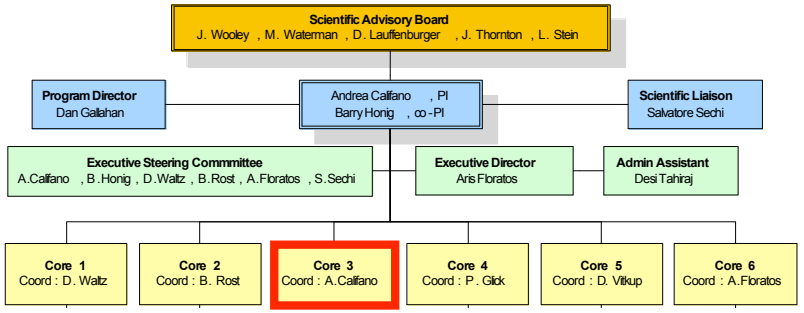
Core III: Driving Biological Projects

Coordinator: Califano
Leaders: Shapiro, Dalla Favera, Gilliam

- ***Cell Adhesion*** **-** Structural and energetic basis of cadherin binding specificity: A combined computational and experimental study
- ***Pathway Dysregulation*** **-** Regulatory Modules in Normal and Transformed B-Cells
- ***Complex Diseases*** **-** Genomic and Bioinformatics Solutions to the Search for Genetic Determinants of Common, Heritable Disorders: Alzheimer's Disease and Autism.



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Q1: “well-mapped to big problems”?

- Fills holes in biomedical computation
  - Imaging
  - Machine learning*
- Promotes synergy w/ complementary existing efforts*
  - Structural Biology (NESG, PSI),
  - Cancer Research (ICBP, CABIG),
  - National Biodefense (NBC), as well as the new pathway initiatives (starting to build ties).
- Standardizes+federates in the face of proliferation+balkanization
  - E.g., clustering, ontologies
  - Crucial for ante-disciplinary science:
    - Results **1** - **10** of about **683,000,000** for **biology (19 definitions)**
    - Results **1** - **10** of about **862,000,000** for **physics (16 definitions)**
    - Results **1** - **10** of about **200,000,000** for **systems** biology.

* biased answer

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* biased answer

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Q2: “other initiatives needed”?

- NCBC
  - Science flourishes when model + experiment walk hand-in-hand
  - Requires experimentalists with
    - Driving biological problems
    - Biological intuition to constrain and guide computation
    - Data.
- encourage joint computational/experimental research
  - Recall Rutherford (1871-1937)’s admonition:
    - “If your result needs a statistician then you should design a better experiment.”
  - Both blatantly false/outmoded and wise/timely

* biased answer

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Q3: “What should CS-ers get excited about”?

- Of course subjective answers, but:
  - ML
  - imaging
  - From DM to KD to biology to biomedicine
- On the scale of NCBC’s, needed:
  - Interoperability
  - Open source
  - Open data
  - Standardization+federation
- Some of these are statistical/algorithmic advances; others are software engineering / design.
- Strive to make something “insanely great.”

* biased answer

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Q4: “RO1/R21 wish list”

- See Q2, i.e., NCBC requires experimentalists with
  - Driving biological problems
  - Biological intuition to constrain and guide computation
  - Data. (new techniques and new questions)
    - RNAi,
    - New expression platforms
    - Image data (hopefully promoting ties with other NCBCs+Roadmaps)
- See Q3, I.e.,
  - “insanely great” interoperability

* biased answer

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