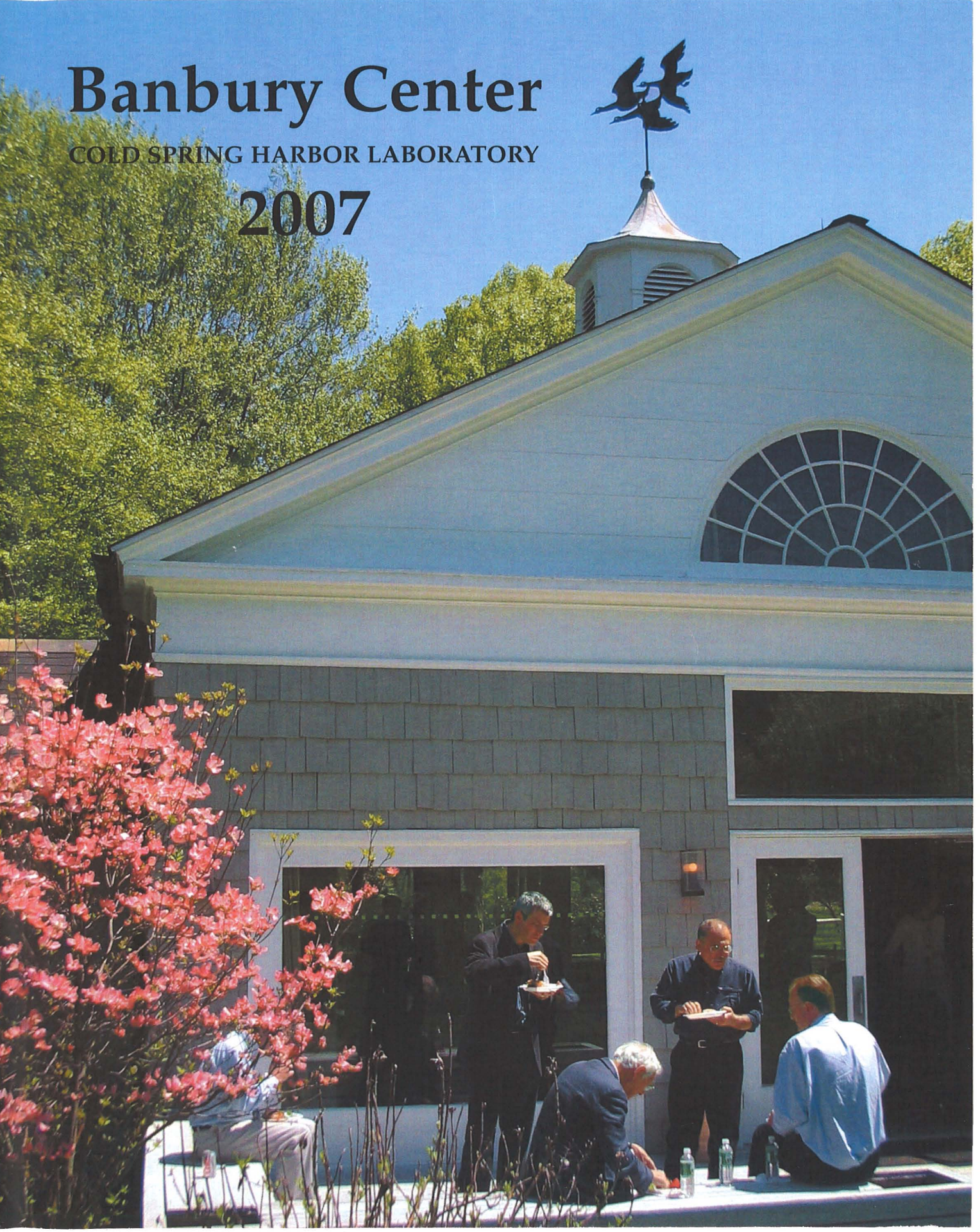
Banbury Center

COLD SPRING HARBOR LABORATORY

2007

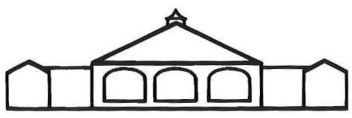


BANBURY CENTER

Banbury Center is a 55-acre estate adjoining the waters of Long Island Sound on the north shore of Long Island, barely 40 miles east of downtown Manhattan and some five miles from Cold Spring Harbor Laboratory. The estate was donated to the Laboratory in 1976 by Charles Sammis Robertson, together with funds for necessary architectural conversions and an endowment to cover upkeep of the grounds and the original estate structures. With the Laboratory's international reputation for research and education, the magnificent Banbury grounds and buildings are an ideal site for small conferences in the areas of molecular biology and genetics, especially as they relate to health, social, and policy issues.

What was once the estate's original seven-car garage is now the Conference Room, containing administrative offices, a small library, and—at its center—a room of an ideal shape and size for workshop-style discussion meetings. Complete with extensive, unobtrusive sound and projection facilities as well as wall-to-wall blackboard space, the room can accommodate as many as 40 participants while remaining equally conducive to either formal presentations or informal give-and-take.

The Robertsons' family house, situated on the final promontory before the grounds descend to the shore of the harbor, now serves as the center for participant accommodations and dining, while the extensive grounds, swimming pool, tennis court, and beach present ample recreational resources. On-site accommodations were supplemented by the opening in 1981 of the Sammis Hall guest house—a modern embodiment of the sixteenth century Palladian villas—designed for the Center by the architectural firm of Moore Grover Harper. In 1997, the Meier House, opposite the Conference Center, was added to provide extra housing so that everyone attending a Banbury Center meeting can stay on the estate.



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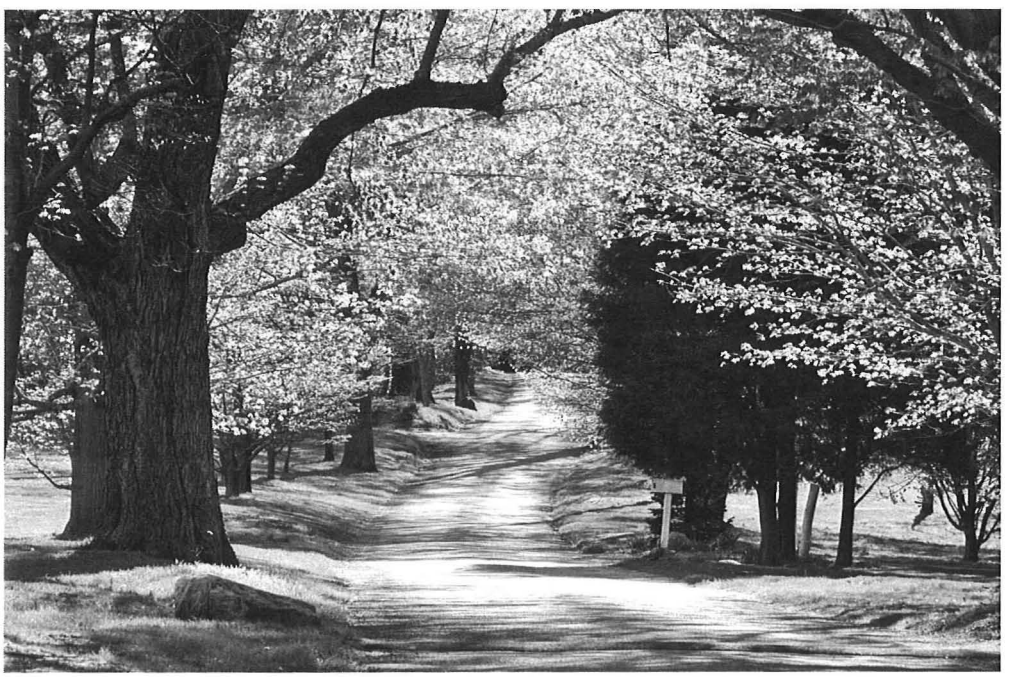
BANBURY CENTER
EXECUTIVE DIRECTOR'S REPORT

The year 2007 marked my 20th year as director of the Banbury Center. The Center continues to be a thrilling place to work, providing opportunities to help develop and promote new and important fields of research. The year proved to be one of the busiest ever in the 30 years since the first meeting was held in 1977. There were 25 scientific meetings, and the Center was used for nine courses. As usual, local organizations, including the Lloyd Harbor Conservation Board and the Cold Spring Harbor School District, made use of the calm of the Center for discussion meetings. Altogether, 36 events were held at Banbury in 2007, and these were attended by 672 participants whose demographics remain very similar from year to year. The proportion of participants from the United States was 77%, drawn from no fewer than 40 states, a record number. As usual, New York, California, Massachusetts, and Maryland provided most of these participants (46%). Foreign participants came from 23 countries, and attendance by scientists from companies was higher than in previous years, comprising 10% of the total.

There were two most interesting and important meetings dealing with social and policy issues relating to the uses of scientific knowledge. *Protecting Public Trust in Immunization*, funded by the Albert B. Sabin Vaccine Institute, has the potential to be one of the most important meetings to be held at Banbury. Vaccination against infectious agents is, unquestionably, the greatest contribution that science has made to improving our health, most especially that of children. Diseases such as polio are virtually forgotten in most countries; smallpox, the great scourge, has been eliminated; and a vaccine against human papillomaviruses is likely to reduce greatly the incidence of cervical cancer. But the absence of infections such as measles, mumps, and rubella has led to a perception that these, too, have disappeared, and the vaccination rates of the MMR (measles, mumps, rubella) vaccine have fallen. This has been accelerated by fears that the MMR vaccine, and/or the mercury once used as a preservative,



Banbury Lane

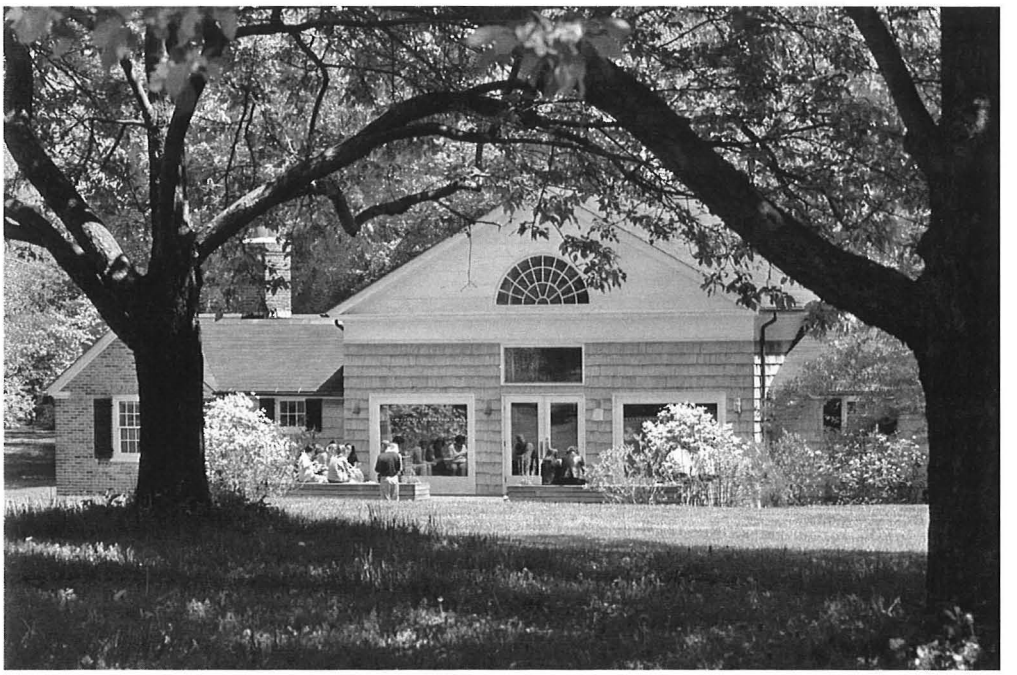
causes autism. Every study has shown that these fears are unfounded, but the perception remains and, as a consequence of the falling use of the MMR vaccine, these diseases are reappearing and killing children. Participants in this meeting discussed what can be done in general to persuade the public of the need for vaccination and to reestablish the public's trust in vaccines. A very distinguished group of participants included representatives of parent advocate organizations, the World Health Organization, the Department of Health and Human Services, Congress, and academic institutions. We were particularly pleased that Louis W. Sullivan, Secretary of Health and Human Services in the administration of George H.W. Bush, attended.

The second science and society discussion meeting also dealt with the vexed issue of how scientific knowledge is used and misused, particularly in the political decision-making process. To what extent should political influences determine what research is done and how scientific data are used? Contemporary examples include the U.S. government's attitudes toward human embryonic stem cell research and global warming. What is needed is a rational approach to decision-making, based on the best evidence available. *Retreat from Reason* reviewed these issues and explored how rationality might be reintroduced into public discourse. The participants were particularly eclectic, drawn from the worlds of science, politics, and the media. They included, for example, Michael Crichton (*Jurassic Park*), Chris Mooney (*Seed Magazine*), Lord Taverne (Sense about Science), and Lee Silver (Princeton University). It was a fascinating occasion.

The Alfred P. Sloan Foundation is noted for the support it gives to fledgling areas of research. The Foundation provides funds at a critical period when such fields may not yet have developed a community and have not produced a body of work sufficient to establish themselves for federal funding. Four years ago, in 2003, the Sloan Foundation supported two workshops at Banbury to discuss molecular "bar codes." These are based on the sequence of a mitochondrial gene, *COXI*, which is identical among individuals of a species but differs sufficiently among species so that it can be used to identify (bar-code) species. The Foundation's initiative has been tremendously successful. There is now a Consortium for the Barcode of Life, with 150-member organizations worldwide, coordinating and standardizing bar-code efforts. It is expected that a half-million species will be bar-coded during the next 5 years. The Sloan Foundation funded a follow-up discussion workshop at Banbury in 2007. Participants discussed both the effectiveness and limitations of bar coding, and it was agreed that bar coding is fulfilling its promise. Indeed, it is progressing so well that a major goal of the meeting was to explore how bar coding can be exploited beyond its present use in taxonomy. There were also important discussions of how to analyze and integrate the large amount of data being produced; effective visualization tools are essential for presenting these data in an interpretable fashion to researchers.

There were two particularly interesting meetings in neuroscience. The Swartz Foundation has supported meetings at Banbury since 1999, and the topics are always fascinating. *New Frontiers in Studies of Nonconscious Processing* was no exception. "Nonconscious processing" seems like a paradox—How can our brains process information without us being aware of it? And if it happens, how can we be aware that we are not aware of it happening?! A little reflection shows that a great deal of our brain activity must be devoted to nonconscious processes. What makes the topic intriguing is its implications for the classic and ever-lasting issue of free will. Experiments have indicated that we reach a decision about how to act before we become aware of the decision. So, our conscious mind, which we generally believe to be "in control" of such decisions, is not; the decision is made and then our conscious mind acts as though it reached the decision. The broad range of the topic was evident in the disciplines represented: social psychologists, cognitive psychologists, neural physiologists, and philosophers.

The second neuroscience meeting that was even broader in its coverage was *Interdisciplinary Memory Symposium in Neurosciences and the Humanities*. The primary focus of the meeting was on memory, the thesis being that, just as neuroscientists explore the physical workings of the brain with the tools of electrophysiology and molecular biology, so writers and artists explore and record the mental experiences of human beings. One thinks immediately of Proust's *À la recherche du temps perdu*. The participants explored the extent to which the insights of those in the humanities might guide neuroscientists in developing and evaluating their models of human memory. We moved from the genetics and



Back of Banbury Center; meeting coffee break

molecular biology of memory in fruit flies, through higher-level processes in more complex brains, to the role memory plays in art, literature, theater, film, and music. It proved to be a fascinating and very successful discussion workshop.

Sydney Gary, who came to Banbury as the first-ever Assistant Director, has been promoted to the position of Director, Research Operations, and is now based on the main Laboratory campus. Sydney took responsibility for the neuroscience programs at Banbury and, most importantly, interacted with David Stewart in developing new forms of the neuroscience lecture courses at Banbury. She did a great job and we are very sorry to lose her.

Banbury Center could not operate at the level that we did in 2007 without the outstanding efforts of many people, most especially Bea Toliver, Ellie Sidorenko, and Sydney Gary at the Conference Room, Basia Polakowski at Robertson House, and Mike Peluso and the grounds crew who look after the Banbury estate. It is only through their hard work and that of the Laboratory's Food Services and Housekeeping that Banbury can continue to fulfill its mission of being the world's best venue for serious discussions of biomedical research.

Jan Witkowski
Executive Director

MEETINGS

Epithelial Mesenchymal Transition

February 25–27

FUNDED BY **OSI Pharmaceuticals, Inc.**

ARRANGED BY **J.D. Haley,** OSI Pharmaceuticals, Inc.
A.J. Dannenberg, New York Presbyterian Hospital, Cornell

A key step in the development of cancer is the epithelial-mesenchymal transition. This reprogramming results in dedifferentiation and ultimately redifferentiation of tumor cells, so that the cells gain the ability to migrate and invade other tissues, i.e., metastasize. These invading mesenchymal-like tumor cells can then redifferentiate, leading to the reacquisition of proliferative self-renewal capacity and tumor growth at metastatic sites. These processes have a major role in the progression of cancer. Participants at this meeting reviewed the clinical and pathobiological significance of the epithelial-mesenchymal transition: the molecular signaling pathways that promote and maintain a mesenchymal-like tumor state and the animal, cell, and pathway models that might be used to further investigate the epithelial-mesenchymal transition.

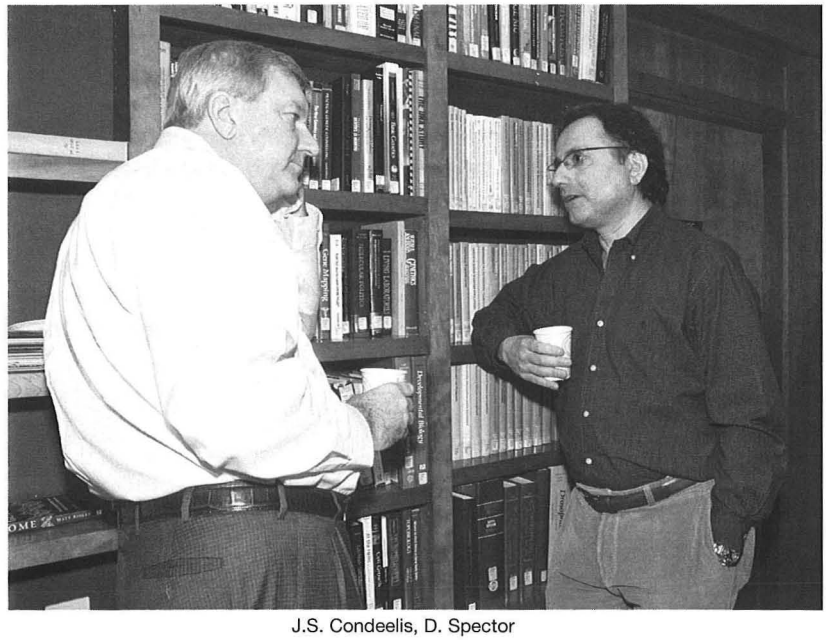
Introductory Remarks and Welcome: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory
D. Epstein, OSI Pharmaceuticals, Inc., Farmingdale, New York

SESSION 1: Molecular Aspects of EMT
Chairperson: R.A. Weinberg, Whitehead Institute for Biomedical Research, Cambridge, Massachusetts

J.D. Haley, OSI Pharmaceuticals, Inc., Farmingdale, New York: EMT: A basis for the design of rational drug combinations.

R.A. Weinberg, Whitehead Institute for Biomedical Research, Cambridge, Massachusetts: Regulators of the EMT.

A. Cano, Instituto de Investigaciones Biomedicas, Madrid, Spain:



J.S. Condeelis, D. Spector

Regulation of EMT by snail and lysyl oxidase-like proteins.
A. Csiszar, Institute of Molecular Pathology, Vienna, Austria: ILEI: A cytokine essential in EMT, tumor formation, and metastasis in epithelial cells.
R. Kalluri, Harvard Medical School, Boston, Massachusetts: Targeting EMT in organ fibrosis.

SESSION 2: Cell Function and EMT
Chairperson: S. Muthuswamy, Cold Spring Harbor Laboratory

D. Radisky, Mayo Clinic Cancer Center, Jacksonville, Florida: Matrix metalloproteinase-induced EMT in breast and lung.
S. Muthuswamy, Cold Spring Harbor Laboratory: Polarity proteins regulate initiation and progression of carcinoma.
J.S. Condeelis, Albert Einstein College of Medicine, Bronx, New York: mRNA targeting is disrupted in metastatic carcinoma cells leading to EMT.

SESSION 3: Pathology and In Vivo Modeling
Chairperson: T. Brabletz, University of Erlangen-Numberg, Germany

T. Brabletz, University of Erlangen-Numberg, Germany: Malignant progression in colorectal cancer: EMT, beta-catenin, and cancer stem cells?
V. Brunton, Beatson Institute for Cancer Research, Glasgow, United Kingdom: Role of Src and FAK tyrosine kinases in tumor progression.
A. El-Naggar, The University of Texas M.D. Anderson Cancer Center, Houston, Texas: p-Src and E-cadherin have a major role in the epithelial-mesenchymal transition of head and neck squamous carcinoma.
S.M. Dubinett, University of California, Los Angeles: Inflammation: Dependent regulation of EMT in lung cancer.

Specific Issues and Priorities
Moderator: D. Epstein, OSI Pharmaceuticals, Inc.. Farmingdale, New York

A. Cano

When Is Amyloid Functional and When Is Amyloidogenesis Pathological?

March 11–14

FUNDED BY **Cold Spring Harbor Laboratory Corporate Sponsor Program**

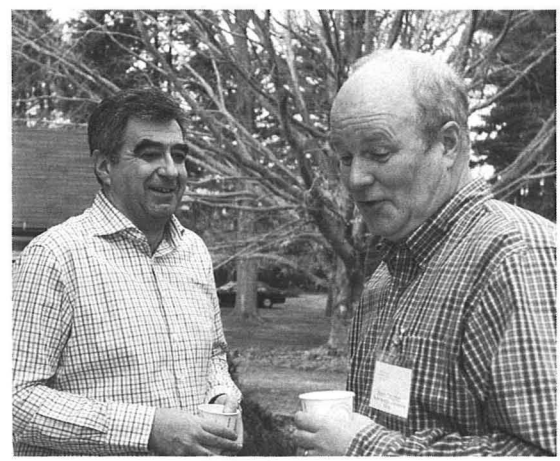
ARRANGED BY **J.W. Kelly,** Scripps Research Institute
K. Hsiao Ashe, University of Minnesota Medical School, Minneapolis

Amyloid has a key role in a number of degenerative disorders, but much is still unknown about the normal functions of amyloid, how the process of amyloidogenesis leads to neurodegeneration, and when amyloid is protective. Participants reviewed what is and what is not known about functional amyloid formation in a variety of tissues and contrasted this with disease-associated amyloid. Pathological amyloidogenesis (and why this process leads to tissue toxicity) was discussed in the context of amyloid, prion, and related diseases and type II diabetes.

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1: Principles of Protein Misfolding
Chairpersons: C. Weissmann, Scripps Florida, Jupiter; **D. Walsh,** University College Dublin, Republic of Ireland

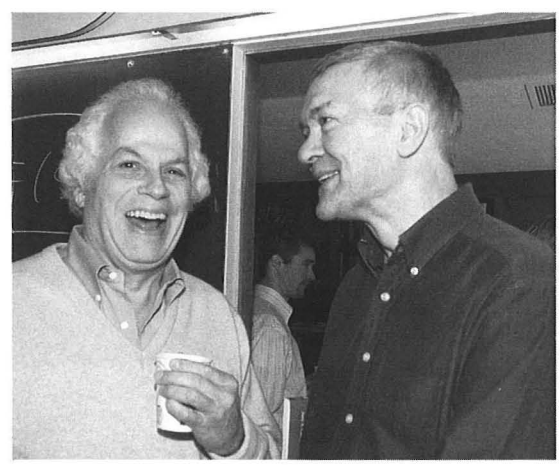
H.A. Lashuel, Swiss Federal Institute of Technology, Lausanne, Switzerland: Understanding the biochemical and structural basis of amyloid toxicity in Alzheimer's and Parkinson's disease.
M. Vendruscolo, University of Cambridge, United Kingdom: Prediction of protein aggregation propensities.
W.E. Balch, The Scripps Research Institute, La Jolla, California: Molecular and structural contributions of membrane trafficking to misfolding disease.
M. Bucciantini, University of Florence, Italy: Cell membranes as primary targets of protein aggregate cytotoxicity.
R.I. Morimoto, Northwestern University, Evanston, Illinois: Toxic protein states and the collapse of protein homeostasis.
E.R. Kandel, HHMI/Columbia University, New York: On the persistence of memory storage.
K. Si, Stowers Institute for Medical Research, Kansas City, Missouri: Does *Drosophila* Orb2 behave like a prion?



J. Collinge, B. Caughey

SESSION 2: Transmissible Prions and Amyloid Proteins
Chairpersons: R.I. Morimoto, Northwestern University, Evanston, Illinois; **G.T. Westermark,** Linkoping University, Sweden

J. Collinge, University College London, United Kingdom: Prion strains, transmission barriers, and neurotoxicity.
C. Weissmann, Scripps Florida, Jupiter: How do cells distinguish between prior strains?
S.B. Prusiner, University of California, San Francisco: Synthetic prions formed from amyloid.
B. Caughey, NIH/NIAID Rocky Mountain Laboratories, Hamilton, Missouri: Prion protein oligomerization and TSE disease.
R. Tycko, National Institute of Diabetes and Digestive and Kidney Diseases, NIH, Bethesda, Maryland: Molecular structure of amyloid and yeast prion fibrils.
M. Jucker, University of Tubingen, Germany: Induction of Aβ-amyloid in transgenic mice.



S. Prusiner, J. Witkowski

SESSION 3: Functional Prions and Amyloids
Chairpersons: S.B. Prusiner, University of California, San Francisco; **W.E. Balch,** The Scripps Research Institute, La Jolla, California

R.B. Wickner, National Institutes of Health, Bethesda, Maryland: Yeast prions (PSI+) and (URE3) are disease agents in yeast.
M. Chapman, University of Michigan, Ann Arbor: Protein misfolding done right: The biogenesis of curli fibers by *E. coli*.
D.M. Fowler, The Skaggs Institute of Chemical Biology, La Jolla, California: Functional amyloid in mammals; the biogenesis of pigmentation.
M. Gebbink, University Medical Centre Utrecht, The Netherlands: Misfolded proteins, hemostasis, and immunogenicity: "The crossbeta pathway."
A.B. Bowman, Vanderbilt University Medical Center, Nashville, Tennessee: Duplication of *Atxn1* suppresses SCA1 neuropathology by decreasing incorporation of polyglutamine-expanded ataxin-1 into native complexes promoting inclusion formation.

SESSION 4: Pathological Amyloids and Misfolding Group 1
Chairpersons: S. Finkbeiner, University of California, San Francisco; **B. Caughey,** NIH/NIAID Rocky Mountain Laboratories, Hamilton, Montana

G. Hotamisligil, Harvard School of Public Health, Boston, Massachusetts: Unfolding story of diabetes, ER stress, and insulin action.
A. Dillin, Salk Institute, La Jolla, California: The genetics of age-regulated proteotoxicity: From worm to mouse.
M. Staufenbiel, Novartis Institutes for Biomedical Research Basel, Switzerland: Amyloid-associated pathological alterations in the brain of APP transgenic mice.
D. Walsh, University College Dublin, Republic of Ireland: Cell-derived Aβ oligomers and their role in Alzheimer's disease.
S. Lesne, University of Minnesota, Minneapolis: Identification and characterization of Aβ*56, a pathological Aβ assembly, causing early memory dysfunction.

SESSION 5: Pathological Amyloids and Misfolding Group 2
Chairpersons: J. Collinge, University College London, United Kingdom; **M. Staufenbiel,** Novartis Institutes for Biomedical Research Basel

P.H. Axelsen, University of Pennsylvania School of Medicine, Philadelphia: Pro-oxidant activity of amyloid-β proteins.
R. Vassar, Northwestern University, Chicago, Illinois: Multiple personalities of Aβ: Positive and negative memory functions, intraneuronal toxicity, and BACE1 elevation in AD.
S. Finkbeiner, University of California, San Francisco: Identifying species of polyglutamine proteins in situ that best predict neurodegeneration.
G.T. Westermark, Linkoping University, Sweden: Formation of intracellular IAPP-amyloid kills the β cells.

Summary
J.W. Kelly, Scripps Research Institute, La Jolla, California
K. Hsiao Ashe, University of Minnesota Medical School, Minneapolis

International Workshop on Conifer Genomics

March 18–21

FUNDED BY **Arborgen, Canadian Forest Service; European Union Evoltree; Genome British Columbia; Genome Canada; Oregon State University; Port Blakeley Tree Farms; Starker Forests; University of California, Davis; University of Georgia; University of Maine; USDA Forest Service**

ARRANGED BY **D.B. Neale,** University of California, Davis
J. Dean, University of Georgia
G.T. Howe, Oregon State University
M.S. Greenwood, University of Maine

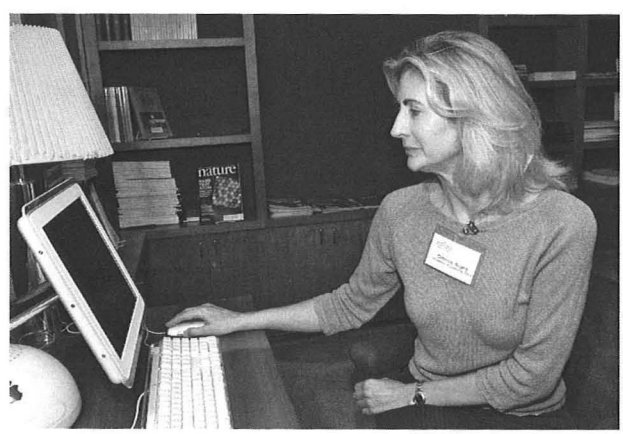
The goals of this workshop were to advance conifer genomics research and the application of genomic tools to increase forest productivity, enhance forest health, and obtain a better understanding of all aspects of forest biology, including adaptation to environmental stresses and climate change. To this end, participants summarized the status of conifer genomics worldwide, examined the strategies pursued in other genome projects, and explored the potential of comparative genomics to advance our understanding of diverse coniferous species. There were also extensive discussions on the steps to be taken: determining priorities, coordinating research, and improving communications among genomic scientists, resource managers, ecologists, forest health specialists, research administrators, and other forest biologists.

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

Welcome and Meeting Objectives: D.B. Neale, University of California, Davis

SESSION 1: Why Conifer Genomics?
Chairperson: G.T. Howe, Oregon State University, Corvallis

M.S. Greenwood, University of Maine, Orono: History of conifer genomics.
G.T. Howe, Oregon State University, Corvallis: Importance of conifers: Who benefits from conifer genomics research?
R. Mangold, USDA Forest Service, Arlington, Virginia: Genomics for forest health.
D.L. Rogers, Genetic Resources Conservation Program, University of California, Davis and Center for Natural Lands Management, Fallbrook, California: Ecological genomics and conservation biology.
R.C. Purnell, Weyerhaeuser Company, Hot Springs, Arkansas: Genomics for forest industry.



D. Rogers

SESSION 2: Organization and Funding of Conifer Genomics Research
Chairperson: B. Goldfarb, North Carolina State University, Raleigh

G.S. Foster, USDA Forest Service, Washington, D.C.: Genomics and the USDA Forest Service.
A. Klein, The National Science Foundation, Arlington, Virginia and Center for Natural Lands Management, Fallbrook, California: Genomics research from competitive grants programs at NSF, DOE, and USDA.
A. Kremer, INRA UMR BIOGECO, Cestas, France: International coordination and funding for genomics research.
N. Wheeler, Molecular Tree Breeding Services, LLC, Centralia, Washington: Genomics education and outreach.
M.J. Morgan, Genome Canada, Ottawa, Canada: Genome Canada's research portfolio in forestry research.

BREAKOUT SESSION 1: Why Conifer Genomics? Organization and Funding of Conifer Genomics Research

SESSION 3: Status of Non-Conifer Genomics
Chairperson: D.B. Neale, University of California, Davis

C.H. Langley, University of California, Davis: Population genomics: Racing technologies and scrambling analysis.
J. McPherson, Baylor College of Medicine, Houston Texas: Sequencing and genomics of large and complex genomes.
R. McCombie, Cold Spring Harbor Laboratory: Maize genomics.
O. Savolainen, University of Oulu, Finland: Genomics of natural populations of *Arabidopsis*.
S.P. DiFazio, West Virginia University, Morgantown: *Populus* genomics.

SESSION 4: Status of Conifer Genomics
Chairperson: M.S. Greenwood, University of Maine, Orono

J. Mackay, University Laval, Canada: Conifer genomics in Canada.
M. Cervera, INIA-CIFOR, Madrid, Spain: Conifer genomics in Europe.
S. Cato, SCION Research, Rotorua, New Zealand: Conifer genomics in Australia and New Zealand.
D.B. Neale, University of California, Davis: Conifer genomics in the United States.

SESSION 5: Key Components of a Conifer Genomics Program
Chairperson: J. Dean, University of Georgia, Athens

J. Dean, University of Georgia, Athens: Introduction and gene discovery.
J. Bohlmann, University of British Columbia, Vancouver, Canada: Gene expression profiling, proteomics, and metabolomics.
D. Nelson, Southern Institute of Forest Genetics, Saucies, Mississippi: Mapping and genome structure.
M. Hinchee, ArborGen LLC, Summerville, South Carolina: Transgenic conifers in the private and public sectors.
K. Ritland, University of British Columbia, Vancouver, Canada: Power of comparative genomics.
S. Gonzalez-Martinez, CIFOR-INIA, Madrid, Spain: SNPs and association genetics.
J. Lee, University of California, Davis: Conifer bioinformatics.
M. Morgante, Universita' di Udine, Italy: Prospects for a conifer genome sequence.

BREAKOUT SESSION 2: Key Components of a Conifer Genomics Program

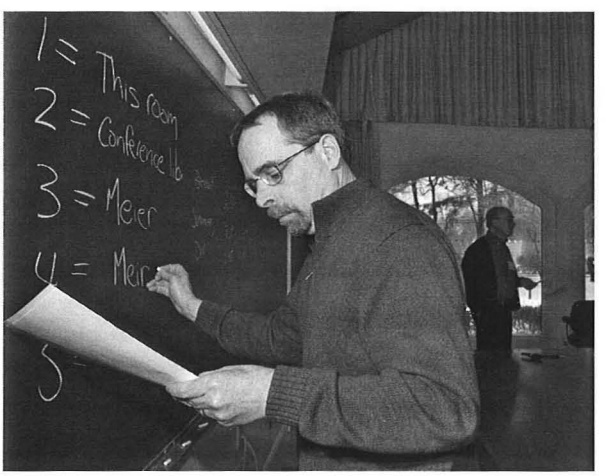
SESSION 6: Future of Conifer Genomics
Chairperson: J. Dean, University of Georgia, Athens

J. Dean, University of Georgia, Athens: Action items for conifer genomics.

BREAKOUT SESSION 3: Future of Conifer Genomics

Breakout session summaries
Large group discussion

MEETING SYNTHESIS
D.B. Neale, University of California, Davis



G. Howe

Neurobiology of Depression: From Molecules to Mood

April 1–4

FUNDED BY **Eli Lilly & Company, Memory Pharmaceuticals, Sepracor Inc., AstraZeneca Pharmaceuticals, Roche Pharmaceuticals, Wyeth Pharmaceuticals**

ARRANGED BY **R.S. Duman,** Yale University School of Medicine
G. Enikolopov, Cold Spring Harbor Laboratory
R. Hen, Columbia University, New York

Depression is a devastating illness that effects 15–20% of the population, resulting in enormous personal suffering and economic loss to society. Despite intensive research, the neurobiological mechanisms underlying the etiology and treatment of major depressive disorders have not been identified. The focus of this meeting was to undertake a comprehensive and integrated assessment of the current state of knowledge of depression research, including analysis of the genetic, molecular, and cellular determinants of mood and depression in animal models and in humans. The neurobiology of stress, which can precipitate or exacerbate depression, was discussed, as well as the behavioral consequences of stress exposure.

Welcome: S. Gary, Banbury Center, Cold Spring Harbor Laboratory,

SESSION 1: Overview/Introduction
Chairperson: H. Akil, University of Michigan, Ann Arbor

Introduction: R.S. Duman, Yale University School of Medicine, New Haven, Connecticut
G. Enikolopov, Cold Spring Harbor Laboratory
R. Hen, Columbia University, New York

R.C. Kessler, Harvard Medical School, Boston, Massachusetts: A brief overview of the epidemiology of depression.
R.R. Krishnan, Duke University Medical Center, Durham, North Carolina: Medical basis of depression.
D.S. Charney, Mount Sinai School of Medicine, New York: Novel targets for antidepressant therapeutic development: Evidence from proof of concept clinical studies.
M. Fava, Massachusetts General Hospital, Boston: How effective are antidepressant drugs?

SESSION 2: Pathophysiology
Chairperson: R.R. Krishnan, Duke University Medical Center, Durham, North Carolina

W.C. Drevets, NIH/NIMH DIRP, Bethesda, Maryland: Neuroimaging studies of depression.
S.H. Lisanby, Columbia University, New York: Targeting the neurocircuitry of depression with focal brain stimulation.
H.K. Manji, National Institute of Mental Health, Bethesda, Maryland: Cellular plasticity cascades: Genes to behavior pathways in the pathophysiology and treatment of severe mood disorders.
G. Sanacora, Yale University School of Medicine, New Haven, Connecticut: Potential contributions of the amino acid neurotransmitter systems to the pathophysiology and treatment of major depressive disorder.
D.R. Rubinow, University of North Carolina, Chapel Hill: Affective dysregulation: Lessons from reproductive neuroscience.

SESSION 3: Stress and Growth
Chairperson: H.K. Manji, National Institute of Mental Health, Bethesda, Maryland

B.S. McEwen, The Rockefeller University, New York: Stress-induced structural remodeling in brains of animals models.
R. Hen, Columbia University, New York: Neurogenesis and depression.
G. Enikolopov, Cold Spring Harbor Laboratory: Neurogenic targets of antidepressant therapies.
R.S. Duman, Yale University School of Medicine, New Haven, Connecticut: Neurotrophic factors in the pathophysiology and treatment of depression.
H. Akil, University of Michigan, Ann Arbor: Searching for novel molecules for mood disorders.

SESSION 4: Genetics and Epigenetics
Chairperson: R. Hen, Columbia University, New York

J. Gingrich, Columbia University, New York: Development contributions to affective disorders.
K.-P. Lesch, University of Wurzburg, Germany: Life stress–serotonin interaction in depression: Evidence from knockout mice and functional imaging.
K. Ressler, Emory University, Atlanta, Georgia: CRH and BDNF systems in depression: Recent genetic and molecular results.
H. Reul, University of Bristol, United Kingdom: Epigenetic mechanisms in stress-induced transcriptional activation and behavioral adaptation.
A. Kumar, University of Texas Southwestern Medical Center, Dallas: Genome-wide epigenetic and genetic changes underlying striatal plasticity associated with mood disorders.

SESSION 5: Cognition/Motivation
Chairperson: R.S. Duman, Yale University School of Medicine, New Haven Connecticut

A. Markou, University of California, San Diego: Psychostimulant drug withdrawal as an inducing condition in models of depression.
W. Carlezon, Harvard Medical School, Belmont, Massachusetts: Importance of CREB-mediated dynorphin regulation in the study and treatment of mood disorders.
J.R. Taylor, Yale University School of Medicine, New Haven, Connecticut: Murine models of depression: Linking molecules to cognitive-motivational function.

SESSION 6: Conclusions/Future Directions
Co-Chairpersons: D.S. Charney, Mount Sinai School of Medicine, New York; **H. Akil,** University of Michigan, Ann Arbor

A. Markou

New Frontiers in Studies of Nonconscious Processing

April 8–11

FUNDED BY **The Swartz Foundation**

ARRANGED BY **T.D. Wilson,** University of Virginia, Charlottesville
A. Dijksterhuis, University of Amsterdam, The Netherlands

There has been a renaissance of research on nonconscious processing, but much of this research is occurring in separate disciplines at different levels of analysis, from behavioral research to studies of neural processes. The goal of this meeting was to bring together people from different disciplines who are interested in nonconscious mental processing and its relationship to consciousness, broadly defined. Even more than is usual for a Banbury Center meeting, a very wide spectrum of disciplines was represented: social psychology, cognitive psychology, neural physiology, and philosophers. The expectation was that these participants would learn from each other, discovering that they had previously unsuspected interests in common, and that this would lead to new research directions and collaborations.

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1
Chairperson: P. Winkielman, University of California, San Diego

Introductory Remarks: T.D. Wilson, University of Virginia, Charlottesville
A. Dijksterhuis, University of Amsterdam, The Netherlands

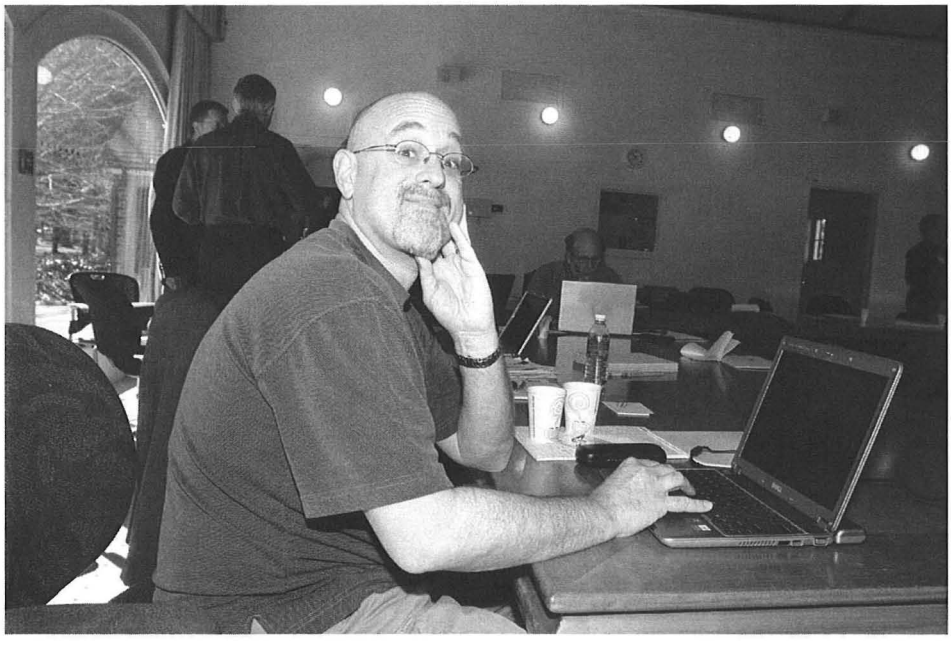
T.D. Wilson, University of Virginia, Charlottesville: The necessity of nonconscious processing.

D.M. Wegner, Harvard University, Cambridge, Massachusetts: Unconscious wellsprings of conscious will.

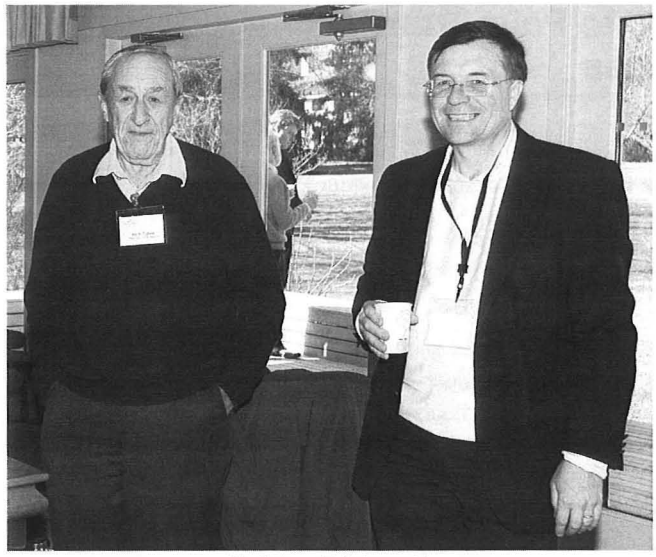
A. Dijksterhuis, University of Amsterdam, The Netherlands: On unconscious thought.

J.W. Schooler, University of British Columbia, Canada: Challenges of distinguishing between unconscious processes and processes that are experienced but in the absence of meta-awareness.

D. Gilbert, Harvard University, Cambridge, Massachusetts: Conscious misprediction of unconscious processes.



D. Gilbert



H. Cohen, T. Sejnowski

SESSION 2
Chairperson: D. Gilbert, Harvard University, Cambridge, Massachusetts

J. Swartz, The Swartz Foundation, East Setauket, New York: The Conscious "pop": A nonconscious processing framework for problem solving.
T. Sejnowski, The Salk Institute for Biological Studies, San Diego, California: Searching for hidden treasure unconsciously.
X.-J. Wang, Yale University School of Medicine, New Haven, Connecticut: Concept of a decision threshold in sensory-motor processes.
A.G. Greenwald, University of Washington, Seattle: Using knockout strategies to reveal conscious function.
M.N. Shadlen, HHMI/University of Washington, Seattle: Decisions, time, probability, and indeterminacy: Big ideas from small experiments.

SESSION 3
Chairperson: J.W. Schooler, University of British Columbia, Canada

R. Hassin, Hebrew University, Jerusalem, Israel: The nonconscious executive.
H. Aarts, Utrecht University, The Netherlands: Implicit motivation and regulation of goals and their pursuit.
S. Dehaene, CEA/SAC/DSV/DRM/Neurospin, Yvette, France: Human brain mechanisms of subliminal processing and conscious access.
T.L. Chartrand, Duke University, Durham, North Carolina: Nonconscious mimicry.

SESSION 4
Chairperson: C.N. Macrae, University of Aberdeen, United Kingdom

M. Ferguson, Cornell University, Ithaca, New York: On implicit evaluation.
P.S. Churchland, University of California, San Diego, La Jolla: Nonconscious imitation and valenced representations.
A. Bell, University of California, Berkeley: Emergence into consciousness viewed from the levels framework.
D.L. Schacter, Harvard University, Cambridge, Massachusetts: Priming, implicit memory, and the brain: A neuroimaging perspective.

SESSION 5
Chairperson: D.M. Wegner, Harvard University, Cambridge, Massachusetts

C.N. Macrae, University of Aberdeen, United Kingdom: When consciousness slips: Priming the absent mind.
K. Berridge, University of Michigan, Ann Arbor: Hidden brain–emotion components in desire and dread.
P. Winkielman, University of California, San Diego: Emotion and awareness.

Molecular Approaches to Pain: Translational Potential and Challenges

April 15–18

FUNDED BY **Cold Spring Harbor Laboratory Corporate Sponsor Program**

ARRANGED BY **M.E. Csete,** Emory University School of Medicine, Atlanta, Georgia
J. Prager, University of California, Los Angeles, School of Medicine

Pain remains a daunting clinical problem, and advances in understanding the molecular underpinnings of pain have not translated easily into new therapies. Much of this can be attributed to communication difficulties among the basic scientists uncovering the mechanisms of pain, the researchers developing new pain treatments, and the clinicians seeking to treat pain. Because advances in managing pain have come from diverse clinical and basic science communities, this meeting was held to foster communication among molecular biologists, neurobiologists, pharmacologists, anesthesiologists, neurologists, and neurosurgeons. Our current understanding of pain initiation and maintenance was reviewed, as well as the molecular biology of distinct pain syndromes, mechanisms of pain relief, and genetic predisposition to pain and responses to therapy.

Introductory Remarks: S. Gary, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1: Systems/Big Picture
Chairperson: M.E. Csete, Emory University School of Medicine, Atlanta, Georgia

J. Prager, University of California, Los Angeles, School of Medicine: Introduction and overview.
K.E. McCarson, University of Kansas Medical Center, Kansas City: Molecular mechanisms of CNS plasticity during persistent pain.
C. Sommer, Julius-Maximilians Universitat, Wuerzburg, Germany: Role of cytokines in chronic pain.
T. Samad, Harvard Medical School and Massachusetts General Hospital, Charlestown: Modulators of inflammatory pain hypersensitivity.
P.P. Mitra, Cold Spring Harbor Laboratory: Signal processing methods for LFP and EEG time series for rapid monitoring of brain state.

SESSION 2: Pathology
Chairperson: J. Prager, University of California, Los Angeles, School of Medicine

M. Garcia, University of Missouri, Columbia: Neurofilament-dependent neuronal growth and death.
A.L. Oaklander, Harvard Medical School and Massachusetts General Hospital, Boston: Major effects of minor distal nerve injuries.
A.S.C. Rice, Imperial College, London, United Kingdom: Modeling HIV-related neuropathies.
J.D. Glass, Emory University School of Medicine, Atlanta, Georgia: Mechanisms of axonal degeneration.

SESSION 3: Channels, Receptors, and Genes
Chairperson: M.E. Csete, Emory University School of Medicine, Atlanta, Georgia

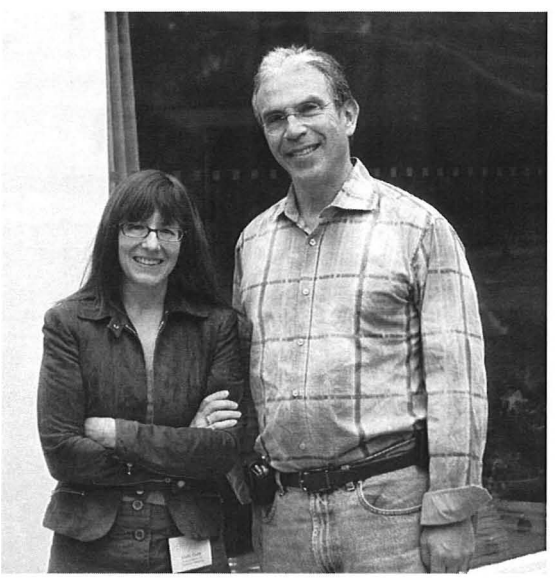
J. Mao, Massachusetts General Hospital, Charlestown: Neuronal glucocorticoid receptor and neuropathic pain.
Q. Ma, Dana-Farber Cancer Institute, Boston, Massachusetts: Runx1 coordinates nocioceptor phenotypes necessary for thermal and neuropathic pain.

SESSION 4: Pharmacology/Therapies/Novel Targets
Chairperson: J. Prager, University of California, Los Angeles, School of Medicine

J. Prager, University of California, Los Angeles, School of Medicine: Neuromodulation: A multitude of targets for modulating the nervous system.
L. Mendell, Stony Brook University: Stopping pain in its tracks.
J. Kurreck, Free University Berlin, Germany: RNA interference for target validation: Investigations of the functional role of TGRPV1 in neuropathic pain.
D. Fink, University of Michigan School of Medicine, Ann Arbor: HSV-mediated gene transfer for the treatment of chronic pain.
M.E. Csete, Emory University School of Medicine, Atlanta, Georgia: Can stem cells treat pain?
R.J. Lewis, The University of Queensland, Indooroopilly, Australia: Analgesic conotoxins: Xen2174 and related stories.

SESSION 5: Clinical/Translation
Chairperson: J. Prager, University of California, Los Angeles, School of Medicine

R.J. Schwartzman, Drexel University College of Medicine, Philadelphia, Pennsylvania: Pathophysiology of CRPS.
R. Gallagher, University of Pennsylvania School of Medicine, Philadelphia: Clinical challenges for translational research.



M. Csete, J. Prager

Interactome Mapping Project for Human and Model Organisms

April 22–25

FUNDED BY **Open Biosystems and individual participants**

ARRANGED BY **M. Vidal,** Dana-Farber Cancer Institute, Boston, Massachusetts

For more than half a century, it has been conjectured that interacting macromolecules form complex systems of functionally interacting components and that the molecular mechanisms underlying most biological processes correspond to particular steady states adopted by such cellular networks. However, until recently, systems-level theoretical conjectures remained largely unappreciated, mainly because of the lack of supporting experimental data. In recent years, new large-scale high-throughput techniques are generating these data at an unprecedented rate. The participants at this meeting reviewed issues in interactome research with the goal of writing a white paper describing the goals and needs of an interactome mapping project for human and model organisms.

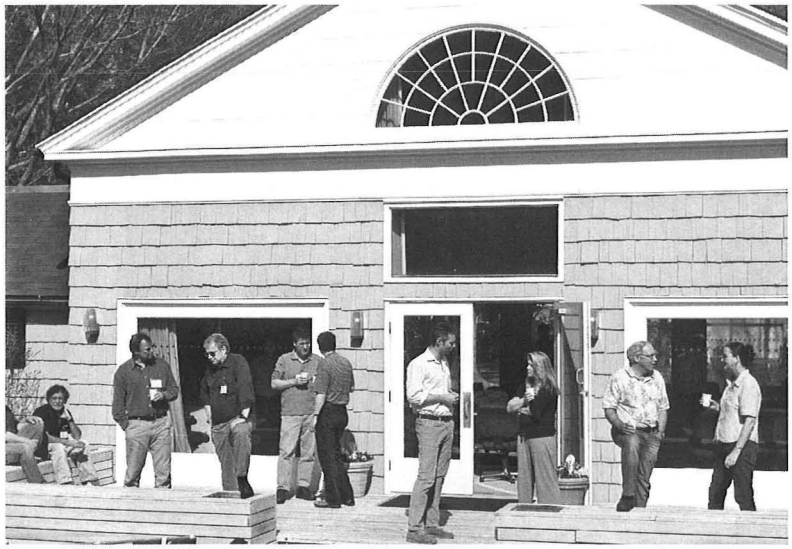
M. Vidal, B. Chait

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1: Biological Networks Properties I
Chairperson: M. Vidal, Dana-Farber Cancer Institute, Boston, Massachusetts

M. Gerstein, Yale University, New Haven, Connecticut: Understanding protein function on a genome-scale using networks.

T. Ideker, University of California, San Diego: Protein interaction networks.



Interactome meeting coffee break

SESSION 2: Cocomplex Membership Maps
Chairperson: M. Vidal, Dana-Farber Cancer Institute, Boston, Massachusetts

M. Walhout, University of Massachusetts Medical School, Amherst: Large-scale transcription factor–DNA interaction mapping using gene-centered protein–DNA interactome mapping.
J. Greenblatt, University of Toronto, Canada: Protein purification and genetic interactions to define protein complexes and functional pathways.
N. Krogan, University of California, San Francisco: Unbiased biology: Functional insights from quantitative physical and genetic interaction data sets.
T. Pawson, Mt. Sinai Hospital, Toronto, Canada: Domain-based interactions.

SESSION 3: Binary Maps
Chairperson: R.L. Finley, Wayne State University, Detroit, Michigan

S. Lalonde, Carnegie Institution of Washington, Stanford, California: Toward a comprehensive *Arabidopsis* protein interactome map: Systems biology of the membrane proteins and signalosomes.
C. Sanderson, University of Liverpool, United Kingdom: High-resolution human protein interaction networks.
R.L. Finley, Wayne State University, Detroit, Michigan: Completing the *Drosophila* protein interaction map.
E. Wanker, Max Delbrück Center for Molecular Medicine, Berlin, Germany: Automated yeast two-hybrid interaction mapping.
G. Wright, Cell Surface Signaling Laboratory, Cambridge, United Kingdom: Filling the blind spot: High-throughput identification of extracellular low-affinity interactions.

SESSION 4: Biological Networks Properties II
Chairperson: M. Vidal, Dana-Farber Cancer Institute, Boston, Massachusetts

P. Bork, EMBL, Heidelberg, Germany: Temporal aspects of protein networks.
A.-L. Barabasi, University of Notre Dame, Indiana: Human diseasome: Using protein interaction to explore human diseases.
G.F. Temple, National Human Genome Research Institute, Bethesda, Maryland: Human protein expression clones for the research community.
A. Califano, Columbia University, New York: An integrated human B-cell interactome for the dissection of lymphoid malignancies.
F. Roth, Harvard University, Boston, Massachusetts: Combining protein interactions with contextual genomic evidence to predict mammalian gene function.

SESSION 5
Chairperson: M. Vidal, Dana-Farber Cancer Institute, Boston, Massachusetts

B.T. Chait, The Rockefeller University, New York: Rapid immunoisolation of protein complexes.
L. Stein, Cold Spring Harbor Laboratory: The Reactome Database of Biological Pathways.
T. Ito, University of Tokyo, Kashiwa, Japan: Y2H and MS approaches for annotating protein interactions and modifications.
K.C. Gunsalus, New York University, New York: Probing molecular networks in *C. elegans*.

SESSION 6: Lessons from the Human Genome Project
Chairperson: M. Vidal, Dana-Farber Cancer Institute, Boston, Massachusetts

M. Vidal, Dana-Farber Cancer Institute, Boston, Massachusetts: Time for an Interactome Mapping Project!
G.M. Weinstock, Baylor College of Medicine, Houston Texas: Thoughts on the elation of Interactome and Genome projects.

SESSION 7: Summary and Future Developments
Chairperson: B.J. Wold, California Institute of Technology, Pasadena

Fragile-X Syndrome and Mechanisms of Synaptic Translation

April 29–May 2

FUNDED BY **NIH/National Institute of Mental Health (through a grant to the University of Illinois)**

ARRANGED BY **S. Warren,** Emory University, School of Medicine, Atlanta, Georgia
E. Berry-Kravis, Rush University Medical Center, Chicago, Illinois
K. Clapp, FRAXA Research Foundation, Newburyport, Massachusetts

Fragile-X syndrome is an inherited autistic spectrum disorder resulting from the functional absence of the RNA-binding protein FMRP. FMRP normally suppresses the translation of target transcripts, and its absence results in overabundance of some of the encoded proteins. FMRP is found within and at the base of dendritic spines that are involved in synaptic plasticity, and it is believed that FMRP may have a critical role in this process. This meeting focused on the regulation of local protein synthesis at the synapse and its consequences for neurobehavioral phenotypes. Modulation of local protein translation may be one approach for rational drug design for Fragile-X syndrome. Leaders in research on processes involved in synaptic protein synthesis and those involved with FMRP biology participated, to better understand FMRP function at the synapse and the neural behavioral results of its absence.

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

Introducing Fragile-X Patients: K. Clapp, FRAXA Research Foundation, Newburyport, Massachusetts

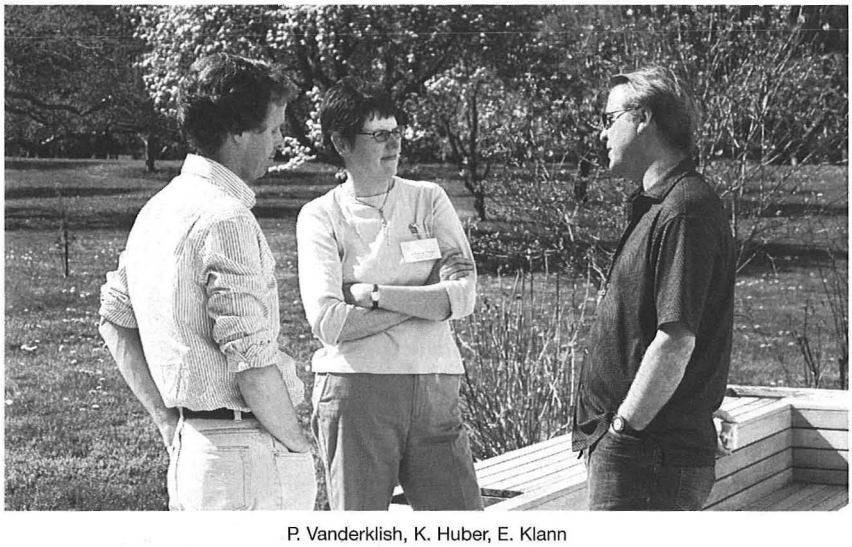
SESSION 1: FXS Phenotypes in Models and Man I
Chairperson: E. Berry-Kravis, Rush University Medical Center, Chicago, Illinois

W.T. Greenough, University of Illinois, Urbana: FMRP-interacting molecules and brain phenotype.

I. Bureau, Cold Spring Harbor Laboratory: Multiple developmental circuit defects in the barrel cortex of Fragile-X mice.

S. Chattarji, National Centre for Biological Sciences, Bangalore, India: Fragile-X mental retardation protein and spine plasticity in the amygdala.

F. Bolduc, Cold Spring Harbor Laboratory, New York: Fragile-X mental retardation protein is selectively required for long-term associative memory.



P. Vanderklish, K. Huber, E. Klann

E. Klann, New York University, New York: Plasticity and behavioral phenotypes in mutant mice with altered translational control.

R.E. Paylor, Baylor College of Medicine, Houston, Texas: Modifying behavioral phenotypes of Fragile-X mouse models.

SESSION 2: FXS Phenotypes in Models and Man II
Chairperson: W.T. Greenough, University of Illinois, Urbana

S. McBride, Albert Einstein College of Medicine, Bronx, New York: Age-dependent cognitive impairment in a *Drosophila* Fragile-X model and its pharmacological rescue.

B.A. Oostra, Erasmus Universiteit Rotterdam, The Netherlands: Behavioral experiments in FRAX mouse and man.

E. Berry-Kravis, Rush University Medical Center, Chicago, Illinois: Modifying behavior, biophysical measures, and cognition with lithium in FXS.

SESSION 3: Neuronal Transport
Chairperson: D.L. Nelson, Baylor College of Medicine, Houston, Texas

G.T. Bassell, Emory University, Atlanta, Georgia: The stimulating travels and functions of FMRP.

E.W. Khandjian, Laval University, Quebec, Canada: Trafficking FMRP-RNP granules in dendrites.

W. Sossin, McGill University, Montreal, Canada: Defining the multiple types of RNA particles/granules that are present in hippocampal neuron's axons.

I. Jeanne Weiler, University of Illinois, Urbana-Champaign: The cargo hypothesis of Fragile X: Applications to testing and analysis.

R.S. Zukin, Albert Einstein College of Medicine, Bronx, New York: AMPA receptor mRNA trafficking in dendrites and dysregulation in Fragile X.

SESSION 4: Functional Studies
Chairperson: B.A. Oostra, Erasmus Universiteit Rotterdam, The Netherlands

T.A. Jongens, University of Pennsylvania School of Medicine, Philadelphia: Role of the siRNA pathway in the regulation of dFMRP expression.

D.L. Nelson, Baylor College of Medicine, Houston, Texas: FXRs and FMR1 function.

R.B. Darnell, The Rockefeller University, New York: Cross-linking-IP studies on Nova.

P.W. Vanderklish, Scripps Research Institute, La Jolla, California: High-throughput proteomics: Comparison of synaptic fractions from wild-type and Fmr1 KO mice—new differences and maybe some new targets.

SESSION 5: Mechanisms of Translation
Chairperson: G.J. Bassell, Emory University, Atlanta, Georgia

S.T. Warren, Emory University School of Medicine, Atlanta, Georgia: FMRP dephosphorylation reveals an immediate-early dendritic signaling pathway.

R.D. Blitzer, Mount Sinai School of Medicine, New York: Stimulation-dependent regulation of dendritic translational capacity by mTOR.

M. Costa-Mattioli, McGill University, Montreal, Canada: Translational control of long-term synaptic plasticity and memory storage.

H. Tiedge, State University of New York, Brooklyn: Dendritic BC1 RNA in translational control mechanisms.

E.M. Schuman, California Institute of Technology, Pasadena: Regulation of local protein synthesis by synaptic transmission.

J.D. Richter, University of Massachusetts Medical School, Worcester: Translational control by CPEB.

SESSION 6: Studies of Synaptic Mechanisms and Activity
Chairperson: S.T. Warren, Emory University School of Medicine, Atlanta, Georgia

K.M. Huber, University of Texas Southwestern Medical Center, Dallas: Conservation of LTD mechanisms utilized by Gq-coupled receptors: Implications for Fragile X.

K. Broadie, Vanderbilt University and Medical School, Nashville, Tennessee: mGluR-dependent and -independent translation regulation by dFMRP in synaptic mechanisms.

C. Portera-Cailliau, University of California, Los Angeles: Imaging the origin of dendritic spine abnormalities in Fragile-X syndrome.

G. Dolen, Massachusetts Institute of Technology, Cambridge: Correction of Fragile-X syndrome in mice by reduced expression of mGluR5.

R.K.S. Wong, State University of New York, Downstate Health Science Center, Brooklyn: Divergent mGluR signaling and physiological responses.

Retreat from Reason

May 5–6

FUNDED BY **Private support**

ARRANGED BY **J. Morris,** International Policy Network, London
G. Ohrstrom, Ohrstrom Foundation Inc., New York
M. Ridley, Newcastle, United Kingdom
J. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

Modern technologies—especially biotechnology—are providing important benefits to society and will continue to do so. However, public perception of these technologies in both Europe and the United States, and the legal and regulatory environment in which they are developed, is increasingly hostile. As a result, access to those technologies in Europe and the United States is becoming increasingly restricted, and investments in research and development of new technologies are being curtailed or redirected to less hostile environments. The purpose of this seminar is to bring together researchers and communicators with a deep interest in the development and dissemination of new technologies. The hope is that through this discussion, a greater understanding of the causes of hostility to modern technologies will emerge, and paths forward for improving public perception and legal/regulatory environments will be identified.

Introduction to Banbury Center: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

Chairperson: G. Ohrstrom, Ohrstrom Foundation, Inc., New York

Keynote Address: L.M. Silver, Princeton University, New Jersey

Panel 1: Attacks on Technology: What Have We Learned?
Chairperson: J. Morris, International Policy Network, London, United Kingdom

Panelists: **B. Ames,** Children's Hospital Oakland Research Institute, California
P. Reiter, Institut Pasteur, Paris, France
D. Taverne, House of Lords, London, United Kingdom

Panel 2: Media Representation of Technology Issues
Chairperson: J. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

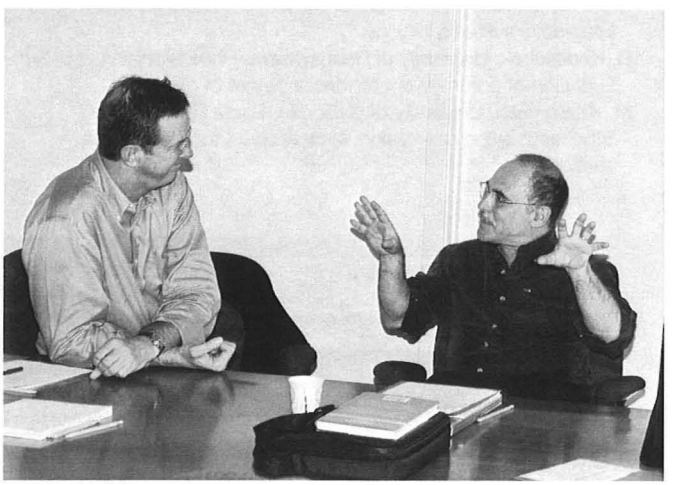
Panelists: **R. Bailey,** Reason Magazine, Charlottesville, Virginia
V. Postrel, Dynamist, Dallas, Texas
C. Mooney, Seed Magazine, Washington, D.C.

Chairperson: G. Ohrstrom, Ohrstrom Foundation Inc., New York

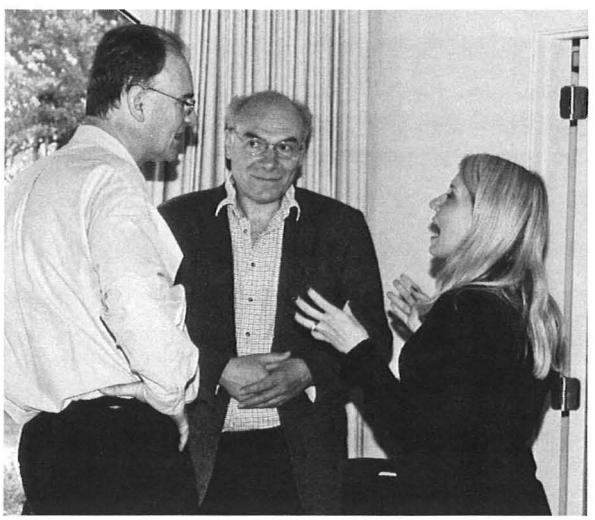
Keynote Address: V. Postrel, Dynamist, Dallas

Panel 3: Psychology of Acceptance of and Opposition to Technology
Chairperson: M. Ridley, Newcastle, United Kingdom

Panelists: **M. Crichton,** Santa Monica, California
T. Kealey, The University of Buckingham, United Kingdom
S. Dudley, Office of Management & Budget, Washington, D.C.



M. Crichton, L. Silver



M. Ridley, T. Kealey, V. Postrel

Design Principles in Biological Systems

May 6–8

FUNDED BY **The National Science Foundation**

ARRANGED BY **P.P. Mitra,** Cold Spring Harbor Laboratory
M.W. Kirschner, Harvard Medical School, Boston, Massachusetts
R.M. Murray, California Institute of Technology, Pasadena

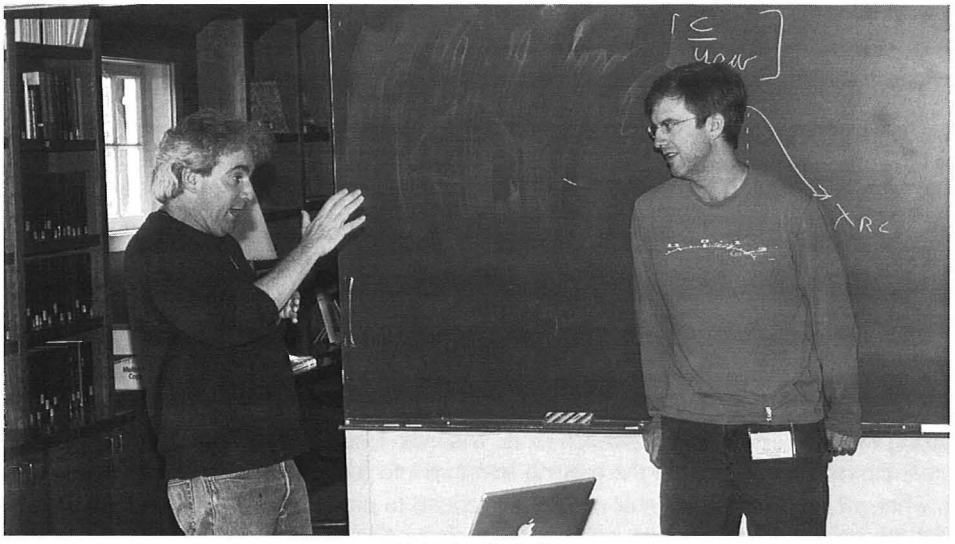
This workshop brought together scientists with strong theoretical or mathematical backgrounds and an active interest in applying engineering principles to the study of biological systems. Discussions and presentations at the workshop focused on the premise that evolutionary solutions or designs, although not themselves engineered, may nevertheless be studied in their existing forms in the framework of theories developed for human-engineered systems. The workshop provided an opportunity for biological researchers to learn about engineering theories that may be relevant to their work and to promote collaborations by bringing interesting biological problems to the attention of engineering theorists and computer scientists.

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

Introduction to Meeting: P.P. Mitra, Cold Spring Harbor Laboratory

SESSION 1: Engineering and Biology
Chairperson: R.M. Murray, California Institute of Technology, Pasadena

R.J. Full, University of California Berkeley: Challenges of an integrative systems biology.
D. Koditschek, University of Pennsylvania, Philadelphia: Evolution of a framework for development of gaits.
M. Khammash, University of California, Santa Barbara: Stochastic gene expression: New analysis tools and case studies.
R. Milo, Harvard Medical School, Boston, Massachusetts: Energy optimization and the design of photosynthesis.
D. Kleinfeld, University of California, San Diego: Topology, dynamics, and neuronal control of cortical blood flow.
C. Myers, Cornell University, Ithaca, New York: Polymorphic programming in biology and engineering.



M. Levine, D. Endy

SESSION 2: Evolution
Chairperson: P.P. Mitra, Cold Spring Harbor Laboratory

M.W. Kirschner, Harvard Medical School, Boston, Massachusetts: Physiological and evolutionary adaptation in hemoglobin.
M. Levine, University of California, Berkeley: Gene networks in animal development and evolution.
C. Queitsch, Harvard University, Cambridge, Massachusetts: Chaperone Hsp90 as a molecular mechanism of genetic and environmental canalization.
S.C. Stearns, Yale University, New Haven, Connecticut: Evolutionary principles of phenotypic design.
P. Niyogi, University of Chicago, Illinois: Computational nature of language learning and evolution.

SESSION 3: Evolution in Engineering
Chairperson: M.W. Kirschner, Harvard Medical School, Boston, Massachusetts

J. Doyle, California Institute of Technology, Pasadena: Robust and evolvable architectures.
R.M. Murray, California Institute of Technology, Pasadena: Systems engineering and architecture.

SESSION 4: Engineering and Biology (with an Emphasis on Evolution)
Chairperson: J. Carlson, Clay Mathematics Institute, Cambridge, Massachusetts

M.A. Savageau, University of California, Davis: Quantitative evolutionary design of an oxidative stress response system in human erythrocytes.
A. Sengupta, Rutgers, The State University of New Jersey, Piscataway: Geometry of parameter space in regulatory networks: Investigating measures of robustness.
H. Karten, University of California, San Diego, La Jolla: Multiple "systems" in the visual "system": An attempt to break the bottleneck.
B. Mishra, New York University, New York: Evolutionary models and systems biology.
C. Myers, University of Utah, Salt Lake City: Engineering genetic circuits.
C.C. Hilgetag, Jacobs University Bremen, Germany: Spatial organization of neural connectivity.

SESSION 5: Synthetic Biology (with Thoughts on Evolution)
Chairperson: M.E. Csete, Emory University School of Medicine, Atlanta, Georgia

C.D. Smolke, California Institute of Technology, Pasadena: Engineering RNA devices as communication and control systems.
D. Endy, Massachusetts Institute of Technology, Cambridge: Very small-scale integrated biological systems.
P.A. Silver, Harvard Medical School, Cambridge: Designing biological memory and logic.

The Brain Architecture Project

May 20–22

FUNDED BY **The W.M. Keck Foundation**

ARRANGED BY **P.P. Mitra,** Cold Spring Harbor Laboratory
L. Swanson, University of Southern California, Los Angeles
H. Breiter, Massachusetts General Hospital, Charlestown
J. Doyle, California Institute of Technology, Pasadena
C. Allen, Cold Spring Harbor Laboratory

This Project is a new collaborative effort in human neuroanatomical research supported by the W.M. Keck Foundation. The initial goal of the project is to produce a draft of the "connectivity matrix" of the human brain, along with analytical and visualization tools. The main focus was collation and integration of human neuroanatomical information in the existing literature into a comprehensive database. This was the first in what will be a series of annual meetings intended to promote the development of useful resources for the neuroscience research and clinical communities, as well as to receive valuable feedback and input from collaborators and invited external advisors. Progress to date was reviewed, and there were sessions focused on the reconciliation of classical neuroanatomical and MRI morphometry-based systems of nomenclature.

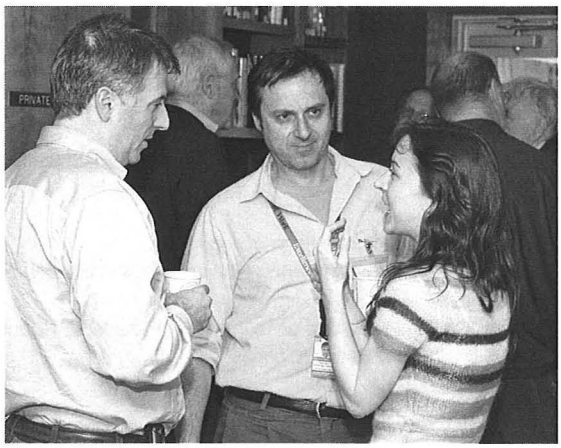
Opening Session: Introducing the Brain Architecture Project

Introduction of Project and Goals: P.P. Mitra, Cold Spring Harbor Laboratory

Overview of Progress and Meeting Agenda; Introductions to Project Members and Meeting Participants: C.B. Allen, Cold Spring Harbor Laboratory

Additional Remarks: H. Breiter, Massachusetts General Hospital, Charlestown
L.W. Swanson, University of Southern California, Los Angeles

Introductory Remarks: S. Gary, Banbury Center, Cold Spring Harbor Laboratory



N. Schiff, C. Allen, D. Herrera

SESSION 1: Related Projects
Chairperson: G. Burns, University of Southern California, Los Angeles

D.M. Bowden, University of Washington, Seattle: Terminological needs of a portal to neuroscience on the Web.

L.W. Swanson and M. Bota, University of Southern California, Los Angeles: Classical nomenclature and the Brain Architecture Management System (BAMS).

C.B. Allen, Cold Spring Harbor Laboratory: Overview of the CoCoMac database.

C.C. Hilgetag, Jacobs University Bremen, Germany: Perspectives on CoCoMac from an end-user.

S. Habeer, University of Rochester, New York: Three-dimensional models of projection pathways in the macaque brain.

D. Kennedy, N. Makris, and H. Breiter, Massachusetts General Hospital, Charlestown: MRI-based neuroanatomic parcellation and labeling systems: Implications for broad, community-based utility.

SESSION 2: Proposed Scenarios for Nomenclature Reconciliation
Chairperson: C.B. Allen, Cold Spring Harbor Laboratory

Direct comparison of MRI parcellation systems (BAP members)
Reconciliation Scenarios (BAP members)
Moderated Discussion

SESSION 3: Networks
Chairperson: C.B. Allen, Cold Spring Harbor Laboratory

P.P. Mitra, Cold Spring Harbor Laboratory: Structure and dynamics of networks: An informal review of models and analysis tools.

SESSION 4: Coordinating with Atlasing Projects
Chairperson: H. Barbas, Boston University, Massachusetts

E.G. Jones, University of California, Davis: Brain atlases and terminology.
D.C. Van Essen, Washington University School of Medicine, St. Louis, Missouri: Cortical partitioning and connectivity analyzed using surface-based atlases and approaches.
A.W. Toga, Laboratory of Neuro Imaging, Los Angeles, California: Multisubject, multisite brain atlasing projects: Past and future experiences.

SESSION 5: Advisor Input: Open discussion with advisors on overall project goals and plan.

SESSION 6: White Paper Input: Open discussion to voice the needs of neuroanatomy and connectivity research.

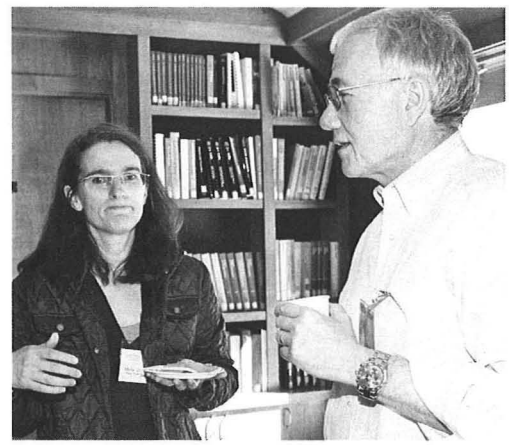
The Laboratory Diagnosis of Lyme Disease

September 9–12

FUNDED BY **Centers for Disease Control and Prevention and NIH—National Institute of Allergy and Infectious Diseases**

ARRANGED BY **P.J. Baker,** NIAID, National Institutes of Health, Bethesda, Maryland
R.J. Dattwyler, New York Medical College, Valhalla
B.J.B. Johnson, CDC, DVBID, Fort Collins, Colorado

Lyme disease continues to be a difficult infection to diagnose and treat, even 25 years after the discovery that it was caused by a spirochete transmitted by tick bites. Banbury Center has been the venue for Lyme disease discussion meetings almost annually since 1991, and it is fascinating to see how the topics for meetings have cycled through basic research, diagnosis, and treatment. This year, the meeting returned to the problems and possible solutions of diagnosis. This is clearly a matter of the greatest importance in infectious diseases. The correct diagnosis must be made as early as possible so that the correct treatment can be administered as soon as possible.



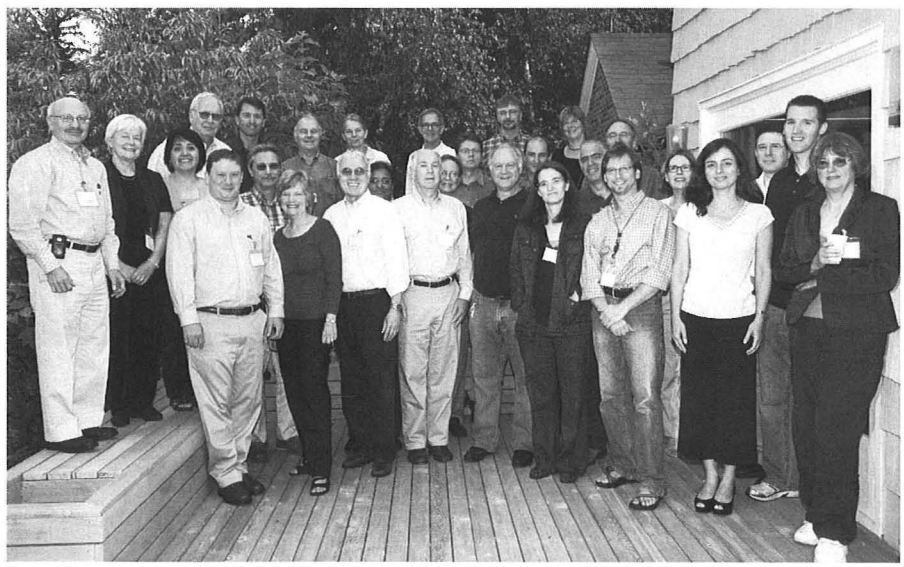
M. Gomes-Solecki, R. Dattwyler

Introductory and Welcoming Remarks

J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory
P.J. Baker, NIAID, National Institutes of Health, Bethesda, Maryland

Goals for the Conference

B.J.B. Johnson, CDC, DVBID, Fort Collins, Colorado
R.J. Dattwyler, New York Medical College, Valhalla



SESSION 1: Serodiagnosis of Lyme Disease in Clinical Practice I
Chairperson: A.C. Steere, Massachusetts General Hospital, Boston

B.J.B. Johnson, CDC, DVBID, Fort Collins, Colorado: Initial efforts to standardize the serodiagnosis of Lyme disease: Rationale, history, and retrospective studies.
M. Aguero-Rosenfeld, Westchester County Medical Center, Valhalla, New York: Lyme serology: Two-tier revisited.
M.J. Binnicker, Mayo Clinic, Rochester, Minnesota: Evaluation of automated western blot processing, scanning, and interpretive systems in the serologic diagnosis of Lyme disease.
A.C. Steere, Massachusetts General Hospital, Boston: Prospective study of serologic tests for Lyme disease.
J.A. Branda, Massachusetts General Hospital, Boston: A new approach to antibody testing in the diagnosis of Lyme disease.

SESSION 2: Serodiagnosis of Lyme Disease in Clinical Practice 2
Chairperson: S. O'Connell, Southampton General Hospital, United Kingdom

B. Wilske, University of Munich, Germany: Diversity of *B. burgdorferi* sensu lato in Europe and implications for diagnosis of Lyme borreliosis.
S. O'Connell, Southampton General Hospital, United Kingdom: Lyme diagnostics and clinical advice provision in the U.K.: Experience of a reference laboratory.
H. Hofmann, University of Munich, Germany: Serological follow up in patients with early and late Lyme borreliosis: Densitometric evaluation of a new Line Blot compared to quantitative ELISA.
P.J. Krause, Connecticut Children's Medical Center, Hartford: Absence of serologic cross-reactivity between *B. burgdorferi* and *B. microti*.
A.R. Marques, LCI, NIAID, National Institutes of Health, Bethesda, Maryland: Evaluation of CSF in the diagnosis of neuroborreliosis.
C.P. Quinn, CDC, Atlanta, Georgia: Development and validation of quantitative serological assays.

SESSION 3: VosE and C6 Peptide
Chairperson: M.T. Philipp, Tulane University Health Sciences Center, Covington, Louisiana

M.T. Philipp, Tulane University Health Sciences Center, Covington, Louisiana: Comparative antigenicity of VlsE, C6, and other VlsE invariant regions and domains.
G.P. Wormser, New York Medical College, Valhalla: C6 vs. two-tier testing: A multicenter study.
S.J. Wong, New York State Department of Health, Albany: Comparison of Athena Multi-Lyte *B. burgdorferi* VlsE1 IgG+ pepC10 IgM test system to two-tier Lyme serology.
M.J. Gomes-Solecki, New York Medical College, Valhalla: Multiantigenic peptide assay for the serodiagnosis of Lyme disease.
P. Lahdenne, University of Helsinki, Finland: Improved serodiagnosis of Lyme disease with recombinant protein variants from different borrelial genospecies.

SESSION 4: Future Directions
Chairperson: A.G. Barbour, University of California, Irvine

R.B. Porwancher, Infectious Disease Consultants, P.C., Mercerville, New Jersey: Improving Lyme disease diagnosis through bioinformatics.
I. Schwartz, New York Medical College, Valhalla: Host-gene expression as a diagnostic test for *B. burgdorferi* infection.
P.L. Felgner, University of California, Irvine: Whole proteome microarrays for serodiagnostic antigen discovery.
A.G. Barbour, University of California, Irvine: Discovery and rediscovery of *B. burgdorferi* antigens: A genome-wide array approach.
J. Carroll, University of Pittsburgh, Pennsylvania: Paralogous gene family 54 and proteomic approaches to serodiagnosis.

SESSION 5: Future Directions II
Chairperson: S.E. Schutzer, UMDNJ–New Jersey Medical School, Newark

A.R. Marques, LCI, NIAID, National Institutes of Health, Bethesda, Maryland: B-cell-attracting chemokine CXCL 13 in patients with post-Lyme disease syndrome.
M. Eshoo, Ibis Biosciences, Carlsbad, California: Identifying unknown pathogens by mass spectrometry.
S.E. Schutzer, UMDNJ–New Jersey Medical School, Newark: Proteomics of Lyme disease.

Special Presentation: Populist syndromes: Toxic mold and chronic Lyme disease
M. Edesess, International Development Enterprises, Lakewood, Colorado

SESSION 6: Regulation of Diagnostic Testing
Chairperson: B.J.B. Johnson, CDC, Fort Collins, Colorado

S. Hojvat, FDA/CDRH/OIVD, Rockville, Maryland: FDA regulation of Lyme disease serological tests for the detection of *B. burgdorferi* antibodies.

SESSION 7: Recommendations of the Conferees

Roundtable: Session chairs and conveners

Champalimaud Foundation: Neuroscience

September 13–14

FUNDED BY **The Champalimaud Foundation**

ARRANGED BY **A. Damasio,** University of Southern California, Los Angeles
J.D. Watson, Cold Spring Harbor Laboratory

The Champalimaud Foundation has decided to establish an international institute of research and clinical practice, focused on cancer and neurological illnesses. Initial plans are under way, including the formation of partnerships with a number of outstanding international universities, teaching hospitals, and research institutions. As part of these initial plans, the Foundation held two discussion workshops at Banbury, the first on neuroscience and the second on cancer (see next page). The following critical questions were put to the invited experts: What kind of science should be pursued? What should the balance be between clinical work and basic research? What new technologies or concepts can best be developed and applied?

Introduction: A. Damasio, University of Southern California, Los Angeles
J.D. Watson, Cold Spring Harbor Laboratory

Chairperson of Meeting: A. Damasio, University of Southern California, Los Angeles

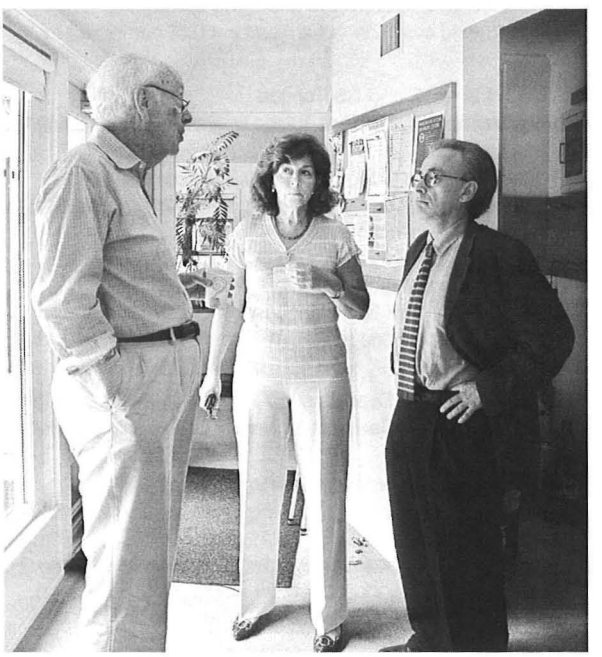
SESSION 1: Current Plans from Champalimaud Foundation I

Neuroscientists (led by Z. Mainen) and reaction from the Group of Advisors

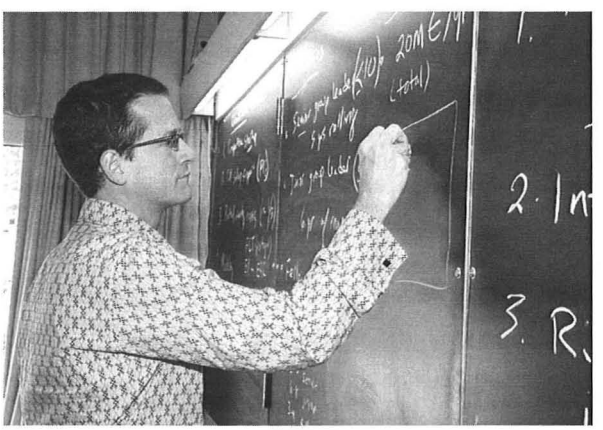
SESSION 2: Current Plans from Champalimaud Foundation II

SESSION 3: Building a Successful Neuroscience Program: Useful Paths and Pitfalls

SESSION 4: Final Discussion and Recommendations



J. Watson, L. Beleza, A. Damasio



Z. Mainen

Champalimaud Foundation: Cancer Research

September 15–16

FUNDED BY **The Champalimaud Foundation**

ARRANGED BY **C. Caldas,** Cancer Research UK, Cambridge
J.D. Watson, Cold Spring Harbor Laboratory

Introduction—The Champalimaud Foundation Cancer Program
J.D. Watson, Cold Spring Harbor Laboratory
C. Caldas, Cancer Research UK, Cambridge

Chairperson of Meeting: C. Caldas, Cancer Research UK, Cambridge

SESSION 1: Cancer Genomes and Epigenomes in the Era of Very Cheap Sequencing

Discussion Leaders:
B.J. Ponder, Cancer Research UK, Cambridge: Germ-line genomics.
M. Loda, Dana-Farber Cancer Institute, Boston, Massachusetts: Somatic genomics.

SESSION 2: Cancer Microenvironment: Angiogenesis and More

Discussion Leaders:
J. Folkman, Children's Hospital, Boston, Massachusetts: Angiogenesis.
D. Hanahan, University of California, San Francisco: Tumor stroma.

SESSION 3: Cancer Imaging: Seeing It All Noninvasively

Discussion Leader:
R. Blasberg, Memorial Sloan-Kettering Cancer Center, New York: State of the art in molecular imaging.

SESSION 4: Cancer Models: Building Mice with "Humanized" Cancer

Discussion Leaders:
S. Lowe, Cold Spring Harbor Laboratory: RNAi in mice.
D.A. Tuveson, Cancer Research UK, Cambridge: Engineering mice with "human-like" tumors.

SESSION 5: Experimental Cancer Therapeutics: The Way Ahead

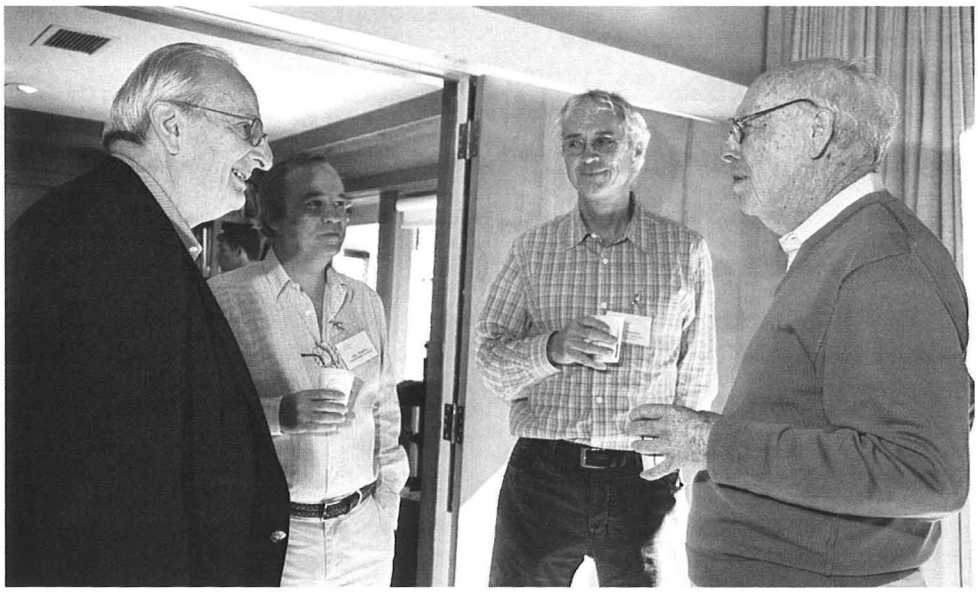
Discussion Leaders:
C.J. Marshall, Institute of Cancer Research, London, United Kingdom: A systems approach to targeting kinase pathways.
S. Aparicio, BC Cancer Research Centre, Vancouver, Canada: Image-based high-throughput "synthetic-lethal" screens.

SESSION 6: Cancer Stem Cells: Does It Matter?

Discussion Leaders:
C. Eaves, BC Cancer Research Centre, Vancouver: Breast stem cells and the molecular phenotypes of breast cancer.
P.G. Pelicci, European Institute of Oncology, Milan, Italy: PML and leukemia stem cells.

SESSION 7: Final Discussion: The Ideal Cancer Research Institute—Balancing Fundamental and Applied Research

Discussion Leaders:
B.J. Ponder, Cancer Research UK, Cambridge
P. Marks, Memorial Sloan-Kettering Cancer Center, New York



J. Folkman, J. Botelho, D. Hanahan, J. Watson

Drug Discovery, Biomarkers, and Clinical Trials for ALS

September 23–26

FUNDED BY **Greater New York Chapter of the ALS Association**

ARRANGED BY **E.P. Pioro,** The Cleveland Clinic, Ohio
M.D. Cudkowicz, Harvard Medical School, MGH, Boston, Massachusetts
L. Bruijn, The ALS Association, Palm Harbor, Florida
N. Kayadjanian, The ALS Association, San Diego, California

As we understand more about the underlying mechanisms involved in cell death in ALS, several new targets for therapeutic development have been identified. Some of the key challenges associated with the development of therapies for ALS include the degree of cell death at the time of diagnosis and the length of clinical trials required to determine whether the drug is effective in slowing disease progression. This workshop evaluated some of the exciting new areas and opportunities for drug discovery and development, and explored the development of biomarkers and clinical trial design.

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1: Drug Discovery Efforts in ALS
Chairperson: J.D. Rothstein, The Johns Hopkins University School of Medicine, Baltimore, Maryland

L. Bruijn, The ALS Association, Palm Harbor, Florida: Introduction.
R. Pacifici, MRSSI/CHDI, Inc., Los Angeles, California: Drug discovery and development in other orphan diseases such as Huntington's disease: Opportunities and challenges.
P.T. Lansbury, Link Medicine, Corporation, Cambridge, Massachusetts: Therapeutic strategies for slowing ALS progression.
J.M. McCall, PharMac LLC, Kalamazoo, Michigan: Drug discovery and development: Challenges and opportunities.
J.D. Rothstein, The Johns Hopkins University School of Medicine, Baltimore, Maryland: Modulation of astroglial function in ALS: Small-molecule discovery, relevant biomarkers and PET.

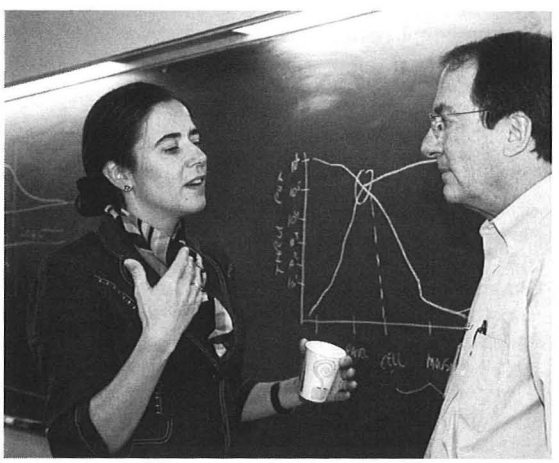
SESSION 2: High-throughput Screening
Chairperson: R. Pacifici, MRSSI Inc., Los Angeles, California

D.F. Fischer, BioFocus DPI, Leiden, The Netherlands: High-throughput target and drug discovery in human stem-cell-derived motor neurons.
J. Staunton, CombinatoRx, Inc., Boston, Massachusetts: Platform for testing combination therapies in high-throughput cell-based assays.

SESSION 3: Delivery Systems
Chairperson: M.D. Cudkowicz, Harvard Medical School, MGH, Boston, Massachusetts

D. Drummond, Hermes Biosciences, Inc., South San Francisco, California: Immunotargeted lipid nanocarriers for small-molecule and nucleic acid therapeutics.
Z. Xu, University of Massachusetts Medical School, Worcester: RNAi therapy for ALS.
T.M. Miller, Washington University School of Medicine, St. Louis, Missouri: Antisense and ALS.

General Discussion
M.D. Cudkowicz, Harvard Medical School, MGH, Boston, Massachusetts



P. Kauffman, J.M. McCall

SESSION 4: Clinical Trials in ALS
Chairperson: P. Kaufmann, The SMA Clinic, Columbia University Medical School, New York

M.D. Cudkowicz, Harvard Medical School, Massachusetts General Hospital, Boston: Overview.
W.W. Bryan, Biologics Consulting Group, Inc., Rockville, Maryland: Is ALS one disease or many different diseases?
B. Ravina, Strong Health Medical Center, Rochester, New York: Clinical trial designs in Parkinson's disease.
S. Wieland, CytRx Corporation, Los Angeles, California: Clinical trial design in ALS for product approval.
B. Levin, Columbia University, New York: Sequential statistical designs for selecting from competing therapies.
D.A. Schoenfeld, Harvard School of Public Health, Boston, Massachusetts: Design considerations for trials of ALS therapies.

SESSION 5: Biomarkers I
Chairperson: N. Kayadjanian, The ALS Association, San Diego, California

E.P. Pioro, The Cleveland Clinic, Ohio: Overview.
M. Benatar, Emory University, Atlanta, Georgia: Strategies for presymptomatic biomarker identification in familial ALS.
M. Strong, UH-LHSC, London, Ontario, Canada: FTD-TDP43 and other clues as biomarkers/pathology.
J.S. Paulsen, University of Iowa, Iowa City: Lessons from other diseases: Huntington's disease.
M. Lowe, The Cleveland Clinic Foundation, Ohio: Imaging techniques.
J.M. Shefner, State University of New York, Upstate Medical University, Syracuse: Physiological outcome measures in ALS clinical trials.

General Discussion:
E.P. Pioro, The Cleveland Clinic, Ohio

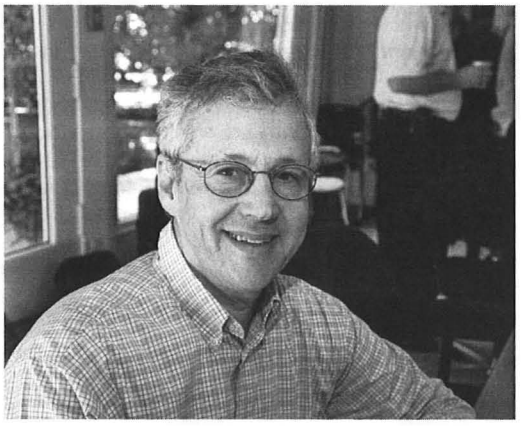
SESSION 6: Biomarkers II
Chairperson: E.P. Pioro, The Cleveland Clinic, Ohio

R.H. Brown, Massachusetts General Hospital, Charlestown: Overview.
R. Bowser, University of Pittsburgh School of Medicine, Pennsylvania: Use of biomarkers to identify therapeutic targets and monitor disease progression.
B. McCreedy, Metabolon, Inc., Research Triangle Park, North Carolina: Metabolomic approach to biomarkers for ALS.

SESSION 7: Animal Models
Chairperson: L. Bruijn, The ALS Association, Palm Harbor, Florida

D.S. Howland, High Q Foundation, New York: Standardization of preclinical testing in mouse models of ALS and HD: A pipeline for targets and compounds.

Panel Discussion: Challenges for Preclinical and Clinical Development of Therapies for ALS
Chairperson: M.D. Cudkowicz, Harvard Medical School, MGH, Boston, Massachusetts
Panelists: **J. McCall,** PharMac LLC, Kalamazoo, Michigan: Drug development.
B. Ravina, University of Rochester, New York: Clinical trials.
R.H. Brown, Massachusetts General Hospital, Charlestown: All aspects.
W.W. Bryan, Biologics Consulting Group Inc., Rockville, Maryland: Regulatory issue.
D.S. Howland, High Q Foundation, New York: Animal models.


D.F. Fischer

Wrap Up and Closing Remarks
L. Bruijn, The ALS Association, Palm Harbor, Florida

Science: Get It Across!

September 28–October 3

FUNDED BY **Boehringer Ingelheim Fonds Foundation for Basic Research in Medicine**

ARRANGED BY **H. Fröhlich,** Boehringer Ingelheim Fonds, Heidesheim, Germany
C. Walther, Boehringer Ingelheim Fonds, Heidesheim, Germany

The Boehringer Ingelheim Foundation returned to the Banbury Center for their biannual fellows meeting in North America. In addition to providing training for their fellows, the Foundation very generously supported a special lecture by a visiting young scientist, given in Grace Auditorium and open to all CSHL scientists. The first recipient of this honor was Jennifer A. Zallen, Head of the Morphogenesis and Polarity Laboratory at Memorial Sloan-Kettering Institute, who spoke on "Shaping the embryo: Cellular dynamics in development."

Opening Remarks: H. Fröhlich, Boehringer Ingelheim Fonds, Heidesheim, Germany

Introduction: C. Walther, Boehringer Ingelheim Fonds, Heidesheim, Germany

Speakers

W. Wells, Global Alliance for TB Drug Development, New York: Basic lecture on writing techniques and how to structure papers.

H. Ploegh, Whitehead Institute, Cambridge, Massachusetts: What makes success in science?

B. Tansey, Cold Spring Harbor Laboratory: Representation of scientific information: Graphic and rhetoric.

B. Tansey, Cold Spring Harbor Laboratory: Group A starts the graphic assignment and Group B delivers 10-minute-presentation.

B. Tansey, Cold Spring Harbor Laboratory: Review of the videotaped presentations (Group B).

B. Tansey, Cold Spring Harbor Laboratory: Group B starts the assignment and Group A delivers 10-minute-presentation.

B. Tansey, Cold Spring Harbor Laboratory: Review of the videotaped presentations (Group A).

J.A. Zallen, Memorial Sloan-Kettering Cancer Center, New York: Shaping the embryo. Cellular dynamics in development.

Sammis Hall in the fall

Genetics of Crop Domestication

October 14–17

FUNDED BY **Cold Spring Harbor Laboratory Corporate Sponsor Program**

ARRANGED BY **M.D. Purugganan,** New York University
E.S. Buckler, Cornell University, Ithaca, New York

The development of domesticated species was a pivotal event in the rise of human civilizations and has served as a metaphor for the evolution of new taxa. In recent years, geneticists and plant scientists have made significant advances in identifying genes associated with domestication, as well as using molecular data to explore the evolutionary process of domestication. Archaeologists have also made strides in unraveling the record of crop and farm animal use in many sites across the world and have begun to explore the cultural, ecological, and evolutionary patterns associated with domestication. As for many Banbury meetings, the organizers ensured an interesting meeting by having participants from varied backgrounds—genomic scientists, molecular biologists, plant breeders, evolutionary geneticists, and archaeologist—in this case, to explore the origins and evolution of domesticated plant and animal species.

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1: Plant and Animal Domestication and the Archaeological Record
Chairperson: J.F. Wendel, Iowa State University, Ames

D.Q. Fuller, University College London, United Kingdom:
Progress and challenges in the Archaeobotany of Asian rice: Spikelet bases, immature harvests, and inferring domestication process.

B.D. Smith, Smithsonian Institution, Washington, D.C.:
Combing genetics and archaeology in documenting the early

history of four crop plants in the Americas: Bottle gourd, squash, maize, and sunflower.

M.A. Zeder, Smithsonian Institution, Washington, D.C.: Defining domestication: How advances in genetics and archaeology are reshaping our understanding of domestication and its origins.

G. Wilcox, National Centre for Scientific Research, Saint-Paul-le-Jeune, France: Origins of cultivation and domestication of cereals and pulses: Evidence from Near Eastern archaeological sites.

P. Gepts

SESSION 2: Origins of Agricultural Species: Molecular Data
Chairperson: D.Q. Fuller, University College London, United Kingdom

P.L. Morrell, Monsanto Company, Chesterfield, Missouri: Genetic evidence for a second domestication of barley (*Hordeum vulgare*) east of the Fertile Crescent.

P. Gepts, University of California, Davis: A Phaseoulus perspective on crop domestication.

D.G. Bradley, Trinity College Dublin: Genetic hoof prints; genetic insight into bovine domestications.

G. Larson, Uppsala University Biomedical Center, Sweden: Breaking down genomic barriers: How domestication affects an organism's ability to hybridize with multiple wild species.

R.K. Wayne, University of California, Los Angeles: Dog origins, domestication, and evolution.

J.F. Wendel, Iowa State University, Ames: Jeans, genes, and parallel domestication of cultivated cottons.

P. Tiffin, University of Minnesota, St. Paul: Population genetics of the progenitor: Geographic structure and diversity in teosinte.

SESSION 3: Selection in Domesticated Genomes
Chairperson: P. Tiffin, University of Minnesota, St. Paul

C.D. Bustamante, Cornell University, Ithaca, New York: Statistical methods for inferring demographic history of domesticated plant and animal species from SNP genotype data: Preliminary data, potential pitfalls, and possible solutions.

Y. Kim, Arizona State University, Tempe: The pattern of selective sweeps in derived populations.

A.L. Caicedo, University of Massachusetts, Amherst: Genome-wide patterns of nucleotide polymorphism in domesticated rice.

M.D. Purugganan, New York University, New York: Nature of selection in the rice genome.

S.I. Wright, York University, Toronto, Canada: Demographic history and selection during maize domestication.

T. Brown, University of Manchester, United Kingdom: Using computer simulations to test models of crop origins.

SESSION 4: Genetic Architecture and Molecular Genetics of Domestication
Chairperson: A.L. Caicedo, University of Massachusetts, Amherst

T. Sang, Michigan State University, East Lansing: Genetics and phylogenetics of rice domestication.

S. McCouch, Cornell University, Ithaca, New York: Emerging story of rice domestication.

J.M. Burke, University of Georgia Plant Biology, Athens: Genetics and the domestication of sunflower.

W. Powell, National Institute of Agriculture Botany, Cambridge, United Kingdom: Evolution and domestication of barley and wheat: New insights from population-based resequencing of candidate genes.

E.S. Buckler, Cornell University, Ithaca: Genetic architecture of maize trait variation.

L. Andersson, Uppsala University, Sweden: Molecular characterization of trait loci gives new insight in chicken domestication.

K.M. Olsen, Washington University in St. Louis, Missouri: Molecular evolution of an adaptive cyanogenesis polymorphism in white clover.

N. Weeden, Montana State University, Bozeman: Genetic basis of morphological and physiological changes associated with the domestication of pea, *P. salivum L.*

Meeting Wrap Up and Discussion of Future Research

Protecting Public Trust in Immunization

October 17–19

FUNDED BY **Albert B. Sabin Vaccine Institute, with support from the Robert Wood Johnson Foundation and Autism Speaks**

ARRANGED BY **L.Z. Cooper,** Sabin Vaccine Institute, New York
H. Larson, Harvard Center for Population & Development, Cambridge, Massachusetts
S.L. Katz, Duke University Medical Center, Durham, North Carolina

Vaccine preventable diseases (with few exceptions) are at an all time low in the United States. This success reflects the biologic effectiveness of specific vaccines, sound public policy, implementation in delivering vaccines to target audiences, and a history of high levels of public trust in vaccine safety and efficacy. This trust is an expression of a special social contract that is key to the success of immunization programs. However, we cannot be complacent in assuming trust in public health recommendations, and, indeed, a significant number of parents have serious concerns about safety. Antivaccine activists are gaining momentum. Given these recent trends, it is critical to take a closer look at public trust in vaccines. This discussion meeting reviewed the status of public trust in immunization, clarified its strengths and weaknesses, identified strategies to increase trust, and made recommendations to stakeholders in the "vaccine endeavor."

Keynote Speaker: H.R. Shepherd, Sabin Vaccine Institute, New Canaan, Connecticut

Introduction of Speaker: Robert Wright, Autism Speaks, New York

SESSION 1: A Frame of Reference
Chairperson: S.L. Katz, Duke University Medical Center, Durham, North Carolina

L.Z. Cooper, Sabin Vaccine Institute, New York: Why Sabin convened this colloquium?
D.G. Salmon, National Vaccine Program, DHHS, Washington, D.C.: Government roles in protecting public trust in immunization.
D. Pineda, Immunizations for Public Health, Galveston, Texas: Words matter: Risk communication and public trust.

Group General Discussion and charge to Breakout Group A: What should be key features immunization programs to sustain public trust of individuals to be served?

Group's Report

SESSION 2: Painful Examples: Evolution of Distrust and Lessons to be Learned
Chairperson: L.Z. Cooper, Sabin Vaccine Institute, New York

Discussion: Autism—The MMR Questions Evolution of Chimerical Concerns
Panel: N. Halsey, The Johns Hopkins University School of Hygiene & Public Health, Baltimore, Maryland
G. Nowak, Centers for Disease Control and Prevention, Atlanta, Georgia
S. Bernard, SafeMinds, Tyrone, Georgia
A. Shih, Autism Speaks, New York
M. McCormick, Harvard School of Public Health, Boston, Massachusetts: A special perspective: The IOM-ISRC experience—Trust, a steep hill.

SESSION 3: Global Issues: Biologic and Sociocultural/Political Complexities Challenge Public Trust

A. Polio and Beyond, Tetanus and Hepatitis Vaccines
Chairpersons: A. Bentsi-Enchill, World Health Organization, Geneva, Switzerland
H. Larson, Harvard Center for Population & Development, Cambridge, Massachusetts
N. Khuri-Bulos, Jordan University Hospital, Amman
K. Hartigan-Go, The Zuellig Foundation, Makati City, Philippines

B. Other Challenges, Including Balancing National vs. International Interests
Chairperson: S.L. Katz, Duke University Medical Center, Durham, North Carolina

J.D. Grabenstein, Merck Vaccines & Infectious Diseases, West Point, Pennsylvania: HPV, a new primary audience, different challenges.
D.R. Johnson, Sanofi Pasteur, Swiftwater, Pennsylvania: Ups, downs, and ups with totavirus vaccine.
L. Sullivan, Morehouse School of Medicine, Atlanta, Georgia: A broader perspective on public trust and immunization.

Brief Comments from the "Communicators"
Chairperson: C.D. DeAngelis, Journal of the American Medical Association, Chicago, Illinois
Panel: C. Cole, Sesame Workshop, New York
L. McNeill, Food and Drug Administration, Rockville, Maryland
B. Mulach, NIAID, National Institutes of Health, Bethesda, Maryland
G. Nowak, Centers for Disease Control and Prevention, Atlanta, Georgia
D. Pineda, Immunizations for Public Health, Galveston, Texas

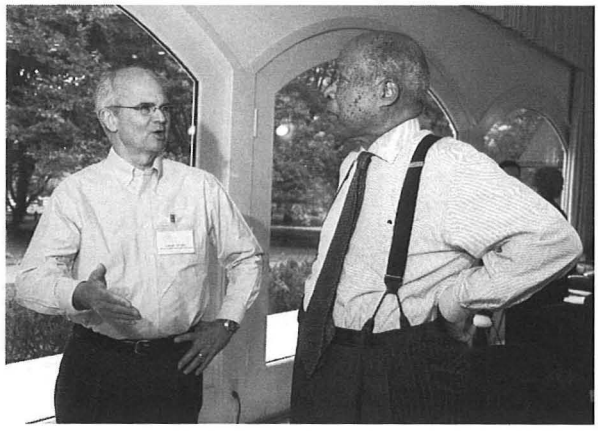
Breakout Group B
What are the lessons to be learned from these recent challenging examples? Reflect on both the processes of communication and the specific content of the information.

Breakout Group B Reports and Open Discussion

Breakout Group C
Since immunization science provides content essential for communication and building public trust, what are solutions for enhancing immunization safety science?

Group's Report and Group Discussion: Selecting most important solutions

Open Comments: What have we missed? What will you take away? What will you do toward protecting public trust?
Panel: L.Z. Cooper, Sabin Vaccine Institute, New York
S.L. Katz, Duke University Medical Center, Durham, North Carolina
H. Larson, Harvard Center for Population & Development, Cambridge, Massachusetts: Wrap up by the organizers, including next steps and final group discussion.



L. Gordon, I. Sullivan

Microbial Forensics: Enduring Research Pathways

October 21–24

FUNDED BY **U.S. Department of Homeland Security and individual participants**

ARRANGED BY **S. Schutzer,** UMDNJ–New Jersey Medical School, Newark
B. Budowle, Federal Bureau of Investigation Laboratory, Quantico, Virginia

A major thrust of microbial forensics is the continuing quest for technologies and strategies that can improve the characterization of samples. At present, these fall into two major categories: nucleic-acid-based assays and chemical assays. The former enable association (or elimination) of a pathogen with specific sources using genetic information, and the latter provides information on the processes used to grow, stabilize, and/or disseminate the agent. In both areas, technologies are needed for rapid, high-sensitivity, and highly specific analysis of pathogens in limited and complex samples. Participants sought to identify the requirements of such technologies, to better guide the community in research and development and administrators in selecting what to support.

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1: Overview
Chairperson: S. Schutzer, UMDNJ–New Jersey Medical School, Newark

B. Budowle, Federal Bureau of Investigation, Quantico, Virginia: Microbial forensics and enduring technologies.
P.T. Pesenti, U.S. Department of Homeland Security, Washington, D.C.: DHS program for long-term needs to support field and goals.
J.P. Burans, U.S. Department of Homeland Security, Frederick, Maryland: National labs and NBFAC efforts in enduring technology.

SESSION 2: Proteomics
Chairperson: B.L. Marrone, Los Alamos National Laboratory, New Mexico

J.N. Adkins, Pacific Northwest National Laboratory, Richland, Washington: Mass spectrometry identification of forensic material.
K.L. Wahl, Pacific Northwest National Laboratory, Richland, Washington: Mass spectrometry tool for identifying nonprotein non-DNA signatures.

SESSION 3: DNA Typing Technologies
Chairperson: J.J. Dunn, Brookhaven National Laboratory, Upton, New York

W.R. McCombie, Cold Spring Harbor Laboratory: Comparison of high-throughput sequencing capabilities.
M. Srinivasan, 454 Life Science, Bradford, Connecticut: 454 sequencing.
M.R. Furtado, Applied Biosystems, Foster City, California: Solid and multiplex SNP technologies.

SESSION 4: Threat Assessment and Legal Issues
Chairperson: P.J. Jackson, Los Alamos National Laboratory, New Mexico

J. Smith, Federal Bureau of Investigation, Washington, D.C.: Credible threat assessments: Bases and practices.
R.P. Harmon, Alameda County District Attorney's Office, Oakland, California: Legal issues for technologies, routine, new, and one-of-a-kind, Daubert.

SESSION 5: Improving Template Quality for Downstream Assays
Chairperson: R.P. Harmon, Alameda County District Attorney's Office, Oakland, California

M. Eshoo, Ibis Bioscience, Carlsbad, California: Whole-genome amplification.
T.E. Evans, New England BioLabs, Inc., Ipswich, Massachusetts: DNA repair.
S. Schutzer, UMDNJ–New Jersey Medical School, Newark: Integration of proteomics and genomics.
S.P. Velsko, Lawrence Livermore National Laboratory, California: Analytical technologies for nonbio signatures.

SESSION 6: Interpretation
Chairperson: S.A. Morse, Centers for Disease Control and Prevention, Atlanta, Georgia

B. Budowle, Federal Bureau of Investigation, Quantico, Virginia: Needs for interpretation of results.
M.A. Feinberg and J. Bannan, Federal Bureau of Investigation, Quantico, Virginia: Technology and attribution needs for the FBI.

SESSION 7: Bioinformatics
Chairperson: J.P. Burans, U.S. Department of Homeland Security, Frederick, Maryland

O. White, Institute for Genome Sciences, University of Maryland School of Medicine, Baltimore: Bioinformatics tools for genomics for identifying regions, genes, function.
T. Slezak, Lawrence Livermore National Laboratory, California: Bioinformatics tools and the BKC for attribution.

SESSION 8: Distinguishing Natural Outbreaks from Intentional Use
Chairperson: J. Smith, Federal Bureau of Investigation, Quantico, Virginia

P.S. Keim, Northern Arizona University, Flagstaff: Attribution using microbial databases.
S.A. Morse, Centers for Disease Control & Prevention, Atlanta, Georgia: Tracing disease outbreaks.
C.L. Cooke, National Counterproliferation Center, Washington, D.C.: Scenarios on interpretation of DNA evidence.
W.W. Laegreid, University of Illinois, Urbana: Response and interpretation: Finding the tainted mad cow.
D.L. Rock, University of Illinois at Urbana-Champaign: Interpreting FMDV outbreak data.

SESSION 9: Utility of Microbial Population Genetics and Legal Aspects
Chairperson: P.T. Pesenti, U.S. Department of Homeland Security, Washington, D.C.

D.E. Dykhuizen, Stony Brook University, New York: Tipping in phylogenetic analysis.
J. Yadav, University of Cincinnati College of Medicine, Ohio: Genomic approach for microbial pathogen detection and issues of interpretation.
R.P. Harmon, Alameda County District Attorney's Office, Oakland, California: HIV as a microbial forensic model.
T. Cebula, U.S. Food and Drug Administration, Laruel, Maryland: Summary of SWG mock trial: Impression of a day in court.

SESSION 10: Identification and Installation of Promising Technologies
Chairperson: A. Martinez-Fonts, Department of Homeland Security, Washington, D.C.

A. Martinez-Fonts, Department of Homeland Security, Washington, D.C.: Discussion on strategy for identifying promising technologies to support.

Wrap Up
Chairpersons: B. Budowle, Federal Bureau of Investigation, Quantico, Virginia;
S. Schutzer, UMDNJ–New Jersey Medical School, Newark

Using Bar-code Data in Studies of Molecular and Evolutionary Dynamics

October 28–31

FUNDED BY **Alfred P. Sloan Foundation**

ARRANGED BY **D.E. Schindel,** Smithsonian Institution, Washington, D.C.
M. Blaxter, University of Edinburgh, United Kingdom
P. Gilna, University of California, San Diego
R.G. Harrison, Cornell University, Ithaca, New York
D.M. Rand, Brown University, Providence, Rhode Island
M. Veuille, Museum d'Histoire Naturelle, Paris, France

The Barcode of Life Initiative is generating an enormous volume of nucleotide sequence data from an homologous region of the animal mitochondrial genome. These data are being collected to build an information infrastructure for taxonomic research and for the rapid identification of species for diverse applied purposes such as border control of agricultural pests. This body of standardized gene sequence data may present allied fields of research with new and unanticipated opportunities as well. This workshop, the third in the series held at the Banbury Center, brought together population biologists, geneticists, bioinformaticians, and evolutionary biologists for the purpose of exploring the potential "off label" uses of DNA bar-code data.

Historical Background: J.H. Ausubel, The Rockefeller University, New York

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1: Overview of Bar-code Data
Chairperson: P. Gilna, University of California, San Diego

D.E. Schindel, Smithsonian Institution, Washington, D.C.: Linking bar-coded data to multiple users.
R. Hanner, University of Guelph, Ontario, Canada: Bar-code data standard and trace analysis.
S. Ratnasingham, University of Guelph, Ontario, Canada: The Barcode Life Data Systems: An informatics platform for the biodiversity informatics community.
M. Hajibabaei, University of Guelph, Ontario, Canada: Minimalist bar-code sequences.

SESSION 2: Species Boundaries, Speciation Processes, and Models
Chairperson: R.G. Harrison, Cornell University, Ithaca, New York

R.G. Harrison, Cornell University, Ithaca, New York: Multilocus approaches to defining species boundaries.
M. Blaxter, University of Edinburgh, United Kingdom: Defining and constructing MOTUs.
M. Stoeckle, The Rockefeller University, New York: Iterative taxonomy-DNA bar-coding cycle provides insights into species limits in birds.
J. Hey, Rutgers University, Piscataway, New Jersey: Population assignment likelihoods in a phylogenetic and demographic model.
A. Meyer, University of Konstanz, Germany: Sharing of mitochondrial DNA haplotypes in cichlid fishes.

SESSION 3: Phylogeography, Community Evolutions, and the Use of Bar Codes for Multispecies Studies
Chairperson: M. Veuille, Museum d'Histoire Naturelle, Paris, France

M. Veuille, Museum d'Histoire Naturelle, Paris, France: Can we extend intraspecific population genetics to community population genetics?
E. Bermingham, Smithsonian Tropical Research Institute, Balboa, Republic of Panama: Phylogeography of Caribbean birds.
G. Stone, University of Edinburgh, United Kingdom: Beyond the bar code: Setting our sites on reconstructing community evolution.
L. Knowles, University of Michigan, Ann Arbor: Statistical phylogeography.

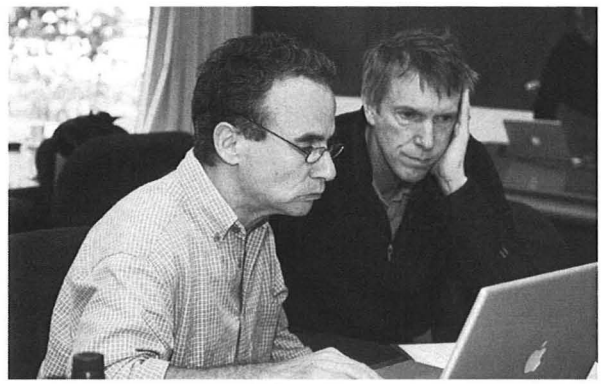
SESSION 4: Selection on and Variation in Mitochondrial DNA Sequences
Chairperson: D.M. Rand, Brown University, Providence, Rhode Island

D.M. Rand, Brown University, Providence, Rhode Island: Bar codes and selection of mtDNA.
T. Barraclough, Imperial College London, Ascot, United Kingdom: Patterns of divergent selection from combined bar-code and phenotypic data.
R. Nielsen, University of Copenhagen, Denmark: Statistical approaches for DNA bar coding.
G. Wallis, University of Otago, Dunedin, New Zealand: Beyond the bar: Roles for a million COI sequences in studies of molecular adaptation.

SESSION 5: Visualization of Large Sequence Data Sets
Chairperson: D.E. Schindel, Smithsonian Institution, Washington, D.C.

M. Hajibabaei, University of Guelph, Ontario, Canada: Visualizing bar-code data.

SESSION 6: Final Discussion of Conclusions, Recommendation, and Action Items
Chairperson: D.E. Schindel, Smithsonian Institution, Washington, D.C.



E. Bermingham, M. Stoeckle

Interdisciplinary Memory Symposium in Neurosciences and the Humanities

October 31–November 2

FUNDED BY **The Selz Foundation, Inc.; The Satenik and Adom Ourian Educational Foundation; Haig R. Nalbantian; Marsh & McLennan Companies—MMC Matching Gifts to Education Program; The Daniel and Joanna S. Rose Fund, Inc.; Mr. and Mrs. Howard Phipps, Jr.**

ARRANGED BY **S. Nalbantian,** Long Island University, Brooklyn, New York
P. Matthews, GlaxoSmithKline, Oxford University, United Kingdom

The subject of human memory offers intriguing and exciting possibilities for interdisciplinary exchanges between the humanities and neuroscience. Just as the neuroscientist explores the physical workings of the brain with the tools of electrophysiology and molecular biology, so writers and artists explore and record the mental experiences of human beings. This interdisciplinary symposium discussed the ways in which the insights of those in the humanities can inform the models of human memory based on neuroscience.

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

Introduction to the Symposium: S. Nalbantian, Long Island University, Brooklyn, New York; **Paul Matthews,** GlaxoSmithKline, Oxford University, United Kingdom

Keynote Address: Representations of Memory in Twentieth Century Art: Painting Modernism's Memories
L. Dalrymple Henderson, University of Texas, Austin

SESSION 1

J. Dubnau, Cold Spring Harbor Laboratory: The genetic basis of memory: Memories of a fly?

J.-P. Changeux, Institut Pasteur and Collège de France, Paris, France: Brain plasticity and the epigenetic variability of memory: Consequences in artistic contemplation and creation.

J.L. McClelland, Stanford University, California: Connectionist modeling of parallel processing and complementary memory systems.

SESSION 2

B. Favorini, University of Pittsburgh, Pennsylvania: The theatre of memory: The scene *is* memory!
S. Nalbantian, Long Island University, Brooklyn, New York: Literature as a laboratory for memory research: Literary case studies as evidentiary material.
J. Burt Foster, George Mason University, Fairfax, Virginia: Memory in the literary memoir: Nabokov, Yeats, Mary McCarthy.

SESSION 3: Interdisciplinary Panel for the Creation of a "Third Discourse" for Memory Research; Discussion
Chairpersons: S. Nalbantian, Long Island University, Brooklyn, New York; **P. Matthews,** Oxford University, United Kingdom

Topics for Discussion:

1. Identification of the most likely areas where humanists can illuminate the memory process in an exploratory or confirmatory fashion.
2. Pertinence of neuroscientific models to humanistic data.
3. Consideration of the way literature and the arts can be used as data with emphasis on artistic and linguistic factors. Possibilities for neuroimaging testing studies of human subjects.
4. Cross-disciplinary vocabulary.
5. Inroads to creativity.
6. Publication of a volume stemming from this symposium.

SESSION 4

F. Vidal, Max-Planck Institute for the History of Science, Berlin, Germany: The Cerebral subject: Memory, self and the brain in film.
Respondent: J.D. Talasek, National Academy of Sciences, Washington, D.C.
P. Matthews, GlaxoSmithKline, Oxford University, United Kingdom: Neuroimaging, memory, and brain disorders.
R. Stickgold, Harvard Medical School, Boston, Massachusetts: Dream analysis memory: Reactivation and reconsolidation.
Respondent: V. Doyère, CNRS, Université Paris Sud, Orsay, France

SESSION 5

D. Hertz, Indiana University, Bloomington: Poetry and music: What makes us remember?
M. Tramo, M.D., Harvard Medical School, Boston, Massachusetts: The neurobiology of memory for music.
P. Michon, Collège International de Philosophie, Paris, France: Epistemological models in social and neuroscientific memory studies: A philosophical inquiry.
Respondent: R. Phipps, Center for Process Studies, Claremont Graduate University, California: Whitehead's philosophy and memory.

J. Pierre-Changeux

From Statistics to Genes: Figuring Out the Molecular Basis of Complex Traits

November 4–7

FUNDED BY **Cold Spring Harbor Laboratory Corporate Sponsor Program**

ARRANGED BY **A. Chakravarti,** The Johns Hopkins University School of Medicine, Baltimore, Maryland
L. Kruglyak, Princeton University, New Jersey

Studies of the genetic basis of complex traits are being transformed by a convergence of two related developments: genome-wide association studies that are providing a growing list of susceptibility loci for common diseases, and, studies of model organisms that are providing increasingly detailed descriptions at the molecular level. Both of these developments are being driven by new technologies, access to genomic sequence, and functional information. This meeting brought together leaders in three areas—human genetics, model systems, and technology—to chart the future course of understanding complex disease.

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory
Overview: A. Chakravarti, The Johns Hopkins University School of Medicine, Baltimore, Maryland; **L. Kruglyak,** Princeton University, New Jersey

SESSION 1: Complex Traits in Model Systems I
Chairperson: L. Kruglyak, Princeton University, New Jersey

L. Steinmetz, EMBL Heidelberg, Germany: Fine mapping and functional characterization of complex traits in yeast.
G. Yvert, CNRS, Lyon, France: Cell-to-cell stochastic variation in gene expression as a complex trait in yeast.
J. McCusker, Duke University Medical Center, Durham, North Carolina: Complex traits in a simple eukaryote.
M. Nordborg, University of Southern California, Los Angeles: Whole-genome association in *Arabidopsis*.

SESSION 2: Complex Traits in Model Systems II
Chairperson: H.G. Parker, CGB/NHGRI/NIH, Bethesda, Maryland

M. Rockman, Princeton University, New Jersey: Complex trait genetics in *C. elegans*.
D. Stern, Princeton University, New Jersey: Morphological evolution through multiple *cis*-regulatory mutations at a single gene.
G.C. Gibson, North Carolina State University, Raleigh: *Drosophila* as a model for complex traits and diseases.
P. Wittkopp, University of Michigan, Ann Arbor: Genomic sources of regulatory variation.

G. Churchill, G. Yvert, M. Nordborg, A. Chakravarti

SESSION 3: Complex Trait Model Systems III
Chairperson: P. Wittkopp, University of Michigan, Ann Arbor

M. Shapiro, University of Utah, Salt Lake City: Genetic basis of parallel evolution in stickleback fish.
H.G. Parker, CGB/NHGRI/NIH, Bethesda, Maryland: The long and short of canine fixed trait mapping.
B.A. Hamilton, University of California, San Diego; School of Medicine, La Jolla, California: Architectures of modifier gene networks: Thoughts from two examples.
G.A. Churchill, The Jackson Laboratory, Bar Harbor, Maine

SESSION 4: Human Complex Trait Dissection and Evolution
Chairperson: L. Pennacchio, Lawrence Berkeley National Laboratory, California

D.B. Goldstein, Duke University, Durham, North Carolina: Genome-wide association studies in host response to HIV.
A.C. Kong, DeCode Genetics, Reykjavik, Iceland: Recent gene discoveries and new challenges.
M. McCarthy, The Churchill Hospital, Oxford, United Kingdom: Thinking big: Genes involved in type-2 diabetes, adiposity, and height.
S. Deutsch, University of Geneva Medical School, Switzerland: Phenotype mapping in cell lines.
S. Tishkoff, University of Maryland, College Park: Genetic and phenotypic variation in Africa.
G. Wray, Duke University, Durham, North Carolina: Genome-wide imprints of selection and the evolution of complex traits in humans.

SESSION 5: New Technologies
Chairperson: A. Chakravarti, The Johns Hopkins University School of Medicine, Baltimore, Maryland

S. Kruglyak, Illumina, Inc., San Diego, California: Tools for whole-genome association studies.
J. Sebat, Cold Spring Harbor Laboratory: Analysis of genome copy-number variation in psychiatric disease.
L. Pennacchio, Lawrence Berkeley National Laboratory, California: Deep resequencing in the Dallas Heart Study.
T.S. Mikkelsen, Broad Institute, Cambridge, Massachusetts: Mammalian epigenomics.

SESSION 6: Final Discussion and Future Directions

Discussion
A. Chakravarti, The Johns Hopkins University School of Medicine, Baltimore, Maryland, and L. Kruglyak, Princeton University, New Jersey.

Second Environment Ontology Workshop

November 14–16

FUNDED BY **U.S. National Science Foundation's Research Coordination Network grant (DBI 0234147) to the Gramene Database**

ARRANGED BY **P. Jaiswal,** Cornell University, Ithaca, New York
N. Morrison, University of Manchester, United Kingdom
D. Field, Oxford University, United Kingdom
S. Lewis, Lawrence Berkeley National Laboratory, California
B. Smith, University at Buffalo, New York
M. Ashburner, University of Cambridge, United Kingdom

An ontology is a controlled, structured vocabulary developed to represent entities in a given domain and the relations between them. The use of a standardized, consistent nomenclature means that information can be searched by computers, enabling them to share and integrate information without human intervention. There is, for example, a Gene Ontology that has been developed so that different genome databases can "talk" to each other. Participants in this workshop are attempting do derive an ontology to describe the environments in which organisms live. Such an ontology would facilitate the retrieval of any biological record anchored to the environment ontology, whether in sequence or genome databases, tissue banks, or museum collections. Developing (and implementing) such ontologies is a far from trivial endeavor and participants learned how Gene Ontology developed as well as planning future steps.

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1
Chairperson: P. Jaiswal, Cornell University, Ithaca, New York

P. Jaiswal, Cornell University, Ithaca, New York: Welcome and introductory remarks.
B. Smith, University at Buffalo, New York: EnvO introduction.
M. Ashburner, University of Cambridge, United Kingdom: Progress on EnvO+GAZ ontology development.
N. Morrison, University of Manchester, United Kingdom: Ontology maintenance and Web site + database logistics.
C. Mungall, Lawrence Berkeley National Laboratory, California: Phenote annotation tool.

Case Studies with EnvO annotations:
P. Dawyndt/Bart van Brabant
L. Schriml/Aaron Gussman
D. Field
N. Sarkar

SESSION 2
Chairperson: N. Morrison, University of Manchester, United Kingdom

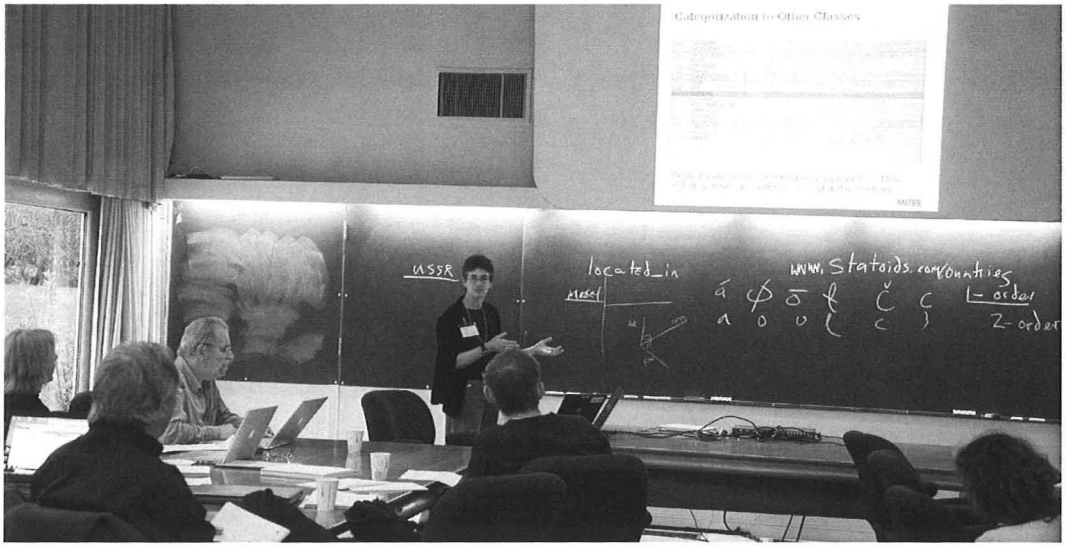
New Case Studies for Potential EnvO Annotations
J. White
S. Greene
L. Hirschman
V. Markowitz
S. Ratnasingham
M. Ashburner, University of Cambridge, United Kingdom: Hands-on work on ontology.

SESSION 3
Chairperson: B. Smith, University of Buffalo, New York

S. Lewis, University of California, Berkeley: Summary from Day-1.
M. Ashburner, University of Cambridge, United Kingdom: Hands-on work on ontology.

SESSION 4
Chairperson: S. Lewis, University of California, Berkeley

M. Ashburner, University of Cambridge, United Kingdom: Hands-on work on ontology.
B. Smith, University of Buffalo, New York: Discussion of funding possibilities.
N. Morrison, University of Manchester, United Kingdom: Identify potential projects, databases, and collaborators.
S. Lewis, University of California, Berkeley: Summarizing the meeting, action items, and wrap up.



L. Hirschman

Podosomes and Invadopodia: Signatures of the Wandering Cell?

November 26–29

FUNDED BY **Cold Spring Harbor Laboratory Corporate Sponsor Program**

ARRANGED BY **G. Jones,** King's College, University of London, United Kingdom
J.S. Condeelis, Albert Einstein College of Medicine, Bronx, New York
A. Huttenlocher, University of Wisconsin, Madison

Examples of cell migration include leukocytes involved in immune surveillance and innate immunity, and other cell types during morphogenetic movements of embryonic development, in wound healing, and in the invasion and dispersal of metastatic tumor cells. To a large extent, these cell movements depend on the degradation of extracellular matrix components by focal secretion of matrix metalloproteinases. Localized degradation of the matrix is found at adhesive (podosomes) and protrusive (invadopodia) locations in a variety of cell types including leukocytes and invasive carcinoma cells. Research on the role of these transient membrane-associated organelles in cell motility suggests that they are involved in directed cell migration and chemotaxis in vitro and in vivo. Participants reviewed recent findings and developments and discussed the importance of these structures in cell migration, inflammation, morphogenesis, and metastasis. There was vigorous discussion of the relationship between podosomes and invadopodia.

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1: Principles of Cell Motility
Chairperson: G. Jones, King's College London, United Kingdom

General Discussion on Terminology: Do podosomes = invadopodia = invadosomes?

Discussion Leaders:
G. Jones, King's College, University of London, United Kingdom
J.S. Condeelis, Albert Einstein College of Medicine, Bronx, New York

A. Huttenlocher, University of Wisconsin, Madison: Principles of cell motility: Neutrophil chemotaxis in vivo.

P. Friedl, University of Würzburg, Germany: Invadopods in three-dimensional invasion?

J.S. Condeelis, Albert Einstein College of Medicine, Bronx, New York: Invadopod regulation and function in breast tumor metastasis.

F. Gertler, Massachusetts Institute of Technology, Cambridge:

An invasion-specific Mena isoform promotes cancer cell invasion and potentiates EGF responses.

S. Muthuswamy, Cold Spring Harbor Laboratory: Changes in cell polarity pathways regulate cell invasion.

P. DeCamilli, Yale University, New Haven, Connecticut: Role of dynamin in cell physiology.

SESSION 2: Podosome Regulation
Chairperson: A. Huttenlocher, University of Wisconsin, Madison

G. Jones, King's College London, United Kingdom: Podosomes in myeloid leukocytes.

S. Linder, University of Munich, Germany: Regulation of podosome dynamics in human macrophages.

R. Buccione, Consorzio Mario Negri Sud, Italy: Regulation of invadopodia biogenesis.

D. Cox, Albert Einstein College of Medicine, New York: WASP phosphorylation and podosome regulation.

R. Baron, Yale University, New Haven, Connecticut: Src regulation of podosomes using the osteoclast as a model system.

I.M. Anton, Centro Nacional de Biotecnología/CSIC, Spain: Contribution of WIP to podosome formation in dendritic cells and mature osteoclasts.

S. Tsuboi, Burnham Institute for Medical Research, La Jolla, California: Role of the WASP-WIP complex in podosome formation in macrophages.

SESSION 3: Actin-based Motility
Chairperson: J.S. Condeelis, Albert Einstein College of Medicine, Bronx, New York

L.M. Machesky, Cancer Research UK, United Kingdom: Role of Arp2/3 complex and IRSp53-MIM proteins in actin membrane interactions.

J. Taunton, University of California, San Francisco: Actin-dependent feedback to N-WASP: A signal amplification mechanism for invadopodia expansion.

J.A. Cooper, Washington University, St. Louis, Missouri: Role of cortactin and HS1 in actin assembly in osteoclasts and lymphocytes.

J.E. Bear, University of North Carolina, Chapel Hill: Role of coronins in cancer cell invasion and motility.

J. Theriot, Stanford University, California: Large-scale coordination of actin polymerization, contraction, and adhesion in motile keratocytes.

SESSION 4: Cell Signaling in Invasive Motility
Chairperson: F. Gertler, Massachusetts Institute of Technology, Cambridge

S.A. Courtneidge, Burnham Institute for Medical Research, La Jolla, California: Role of the adaptor protein Tks5 in cancer cell invasion and embryonic development.

A.S. Mak, Queen's University, Kingston, Canada: Calpain-4 in podosome formation.

M.A. Chellaiah, University of Maryland, Baltimore: Podosomes and invadopodia: Role in extracellular matrix degradation and migration in osteoclasts and prostate cancer cells.

E. Genot, Université Bordeaux, Pessac, France: Endothelial podosomes: A new tool for remodeling the vascular bed.

H. Gil-Henn, Yale University School of Medicine, New Haven, Connecticut: Pyk2 in podosome organization and bone remodeling.

S.C. Mueller, Georgetown University Medical Center, Washington, D.C.: Invadopodia: Src and the cell-protease interface.

S.A. Weed, West Virginia University, Morgantown: Phosphoregulation of cortactin function.

SESSION 5: Invadopodia and Cancer Invasion
Chairperson: J.S. Condeelis, Albert Einstein College of Medicine, Bronx, New York

C. Streuli, University of Manchester, United Kingdom: Integrins in breast development and cancer.

E. Sahai, Cancer Research UK, London, United Kingdom: Mechanisms of cell invasion in three-dimensional environments and in living tumors.

A. Weaver, Vanderbilt University Medical Center, Nashville, Tennessee: Microenvironmental regulation of invadopodia.

J.F. Marshall, University of London, United Kingdom: Targeting integrin α-v β-6 for the imaging and therapy of carcinoma.

N. Carragher, AstraZeneca, Loughborough, United Kingdom: Modeling distinct modes of tumor cell invasion for drug discovery.

General Discussion and Terminology: Do podosomes = invadopodia in composition and function?

Discussion Leaders:
A. Huttenlocher, University of Wisconsin, Madison
G. Jones, King's College London, United Kingdom
J.S. Condeelis, Albert Einstein College of Medicine, Bronx, New York

S. Courtneidge, G. Jones

S. Mueller, R. Buccione

Cell Transplantation as a Therapy for Parkinson's Disease

December 9–12

FUNDED BY **Private support**

ARRANGED BY **A. Bjorklund,** University of Lund, Sweden
H. Cline, Cold Spring Harbor Laboratory
O. Lindvall, Lund University Hospital, Sweden

Previous clinical trials have shown that transplants of fetal dopamine neurons can survive and function in the brains of patients with Parkinson's disease. Therapeutically valuable and long-lasting clinical improvement has been observed in subgroups of patients, but troublesome graft-induced dyskinesias have been noted in a significant number of cases. Further development of a dopamine cell replacement therapy for Parkinson's disease will critically depend on the development of alternative sources of cells for grafting. Participants critically examined the issues that need to be resolved in order to bring the cell replacement approach into a clinically successful and competitive therapy for patients with Parkinson's disease.

Introductory Remarks: J.A. Witkowski, Banbury Center, Cold Spring Harbor Laboratory

SESSION 1: Clinical Trials: A Critical Assessment of the Results Obtained in Patients with Fetal DA Neuron Transplants
Chairperson: D. Eidelberg, Feinstein Institute for Medical Research, Manhasset, New York

T.B. Freeman, University of South Florida, Tampa: The Tampa–Mount Sinai trial.
C.R. Freed, University of Colorado School of Medicine, Denver: The Denver–Columbia trial.
I. Mendez, Dalhousie University, New York: The Halifax program.
O. Lindvall, Lund University Hospital, Sweden: The Lund–London–Marburg program.
T.B. Freeman, University of South Florida, Tampa: Neurosurgical aspects.

SESSION 2: What Is Required to Make a Cell Transplantation Therapy Clinically Competitive?
Chairperson: R.A. Barker, University of Cambridge, United Kingdom

G. Nikkhah, Abt. Stereotaktische Neurochirugie, Freiburg, Germany: Pattern and extent of recovery in grafted patients.
S. Dunnett, Cardiff University, South Wales, United Kingdom: Behavioral criteria in rodent models.
D.E. Redmond, Yale University School of Medicine, New Haven, Connecticut: Behavioral criteria in primate models.
A. Bjorklund, University of Lund, Sweden: Necessary properties of grafted cells.

SESSION 3: Generation of Dopamine Neurons from ES Cells
Chairperson: S. Dunnett, Cardiff University, South Wales, United Kingdom

B. Reubinoff, Hadassah University Medical Organization, Jerusalem, Israel: Human embryonic stem cells for Parkinson's disease.
J. Ericson, Karolinska Institute, Stockholm, Sweden: Intrinsic determinants in stem cell engineering.
K.-S. Kim, McLean Hospital, Harvard Medical School, Belmont, Massachusetts: Potential cell sources and animal models for Parkinson's disease.
E. Arenas, Karolinska Institute, Stockholm, Sweden: Reduced proliferation and enhanced dopaminergic differentiation by Wnt5a.

SESSION 4: In Vivo Performance of Stem-cell-derived Dopamine Neurons: Survival, Function, Tumorigenesis
Chairperson: A. Bjorklund, University of Lund, Sweden

L. Studer, Memorial Sloan-Kettering Cancer Center, New York: Directed differentiation and purification of human ES-cell-derived dopamine neurons.
S.-C. Zhang, University of Wisconsin, Madison: Survival and function of DA neurons derived from hES cells.
S.A. Goldman, University of Rochester Medical Center, New York: DA neurons derived from human ES cells in coculture.
J. Takahashi, Kyoto University, Japan: In vivo functional studies in primates.

SESSION 5: Critical Issues for the Development of a Stem Cell Therapy for Parkinson's Disease
Chairperson: O. Lindvall, Lund University Hospital, Sweden

Theme 1: Transplant-induced Dyskinesia

Speaker: K. Steece-Collier, University of Cincinnati, Ohio
Discussant: D. Kirik, University of Lund, Sweden
Open Discussion

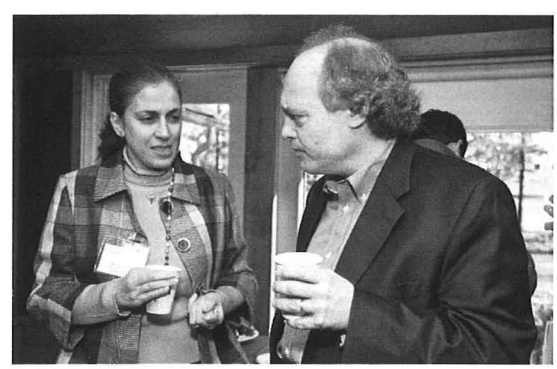
Theme 2: Strategies to Avoid Tumor Formation

Speaker: V. Tabar, Memorial Sloan-Kettering Institute for Cancer, New York
Discussant: J. Takahashi, Kyoto University, Japan
Open Discussion

Theme 3: Patient Selection and Efficacy

Speaker: R.A. Barker, University of Cambridge, United Kingdom
Discussants: D. Eidelberg, Feinstein Institute for Medical Research, Manhasset, New York; **P. Piccini,** Imperial College London, United Kingdom
Open Discussion

P. Piccini



V. Tabar, S. Goldman

BANBURY CENTER GRANTS

Grantor	Program	Duration of Grant	2007 Funding
FEDERAL SUPPORT			
Centers for Disease Control and Prevention (CDC)	The Laboratory Diagnosis of Lyme Disease II	2007	$ 8,900*
NIH–National Institute of Allergy & Infectious Diseases	The Laboratory Diagnosis of Lyme Disease II	2007	17,100*
NIH–National Institute of Mental Health (through a grant to University of Illinois)	Fragile-X Syndrome and Mechanisms of Synaptic Translation	2007	44,564*
The National Science Foundation	Design Principles in Biological Systems–2	2007	47,830*
The National Science Foundation	Second Environment Ontology Workshop	2007	30,000
U.S. Department of Homeland Security	Microbial Forensics: Enduring Research Pathways	2007	9,800*
NONFEDERAL SUPPORT			
Meeting Support			
AstraZeneca Pharmaceuticals	Neurobiology of Depression: From Molecules to Mood	2007	5,000*
Boehringer Ingelheim Fonds Foundation for Basic Research in Medicine	Science—Get It Across!	2007	38,461*
The Champalimaud Foundation	Champalimaud Foundation: Neuroscience and Cancer Research	2007	108,035*
Greater NY Chapter of the ALS Association	Drug Discovery, Biomarkers, and Clinical Trials for ALS	2007	44,787*
The W.M. Keck Foundation	The Brain Architecture Project Annual Meeting	2007	23,964*
Eli Lilly & Company	Neurobiology of Depression: From Molecules to Mood	2007	2,000*
Marsh & McLennan Companies–MMC Matching Gifts to Education Program	Interdisciplinary Memory Symposium in Neurosciences and the Humanities	2007	5,000*
Memory Pharmaceutical Corp.	Neurobiology of Depression	2007	5,000*
Haig R. Nalbantian	Interdisciplinary Memory Symposium in Neurosciences and the Humanities	2007	5,000*
Open Biosystems	Interactome Mapping Project for Human and Model Organisms	2007	3,000*
OSI Pharmaceuticals, Inc.	Epithelial Mesenchymal Transition	2007	19,748*
Mr. and Mrs. Howard Phipps, Jr.	Interdisciplinary Memory Symposium in Neurosciences and the Humanities	2007	10,000*
Private funding	Cell Transplantation as a Therapy for Parkinson's Disease	2007	45,944*
Private funding	Retreat From Reason	2007	17,915*
Roche Pharmaceuticals	Neurobiology of Depression: From Molecules to Mood	2007	10,000*
The Daniel and Joanna S. Rose Fund, Inc.	Interdisciplinary Memory Symposium in Neurosciences and the Humanities	2007	10,000*
Albert B. Sabin Vaccine Institute (with support of the Robert Wood Johnson Foundation)	Protecting Public Trust in Immunization	2007	26,093*
The Satenik and Adom Ourian Educational Foundation	Interdisciplinary Memory Symposium in Neurosciences and the Humanities	2007	3,000*
The Selz Foundation, Inc.	Interdisciplinary Memory Symposium in Neurosciences and the Humanities	2007	1,000*
Sepracor	Neurobiology of Depression: From Molecules to Mood	2007	5,000*
Alfred P. Sloan Foundation	Using Bar-code Data in Studies of Molecular and Evolutionary Dynamics	2007	45,000*
The Swartz Foundation	New Frontiers in Studies of Nonconscious Processing	2007	35,956*
University of Georgia (with support of Arborgen, Canadian Forest Service, European Union Evoltree, Genome British Columbia, Genome Canada, Oregon State University, Port Blakeley Tree Farms, Starker Forests, University of California at Davis, University of Maine, and USDA Forest Service)	International Workshop on Conifer Genomics	2007	27,139*
Wyeth Pharmaceuticals	Neurobiology of Depression: From Molecules to Mood	2007	5,000*

*New grants awarded in 2007

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