ease of use. The levels of foreground noise, background noise, and spot distortion can be set, and algorithms can be evaluated under varying conditions.

Applications:

- Microarray imaging
- Evaluation of gene expression

Advantages:

- Efficient and accurate microarray signal analysis
- Improved detection of weak targets and improved local background estimation for microarray spots

Development Status: Late stage.

Inventors: Yidong Chen (NHGRI) *et al.*

Publication: Y Balagurunathan, ER Dougherty, Y Chen, ML Bittner, JM Trent. Simulation of cDNA microarrays via a parameterized random signal model. J Biomed Opt. 2002 Jul;7(3):507–523.

Patent Status: U.S. Patent No. 7,363,169 issued 22 Apr 2008 (HHS Reference No. E–089–2003/0–US–03).

Licensing Status: Available for exclusive or non-exclusive licensing.

Licensing Contact: Jeffrey A. James, PhD; 301–435–5474; *jeffreyja@mail.nih.gov*.

System for Synergistic Combination of Multiple Automatic Induction Methods and Automatic Re-Representation of Data

Description of Invention: The present application describes a unique prototype of an advanced framework which relates to the field of multidimensional data mining, machine learning, and analysis that has been named COEV (for COEVolutional). COEV synergistically combines different methods of statistical analysis, neural networks, decision trees and genetic algorithms for the resolution of data queries. COEV automatically determines the optimal methods and data representations to apply at each step of inquiry and, as a result, can provide outcomes that are significantly more accurate than can be achieved by use of any one methodology alone. The invention uses an evolutionary learning technology to improve predictive outcomes with continued use. COEV is designed to advance the accuracy, flexibility, speed and ease of use of advanced data analysis technologies.

Characteristics of problems that are appropriate for the application of the COEV method are: (1) Appropriate for machine learning, in that there is a well-defined set of input variables and a clear prediction target; (2) difficult for traditional methods, and where a modest improvement in accuracy over existing machine learning methods (*e.g.*, neural networks) would be significant; (3) there is a large amount of training data, ideally thousands of cases.

Possible application areas of interest include the analysis of high-throughput screening data for pharmaceutical discovery, detecting patterns of fraud in insurance claims, or automating screening of medical images.

This invention requires further R&D and testing to make it a practical system for widespread use.

Applications:

- Machine learning
- High throughput screening analysis for pharmaceutical, biotechnology, and other industries

Advantages:

- More accurate interpretation and analysis of complex data networks
- Improved predictive outcomes with continued use (evolutionary learning)

Development Status: Early stage.

Inventors: Lawrence Hunter (NLM).

Patent Status: U.S. Patent No. 6,449,603 issued 10 Sep 2002 (HHS Reference No. E–118–1996/0–US–03).

Licensing Status: Available for exclusive or non-exclusive licensing.

Licensing Contact: Jeffrey A. James, PhD; 301–435–5474; *jeffreyja@mail.nih.gov*.

Computational Analysis of Nucleic Acid Information Defines Binding Sites

Description of Invention: Many approaches to determine whether a nucleotide change is a benign polymorphism or is associated with a genetic disease rely on sequence comparisons of a substantial number of individuals. This invention embodies a computational method that is able to predict whether a nucleotide change will have a deleterious effect. The claims of this invention relate to a computer program which has the novel feature in that it is designed to calculate the relative importance of a given nucleotide change. This program is unique in that it is capable of predicting the effect that a given nucleotide change would have on a particular sequence such as a known binding site. The method has been successfully applied to predicting the effects of changes at human splice junctions.

Further information is available at *http://www.ccrnp.ncifcrf.gov/~toms/walker/index.html*.

Applications:

- Predictive outcomes for genetic mutations
- Biomedical research

Development Status: Late stage.

Inventors: Thomas D. Schneider (NCI) *et al.*

Patent Status: U.S. Patent 5,867,402 issued 02 Feb 1999 (HHS Reference No. E–080–1995/0–US–01).

Licensing Status: Available for non-exclusive licensing.

Licensing Contact: Jeffrey A. James, PhD; 301–435–5474; *jeffreyja@mail.nih.gov*.

Dated: January 30, 2009.

Richard U. Rodriguez,

Director, Division of Technology Development and Transfer, Office of Technology Transfer, National Institutes of Health.

[FR Doc. E9–2820 Filed 2–10–09; 8:45 am]

BILLING CODE 4140–01–P

DEPARTMENT OF HEALTH AND HUMAN SERVICES

National Institutes of Health

Government-Owned Inventions; Availability for Licensing

AGENCY: National Institutes of Health, Public Health Service, HHS.

ACTION: Notice.

SUMMARY: The inventions listed below are owned by an agency of the U.S. Government and are available for licensing in the U.S. in accordance with 35 U.S.C. 207 to achieve expeditious commercialization of results of federally-funded research and development. Foreign patent applications are filed on selected inventions to extend market coverage for companies and may also be available for licensing.

ADDRESSES: Licensing information and copies of any U.S. patent applications listed below may be obtained by writing to the indicated licensing contact at the Office of Technology Transfer, National Institutes of Health, 6011 Executive Boulevard, Suite 325, Rockville, Maryland 20852–3804; telephone: 301/496–7057; fax: 301/402–0220. A signed Confidential Disclosure Agreement will be required to receive copies of the patent applications.

Constructs for Measuring Activated Arf5 in Cells

Description of Technology: Scientists at the National Institutes of Health have developed a series of fusion protein constructs that can quantify the levels of activated Arf5 in cells. Arf5 is a member of the Arf family of GTP binding proteins and is an important regulator of intracellular trafficking and actin-mediated cell motility. Arf family members have been implicated to play a role in the spread of cancer (metastasis) and in the movement of cancer cells into healthy tissues (invasion). The constructs are DNA sequences of various portions of the carboxyl-terminal end of the Rab11-

family interacting protein 3 (FIP3) expressed in the pGEX2T vector.

Application: Research tool to detect and quantify activated Arf5 in various laboratory procedures to analyze intracellular trafficking and cellular motility.

Advantages: To the best of our knowledge, this technology represents the first reported assay for the detection of activated Arf5.

Inventors: Paul A. Randazzo and Vi L. Ha (NCI).

Publications:

1. H Inoue *et al.* Arf GTPase-activating protein ASAP1 interacts with Rab11 effector FIP3 and regulates pericentrosomal localization of transferrin receptor-positive recycling endosome. Mol Biol Cell. 2008 Oct;19(10):4224–4237.

2. HY Yoon *et al.* In vitro assays of Arf1 interaction with GGA proteins. Methods Enzymol. 2005;404:316–332.

Patent Status: HHS Reference No. E–064–2009/0—Research Tool. Patent protection is not being pursued for this technology.

Related Technologies: Antibodies and Antisera Recognizing Members of the ArfGap Family of Proteins:

- HHS Reference No. E–220–2008/0—Research Tool.
- HHS Reference No. E–220–2008/1—Research Tool.
- HHS Reference No. E–220–2008/2—Research Tool.
- HHS Reference No. E–221–2008/0—Research Tool.
- HHS Reference No. E–221–2008/1—Research Tool.
- HHS Reference No. E–221–2008/2—Research Tool.
- HHS Reference No. E–222–2008/0—Research Tool.
- HHS Reference No. E–242–2008/0—Research Tool.
- HHS Reference No. E–243–2008/0—Research Tool.
- HHS Reference No. E–244–2008/0—Research Tool.
- HHS Reference No. E–245–2008/0—Research Tool.
- HHS Reference No. E–245–2008/1—Research Tool.
- HHS Reference No. E–252–2008/0—Research Tool.

Licensing Status: Available for licensing under a Biological Materials License Agreement.

Licensing Contact: Samuel E. Bish, PhD; 301–435–5282; *bishse@mail.nih.gov.*

Mouse Monoclonal Antibodies to MAD1, a Human Spindle Assembly Checkpoint Protein for Maintaining Chromosomal Segregation

Description of Technology: Scientists at the National Institutes of Health have developed mouse monoclonal antibodies against the human spindle assembly checkpoint protein, MAD1. The spindle assembly checkpoint in mitotic cell division regulates the fidelity of chromosome segregation during cell division. MAD1 is an important component of this checkpoint control, which if compromised, can lead to the initiation of cancer cell growth. These monoclonal antibodies are the first available antibodies against MAD1 and can be used in laboratory research and diagnostics.

Applications:

- Research tool in various laboratory procedures to identify and detect MAD1.
- Diagnostic tool for aneuploidy, the condition of having an abnormal number of chromosomes, which results in birth and developmental defects, such as Down syndrome.

Inventor: Kuan-Teh Jeang (NIAID).

Publication: K Haller *et al.* The N-terminus of rodent and human MAD1 confers species-specific stringency to spindle assembly checkpoint. Oncogene 2006 Apr 6;25(15):2137–2147.

Patent Status: HHS Reference No. E–119–2003/0—Research Tool. Patent protection is not being pursued for this technology.

Licensing Status: Available for licensing under a Biological Materials License Agreement.

Licensing Contact: Samuel E. Bish, PhD; 301–435–5282; *bishse@mail.nih.gov.*

Collaborative Research Opportunity: The NIAID Office of Technology Development is seeking statements of capability or interest from parties interested in collaborative research to further develop, evaluate, or commercialize reagents for studying cell cycle checkpoint factors. Please contact Agnes Rooke at *rookeab@niaid.nih.gov* or by phone at 301–594–1697 for more information.

Dated: January 30, 2009.

Richard U. Rodriguez,

Director, Division of Technology Development and Transfer, Office of Technology Transfer, National Institutes of Health.

[FR Doc. E9–2821 Filed 2–10–09; 8:45 am]

BILLING CODE 4140–01–P

DEPARTMENT OF HEALTH AND HUMAN SERVICES

National Institutes of Health

Government-Owned Inventions; Availability for Licensing

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Prognostic Test for Breast Cancer Based on a 12 Gene Expression Signature

Description of Technology: The clinical course and survival times of patients with breast cancer varies greatly, consequently it is difficult to establish a prognosis for the disease. To improve patient prognosis, much effort has been made to identify biological markers that would allow precise staging of the cancer. When cells cannot repair minor damage to their DNA it leads to genetic instability which can produce gross abnormalities in chromosomes and the onset of a cancer. It is known that the magnitude of the abnormalities is strongly correlated with a negative prognosis for cancer. Thus, genetic instability can serve as a useful biomarker for establishing a prognosis for breast cancer patients. Presently, genetic instability is not directly accounted for in established prognostic tests.

Investigators at the National Cancer Institute (NCI) have developed a compact gene signature that detects genome instability in breast cancer cells. By comparing changes in expression levels of only 12 genes in malignant tissue to levels in normal breast tissue it is possible to detect the genetic abnormalities that are indicative of a poor prognosis. This method has potential to improve markedly the forecasting of clinical outcomes for breast cancer and help improve treatment of this disease.

Applications:

- Precise staging of women with breast cancer prior to commencing treatment.