iIS Update

資訊科學簡訊

Newsletter of the Institute of Information Science, Academia Sinica, Taiwan

Spring/Summer 2012

Message from the Director

The Institute of Information Science (IIS) was established in 1982. We currently have 38 full-time research faculty, 30 post-doctoral research fellows, and slightly more than 300 research associates and specialists. Our research is conducted in eight specialized laboratories: Bioinformatics, Computer Systems, Information Processing and Discovery (iPAD), Multimedia Technology, Natural Language and Knowledge Processing, Network Systems and Services, Programming Languages and Formal Methods, and Computation Theory and Algorithms.

IIS is not a degree-granting academic institution, with the important exception of the international graduate program in bioinformatics, under the auspices of Academia Sinica's Taiwan International Graduate Program. This Ph.D. program was established in 2003 and has enrolled more than 39 students over the last eight years.

Many of our research fellows hold joint faculty appointments at top universities in Taiwan. This allows our institution to play a very significant role in training and fostering advanced research talent in the IT industry and in academia in Taiwan.

DIRECTOR:
Dr. Hsu, Wen-Lian (Acting)

DEPUTY DIRECTORS:
Dr. Ko, Ming-Tat
Dr. Wang, Hsin-Min

GROUP COORDINATORS:
Dr. Sung, Ting-Yi
  Bioinformatics Lab
Dr. Wu, Jan-Jan
  Computer Systems Lab
Dr. Chen, Meng Chang
  Information Processing and Discovery (iPAD)
Dr. Liao, Hong-Yuan Mark
  Multimedia Technology Lab
Dr. Hsu, Wen-Lian
  Natural Language and Knowledge Processing Lab
Dr. Ho, Jan-Ming
  Network Systems and Services Lab
Dr. Wang, Bow-Yaw
  Programming Languages and Formal Methods Lab
Dr. Hsu, Tsan-sheng
  Computation Theory and Algorithms Lab

First of all we would like to welcome Dr. Wen-Tsuen Chen, former president of Tsing-Hua University, who joined our research team in March. We believe his expertise in communication networks will help our related research reach an even higher level.

The Institute of Information Science has a wide diversity of research projects and many activities. Researchers, many from major research groups abroad, frequently visit and present lectures. Each month, for example, the institute invites a world-renowned researcher to visit. These researchers not only present their major research findings through the IIS Distinguished Lecture Series and offer their views and perspectives on their respective fields, but also give advice on how best to conduct research and be successful in their respective fields. This extremely successful and popular series is entering its fourth year this summer.

Almost every week an IIS faculty member will announce his or her research results in a major journal, at a conference, or in a new book. Some outreach programs — such as workshops, tutorials, and summer internships — are also being conducted through various service groups supervised by institute faculty. Our faculty members are also regularly asked to serve as managers of major funding programs with the National Science Council, or as principle investigators or chief executive officers of national research programs, such as the Networked Communications Program (NCP) and the Taiwan e-Learning and Digital Archives Program (TELDAP). This year, Dr. Chung-Yen Lin received backing from the World Cloud Research Collaboration Project, hosted by Microsoft Research, for two projects.

IIS has eight research laboratories. Their research programs cover a wide range of areas, including bioinformatics, network systems, multimedia, computer vision, natural language and knowledge processing, cryptography, Internet gaming, speech processing, cloud computing, data mining, machine learning, programming languages, and formal verification of computer programs. In this issue of the IIS newsletter, we highlight the Intelligent Agent Systems Laboratory and its major research programs. We also introduce two world cloud research collaboration projects and spotlight a young IIS assistant research fellow, Dr. Yuan-Hao Chang.

IIS faculty members continue to receive major awards. For example, Dr. Chung-Laung Liu received the 2011 Phil Kaufman Award for distinguished contributions to electronic design automation; Dr. Jan-Jan Wu received the 2011 Best Paper Award from the Taiwan Association of Cloud Computing; Dr. Tei-Wei Kuo received the 2011 Distinguished Research Award from the National Science Council; Dr. Yennun Huang was elected an IEEE Fellow in 2012 for his contributions to fault-tolerant and failure-avoidance software; Dr. Yi-Hsuan Yang received the 2011 Young Author Best Paper Award from the IEEE Signal Processing Society; and Dr. Wei-Ho Chung received the 2012 WCNC Best Paper Award from the IEEE Communications Society.

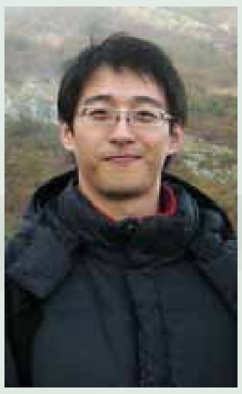
After the long chilly winter, spring has come to Academia Sinica's campus in Nangang, with flowers blooming everywhere. We welcome you to stop by and visit us. We hope you enjoy this issue of the IIS newsletter. As always, please give us your comments and feedback.

Honors and Awards

Corresponding Research Fellow Dr. **Chung-Laung Liu** receiving this year's Phil Kaufman Award for Distinguished Contributions to Electronic Design Automation (EDA)

Dr. **Jan-Jan Wu** receiving the 2011 Best Paper Award from Taiwan Association of Cloud Computing

Dr. **Wen-Tsuen Chen**, a former President of Tsing Hua University, joining IIS as a new Distinguished Research Fellow, March 2012



Dr. **Yi-Hsuan Yang** receiving the 2011 SPS Young Author Best Paper Award from the IEEE Signal Processing Society

Dr. **Chung-Yen Lin** receiving the World Cloud Research Collaboration Project hosted by Microsoft Research

Dr. **Yennun Huang** being elected as Fellow of IEEE 2012

Dr. **Tei-Wei Kuo** receiving the Distinguished Research Award 2011 from National Science Council (NSC)

Distinguished Lecture Series

April **Gerald J. Holzmann** NASA/JPL, Laboratory for Reliable Software, and Caltech CS, Pasadena, CA
Software reliability and software analysis methods, Formal verification, Logic model checking, Distributed systems design , Analysis of multi-threaded software, Requirements capture and analysis, Algorithms, Text processing, Image processing

May **Dan Reed** Corporate Vice President, Microsoft
Computer security, Cryptography, Operating system design, Parallel programming models, Cloud software, Data center architectures, Natural user interfaces

July **Thomas S. Huang** Department of Electrical and Computer Engineering, University of Illinois at Urbana-Champaign
Computer vision, Image compression and enhancement, Pattern recognition, Multimodal signal processing

Genome-Wide DNA Methylation on Cloud

Precise Mapping for Reduced Representation Bisulfite Sequencing (RRBS) and Paired-End Reads

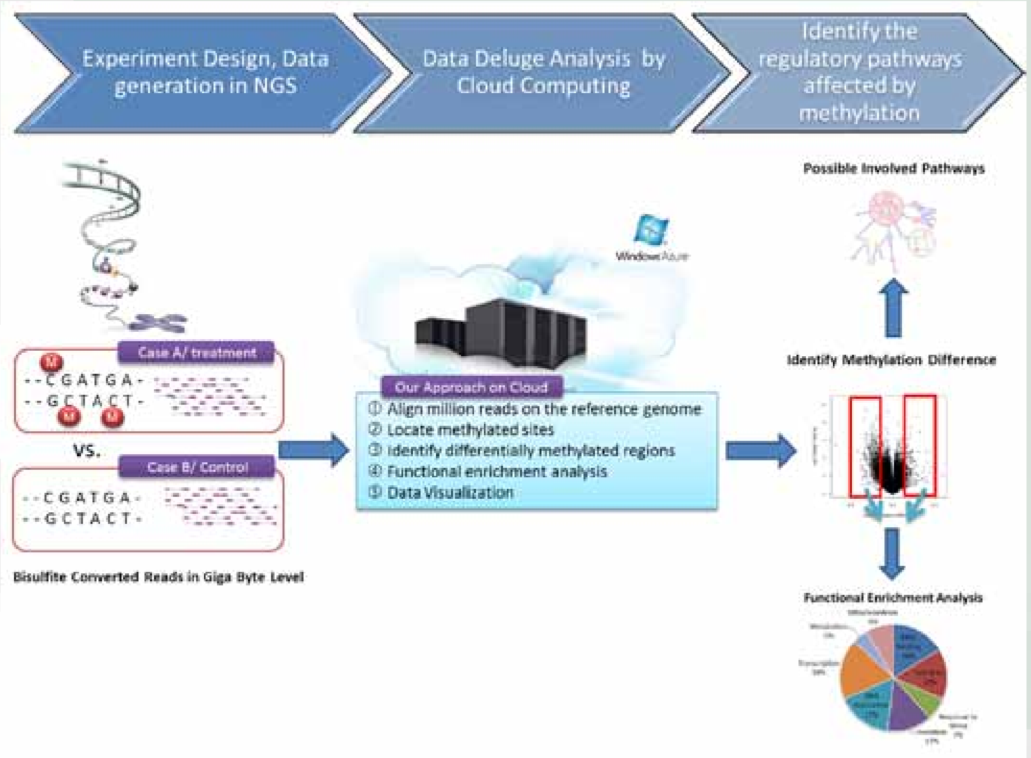
Project Coordinator
Dr. Chung-Yen Lin
Collaborated with
Pao-Yang Chen, Liudmilla Rubbi,
Amit K. Ganguly, Sherin Devaskar,
Matteo Pellegrini at UCLA.
Related URL: http://eln.iis.sinica.edu.tw

Epigenetic regulation, such as cytosine DNA methylation, is important in gene regulation. Precise measurements of genome-wide DNA methylation at single-base resolution have only recently become possible with next generation based bisulfite sequencing (BS-seq). However, aligning bisulfite converted reads (single end and paired ends) remains technically challenging. Here we extend our bisulfite aligner, BS Seeker, to accommodate paired-end mapping. We further propose RRBS-Seeker for mapping reads that are generated from reduced representation bisulfite sequencing (RRBS). By mapping synthetic RRBS reads against the enzyme-digested fragments, RRBS-Seeker yields a higher mappability and a higher accuracy than mapping the reads directly against the genome. To demonstrate the usefulness of RRBS-Seeker we mapped six mouse RRBS lanes. The result reveals lower methylation levels in mice of mothers with caloric restrictions, suggesting nutrition intake in parents may alter the epigenetic profiles of offspring.

DNA methylation plays a critical role in cell differentiation, cancer development, and aging. Using BS-seq approaches [1] we are able to generate genome-wide methylation profiles at single-base resolution. In bisulfite converted reads from BS-seq data unmethylated Cs are converted to Ts, while methylated Cs remain unchanged. Traditional aligners are not able to map this type of read . The team's previously published aligner — BS Seeker [2], which is based on three-letter alignments — was developed explicitly for this task. Since the latest TruSeq library generation kit from Illumina provides only paired-end adaptors, this project extended BS Seeker to allow paired-end mapping. However, as the cost of whole-genome BS-seq is still high, especially for mapping mammalian genomes, less expensive alternative approaches have been developed. One such approach is reduced representation bisulfite sequencing (RRBS) [3], which sequences only enzyme-digested fragments that are enriched for CpG di-nucleotides and promoters, which represent about 1% of the genome. The project developed a variant of BS Seeker, RRBS-Seeker, which maps RRBS reads only to these fragments, and evaluated its mapping

Mapping synthetic RRBS reads to preprocessed (fragments) and to the unpreprocessed genome (chr 21)

	Mapability		Accuracy	
	Against fragments	Against chr 21	Against fragments	Against chr 21
No sequencing error	86.63%	83.70%	100%	100%
With sequencing errors	83.48%	80.80%	99.60%	99.40%



Genome-wide DNA methylation analysis on Cloud

accuracy using synthetic reads. This also has been applied to analyzing six mouse RRBS libraries.

Materials and Methods

The three-letter alignment implementation maps C/T converted (converting Cs to Ts) reads to the two strands of the genome that are also C/T converted , followed by post-processing to keep only uniquely mapped reads and to extract methylation information. To map the second ends in paired end bisulfite converted reads, the reverse compliment of the second end is mapped against the forward strand to a position close to the mapped position of the first end. RRBS-Seeker first masks out the unmappable regions in the genome, i.e., those that are not covered by the enzyme-digestion. It then maps the RRBS reads only to the mappable regions and keeps track of the mapped fragments for downstream analysis.

Results and Discussion

The project mapped 100,000 synthetic RRBS reads from human chr21 directly to the fragments using RRBS-Seeker, and compared the result to those obtained by mapping to the whole chromosome (Table). Mapping only against the fragments yields advantages in both mappability and accuracy, suggesting that an explicit bisulfite aligner is optimal for RRBS mapping.

Conclusions

The project extended BS Seeker to paired end mapping and developed a variant, RRBS-Seeker, for accurately aligning RRBS reads. Synthetic RRBS reads are generated to assess the performance of RRBS-Seeker; and the results demonstrate an improved mappability and accuracy compared to a whole-genome alignment. In the analysis of six mouse placenta samples, lower methylation levels were observed in cases with caloric restriction, indicating an epigenetic change in offspring that was due to the diet of the mothers . The current RRBS-seeker will be released as standalone program (aligner, Python scripts, and analyzer). Because the high-throughput sequencer generates a deluge of data, completing the analysis requires users to have a powerful machine and strong IT support. Yet many wet-lab researchers lack these. Thus, we hope to provide services that will help people work around this; we propose to (1) move RRBS-seeker to the cloud and optimize tasks for parallel computation to increase performance; (2) provide pre-calculated genome references for the most-requested species, such as human and mouse; and (3) guide the data-analysis process via a user-friendly Web interface. Then scientists would need only submit BS-sequences with parameters and essential items; the cloud version of RRBS-seeker would present the results in genome-wide scale to reveal how genes regulate under the different scenarios.

References

[1] Cokus et al. Nature (2008) 452 (7184): 215-219.
[2] Chen et al. BMC Bioinformatics (2010) 2010, 11:203.
[3] Gu et al. Nature Methods (2010) 7(2): 133-136

Distinguished Lecture Series

Mining Heterogeneous Information Networks

Jiawei Han — July 20, 2011

" …We show that structured information networks are informatics, and link analysis of such networks is powerful at uncovering critical knowledge hidden in large networks."

Participatory mHealth: Opportunities and Challenges

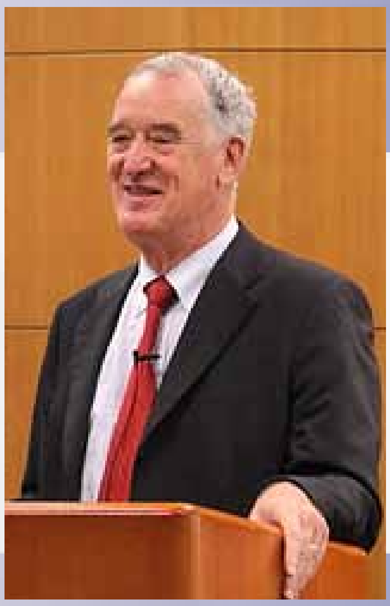
Deborah Estrin — September 22, 2011

"She presents her experience with mHealth pilots and prototypes, and highlights areas in need of significant R&D..."

Towards Trustworthy Systems

Gernot Heiser — October 13, 2011

"He describes NICTA's research agenda for achieving true trustworthiness in systems...."



The Time-Triggered Architecture

Hermann Kopetz — November 23, 2011

"He presents the architecture model of the TTA, explains the design rationale, discusses the time-triggered communication protocols TTP and TTEthernet, and illustrates how transparent fault tolerance can be implemented in the TTA..".

The Power of Abstraction

Barbara Liskov — January 16, 2012

"...Abstraction is at the center of much work in computer science. It encompasses finding the right interface for a system as well as finding an effective design for a system implementation."

The Past and 3½ Futures of NLP

Eduard Hovy — March 13, 2012

"…Where is the heart of NLP? What is the nature of the theories developed in each stream (if any)? What kind of work should graduate students today choose to do?...".

December 28, 2011

Workshop on Music Information Retrieval and Social Network Service

With rapid growth of the development of Web and multimedia techniques, numerous kinds of online music information content and music information retrieval services are prosperously prompted. These online music service platforms are thus more widely and deeply incorporated in human life and interactions. Besides, the number of Web 2.0 websites explosively increased in recent years. These websites, such as Facebook, Twitter, Flicker, YouTube, etc., provide various social network services and result in large impacts in e-commerce. Therefore, many innovative studies emerge and related discussions have attracted much attention in academia and industries. To this end, in this year, 2011, the Institute of Information Science of Academia Sinica, the Department of Computer Science and Information Engineering of National Taiwan University, and the Department of Computer Science and Information Engineering of National Cheng Kung University will cooperatively hold this workshop, which brings together researchers and practitioners to foster the exchange of ideas and the dissemination of emerging techniques in Music Information Retrieval and Social Network Service. The workshop chairs sincerely invite you to participate in this in-depth discussion forum and expand the frontiers of IR.

For further information: http://www.aclclp.org.tw/doc/IR2011_e.htm

Open Source Apps on Mobile

December 28, 2011

Fancy Rich Text Editing on Android
Invited Open Source Software Foundation Talk

Android is an open platform that aims to allow for innovation at every level of its software stack. To serve this purpose it has provided a rich and powerful suite of framework APIs to make app developed.

OPEN HOUSE

In order to help people know more about what is happening at IIS, we have prepared numerous exhibition booths with interesting content to present our work. The open campus event was a great success and we hope that it has sparked many people's interest in information science.

People arrive at the registration area.

Intelligent Agent Systems Lab (IASL) Knowledge Representation and Natural Language Understanding

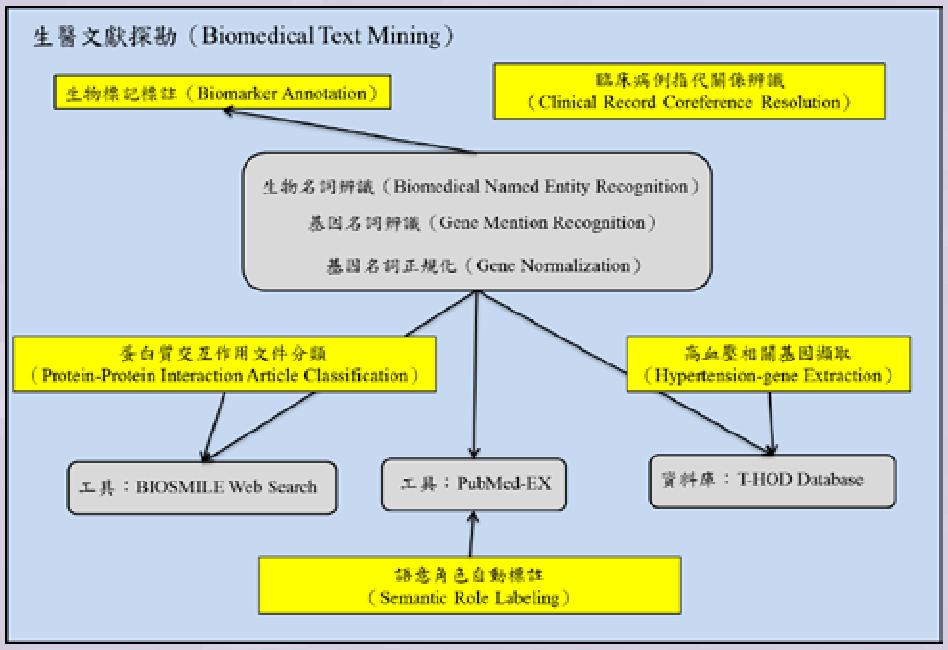
One of the focuses of the Lab (IASL) is knowledge representation and natural language understanding. Combining various advanced machine-learning and rule-based techniques, IASL has rolled out several successful systems, such as Named Entity Recognition, Question Answering, Textual Entailment, and Biological Text Mining.

Named Entity Recognition

Identifying the names of people, locations, and organizations in documents is crucial for natural language understanding. In 2006, IASL won second place in the SIGHAN NER competition for its mature, machine-learning based named entity recognition (NER) system. In recent years, IASL has focused on adopting semantic rules and language patterns to further enhance performance. Our NER has also been applied to the biomedical area. Gene/protein terms within biomedical documents vary widely, which is caused by synonyms, abbreviations, and aliases. The ability to disambiguate recognized named entities has a great impact on the advancement of information extraction problems, such as protein-protein interaction relation extraction and gene-disease relation extraction. Since bio-NER relies heavily on domain knowledge, a Markov-Logic Network has been adopted to integrate various information items, such as lists of key terms from knowledge bases, results from other recognition components, and contextual knowledge. The Markov-Logic Network incorporates the nature of rule-based and machine learning methods, providing more flexibility in the recognition and disambiguation of named entities.

Question Answering

IASL has been working on question answering (QA) for many years. The first such product is the Academia Sinica FAQ System, which can respond to user-entered queries such as “How do I get to Academia Sinica?” After the system locates the answer, it pops open a Web page that contains the relevant transportation information about Academia Sinica. In order to



Biomedical Text Mining

Lab members make efforts to the intelligent QA system.

Welcome to 中央研究院智慧型答詢系統，請輸入您的問題，例如：請問中研院資訊所所長的電話

歡迎來自中研院網域：140.109.19.160的使用者，中研院開放下載自然輸入9 (Going9) 中研院專用版

您的問題：中 研院院 長是誰

你可以參考目前最熱門的前10大問題：

我的回答：以下是我的回答：
答案網址：http://www.sinica.edu.tw/as/person/chwong/index_c.html
若沒有適合的答案，您可以參考關聯性問題，繼續問問題。

關聯性問題

1 院長是誰
2 查詢 現任院長 的相關訊息
3 哪些人是中研院院士
4 是誰成立中央研究院
5 問中央研究院副院長是誰

- 翁啟惠院長
- 彭旭明副院長
- 陳建仁副院長
- 王汎森副院長

翁啓惠 院長

2006年10月19日，翁啓惠院士受總統任命成
院長，在接下院長職務之前，翁院士曾任中
特聘研究員兼主任、美國 Scripps 研究院化

翁院士出生於台灣嘉義，台灣大學學士、台
所碩士、美國麻省理工學院化學博士(指導教

Intelligent QA System.

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關聯性問題

1 院長是誰
2 查詢 現任院長 的相關訊息
3 哪些人是中研院院士
4 是誰成立中央研究院
5 問中央研究院副院長是誰

Textual Entailment

match input questions with their answers, all frequently asked questions are decomposed into concepts in a tree-like structure called InfoMap. In addition to FAQ system, IASL has also been working on a factoid question answering (Factoid QA) system, which is capable of answering a question from a raw text corpus. This requires more complex techniques than those for the basic QA system. The question is analyzed to retrieve related passages from the answer corpus. Relevant NEs are annotated in the corpus. After that, candidate answers are extracted and ranked based on several features. Our QA system twice won first place at New Trends in Computing and Informatics Research conferences (in 2005 and 2007) for Chinese QA shared tasks.

Textual Entailment

Textual entailment (TE) is the task of identifying inferences between two sentences. TE relies heavily on language-processing techniques such as named entity recognition, parsing, part-of-speech tagging, word similarity, and co-reference resolution. By combining various semantic resources and components, IASL developed a semantics-based textual entailment recognition system, which was rated as one of the best systems for shared tasks at NTCIR-9.

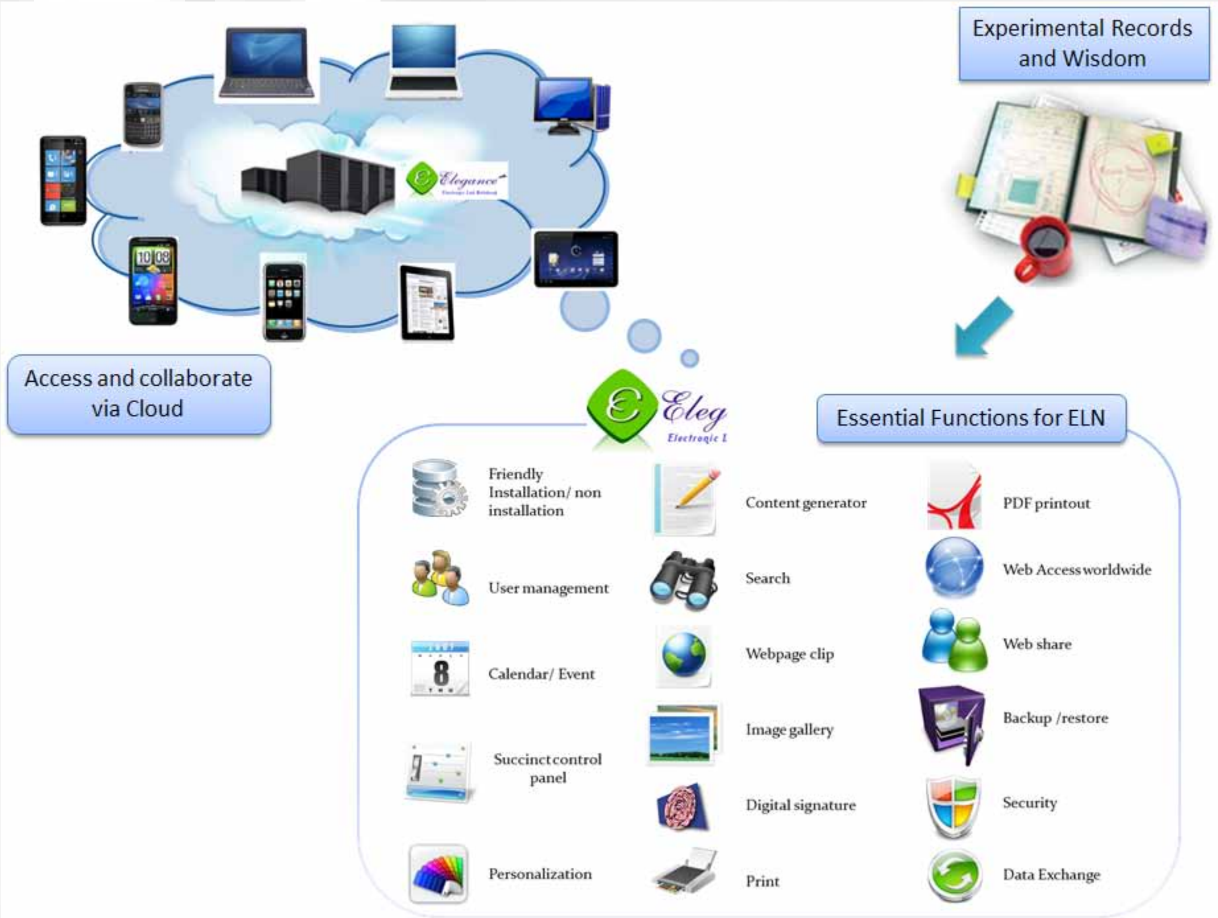
Biomedical Text Mining

Advancements in experimental techniques, accumulation of past experience, and ease of access to publications around the world have all contributed to the acceleration of biomedical studies, resulting in enormous repositories of scientific journals and papers. The field of biomedical literature mining has gained increasing interest, as it has proven to be an efficient method of deriving high-

(cont'd on page 11)

Electronic Laboratory Notebook (Elegance, ELN)
for Biomedical Research Community
on Sharing, Co-working and Inspiriting in Cloud

Project Coordinator
Dr. Chung-Yen Lin
Project URL: http://eln.iis.sinica.edu.tw



The essential functions in cloud ELN for various clients and mobile devices.

Even in the twenty-first century, many scientists are continuing the age-old practice of using a pen to recording their findings, musings, ideas, and inferences in paper-bound laboratory notebooks. This method, however, is inadequate for the increasing volumes and complexity of data that characterize modern research, and it makes it hard to share data among various disciplines and research communities. With the digital deluge generated by high-throughput biology, a platform for a knowledge repository with functions such as search, backup, and reconstruction can be an important tool for laboratory records.

This electronic laboratory notebook (ELN) holds the promise of doing much more than helping scientists with record-keeping. It raises the possibility for new discoveries and problem solving, significantly increasing the competitiveness of whole research teams. Although some ELNs are al-ready available, their prices and lack of user-friendly interfaces are an obstacle to their wider use. But just a few clicks will install the essentials of our ELN: note creating with attached experimental digital output, full-text search with image gallery, succinct user management with digital signature, automatic system backup, calendar with coming event notification, personalized interface with privacy, data sharing and exchange via the Web, duplication and backup of the whole ELN, and many other features. With the support of the NSC since August 2009, we have implemented a draft ELN that can satisfy the needs above and be installed on Windows platforms for personal and small-group use. This prototype enables scientists without specialized computer skills to compile electronic laboratory records quickly, sort notes, compare results, and share information with others. Using Drupal and well-chosen modules, an open source content management system, we exploited Apache, mySQL, PHP, Java, and Ajax to construct a Web-based ELN for various operation systems, including Linux, Windows, and Mac.

Our first version of Web-based ELN can be installed in Linux- and Windows-based environments. The present Windows version ELN is optimized and can be easily deployed on most available PCs, without high hardware and IT-support requirements. Thus, it can be shaped for managing all kind of lab working logs/ experiment data for single researchers or small research teams to construct their own Internet Web services for the public and intranet frameworks to manage experimental results. It can also be used as a platform for sharing work among labs. Most importantly, has been designed to be a content-exchange mechanism. This built-in function can allow two independent ELNs to communicate and share content either manually or automatically.

A further ambitious goal of this ELN project is to help bench scientists manage and share the fruits of their hard work without them needing specialized computer knowledge. Our team has already begun to study how we might implement ELN in the cloud (see figure). We anticipate it will be easy to use and will be accepted like other cloud applications, such as Hotmail and Gmail. To sum up, the ELN developed by our team will substantially help the research community, through such functions as sharing information, reorganizing knowledge, and manifesting actual laboratory work.

The Windows version is available at http://eln.iis.sinica.edu.tw

Screen casts and directions for installation can be found at http://eln.iis.sinica.edu.tw/eln/?q=help

Intelligent Agent Systems Lab

(cont'd from page 9)

quality information from text with the aid of programs and systems. Using literature-mining tools developed by IASL, we are able to automatically achieve goals such as biological entities recognition (in-cluding gene, cell and disease terms) and classification of protein-protein interaction related articles, which may help scientists gain a more thorough understanding of different biological mechanisms. In 2009, IASL won first place in BioCreAtIvE II.5's Interactor Normalization Task category. In applying text-mining techniques to clinical research, IASL also works on gene-disease relation extraction, clinical record co-reference resolution, and biomarker annotation, hoping to benefit clinical research and diagnoses. Several tools have been developed by IASL, such as BIOSMILE Web Search (BWS), PubMed-Ex, and T-HOD Database. BWS is a search interface that is similar to the search engine of PubMed; it combines search results with auxiliary information, such as biological entities recognition and protein-protein interaction related article classification. PubMed-EX is a Firefox plug-in that provides, in real time, annotations of gene and disease terms and the section categorizations of an abstract being viewed.

Combining Dreaming with Hands-On Experience

Dr. Chang, Yuan-Hao, Assistant Research Fellow

Dr. Chang, Yuan-Hao.

Dr. Chang, now that you have been here for a few months, what do you think of the institute?

I like this institute and enjoy working here very much. One of the advantages of working here over universities is that you don't have a teaching load, which saves me a great deal of time.

The colleagues here are very keen on their jobs. Their dedication inspires others to follow suit, which creates a benign circle. People here are not only hardworking, but also very friendly and helpful. Although everyone is busy, they will help you whenever needed. I would like to take the opportunity to give my special thanks to Dr. Jan-Jan Wu, who introduced me to the institute and is serving as a mentor for me in my research.

Briefly introduce yourself.

I was born and bred in a rural area of Tainan, and spent most of my childhood playing in our chicken yard and pigpen. No matter how clean I was at dawn, I would be filthy upon returning home at dusk. The best time for me was playing chess and having tea with my family. I often reminisce about those good old days. Because of chess playing, I enjoy all types of games and things that involve thinking and logical reasoning. Maybe it's the reason I work as a researcher today.

I have always been fascinated by science-fiction novels and movies. The world of the imagination provides a refuge whenever I'm feeling down or tired, and picks me up. I also enjoy listening to classical music, which makes me feel calm and peaceful.

I have two adorable kids — who are two and four years old, respectively — and a beautiful wife. I spent most of my

My happy family.

leisure time walking my two kids, who are both extremely energetic.

Why did you decide to work for Academia Sinica?

Academia Sinica is a research-oriented institute. It provides abundant research resources and a globalized research environment. I can communicate with professors and researchers from around the world and broaden my horizons.

Is there a single event that sparked your interest in the IT field? What did you expect, and what did you want to accomplish?

Ever since I took a micro-processor course taught by Professor Jung-Gen Wu of National Taiwan Normal University, I have been fascinated by computer systems and have enjoyed programming. After finishing my military service, I gave up a stable teaching job to work for Hewlett-Packard, which a lot of people then considered a dumb move. I was doing hardware programming and writing device divers there. That hands-on work allowed me to gain a comprehensive view of computer systems and led me to study computer systems as a doctoral student.

I dream of developing a state-of-the-art computer system one day and contributing to the computer industry.

Please talk a bit about your current research and any difficulties you have encountered.

I hope my research can cater to the needs of Taiwan's industry and make contributions to it from the academic point of view.

My lovely kids with my wife.

My current focus is on embedded computing systems. The major part of Taiwan's IT industry is manufacturing hardware, especially large quantities of electronic consumer products. Enhancing the effectiveness of such products requires an enormous amount of research regarding computer systems and software systems. Unfortunately, relatively few IT students specifically study computer systems, which presents a difficulty because computer-system research needs a lot of brain-power in order to reach the application level.

What advice would you give to those interested in working as researchers in the IT field?

To succeed in computer-system research you will have to be enthusiastic about hands-on computing work. You will need to take many courses related to computer systems. Gaining hands-on experience from hardware circuits, micro-processor controls, and systems software will give you a better perspective on the subject and help a lot when doing computer-system research.

What's your goal in the future?

I expect to focus on theory, algorithms, and architecture in computer-system research. I hope that I can develop very influential and powerful techniques, and build up a team with a worldwide reputation.

Free & Open Source Software Makes Your Life Easier!

More and more people are learning about the world of free and open source software. Although such software has the tremendous benefits of being free to use and redistribute, its greatest advantage is that its source code is available to all. Program developers can easily join open source projects to fix bugs or develop new functions.

The Open Source Software Foundry is an open source project. Its Web site, at www.openfoundry.org, offers many tools for developers to manage their software projects easily. It also provides teaching materials, resource catalogs, and a bi-weekly newsletter, along with sponsoring many activities, including conferences on open source software. The Open Source Software Foundry would love for you to join its community.

LibreOffice

LibreOffice is a multi-platform and open source office software suite. It is compatible with many operating systems (e.g., Windows, Linux, Mac OSX, and Solaris), and is free for download, use, and distribution. It also supports Microsoft Office file formats from version 97 to Office 2007. Its major programs are Writer, Impress, Calc, Draw, Math, and Base.

PDFCreator

PDFCreator easily creates PDFs from any Windows program. Use it like a printer in Word, StarCalc or any other Windows application.

PDFCreator

The bulky and expensive Adobe Acrobat is no longer required to convert files PDF. PDFCreator is free, open source software that easily converts multiple file formats — such as DOC (Word), PPT (Powerpoint), XLS (Excel) and ODT (OpenOffice) — to PDF, simply by simulating a printer. In addition, PDFCreator supports mail-merge printing, merging two different documents into one PDF file, and batch conversion.

GIMP

GIMP (GNU Image Manipulation Program) is a free raster graphics editor. It is primarily employed as an image retouching and editing tool. In addition to offering freeform drawing, GIMP can accomplish essential image workflow steps such as resizing, editing, and cropping photos; combining multiple images; and converting between different image formats. GIMP can also be used to create basic animated images in the GIF format.

Firefox

Mozilla Firefox is a free, cross-platform, graphical Web browser developed by the Mozilla Foundation and hundreds of volunteers. It is a lightweight, fast, and highly extensible standalone browser. This program includes an integrated pop-up blocker, tabbed browsing, live bookmarks, built-in phishing protection, support for open standards, and an extension mechanism for adding functionality and localization for Firefox in different languages.

Free Download Manager

Free Download Manager is an open source download management tool under GNU GPL. It supports HTTP, FTP, and BitTorrent protocols. It accelerates downloads by splitting files into sections and then downloading them simultaneously. According to the program's Web site, download speeds can increase by 600% or even more! Free Download Manager can also resume broken downloads, so users needn't start downloading from the beginning if there was an interruption. It also provides a built-in upload manager for users to share files easily.

Inkscape

Inkscape is an open source vector graphics editor with capabilities similar to those of Illustrator and CorelDraw. Inkscape supports many advanced features of the W3C-standard scalable vector graphics (SVG) file format, including markers, clones, and alpha blending. Great care was taken to produce a streamlined interface that makes it easy for users to edit nodes, perform complex path operations, trace bitmaps, and much more.

FileZilla

Mozilla Firefox is a free, cross-platform, graphical Web browser developed by the Mozilla Foundation and hundreds of volunteers. It is a lightweight, fast, and highly extensible standalone browser. This program includes an integrated pop-up blocker, tabbed browsing, live bookmarks, built-in phishing protection, support for open standards, and an extension mechanism for adding functionality and localization for Firefox in different languages.

PCMan

PCMan is open source BBS software software for Windows. It was created in 2001 by a Chinese software developer. It comes in two versions: PCMan Combo (both Web and BBS) and PCMan Lite (only BBS). Both have standard built-in Unicode-compliant fonts, the capability to convert between traditional Chinese and simplified Chinese characters, and a worldwide Chinese BBS list. Furthermore, PCMan supports tabbed browsing and customizable hotkeys, buttons, and icons.

To promote the development and use of open source software, the Open Source Software Foundry provides a forum that facilitates interaction and collaboration between open source software developers, and serves as a bridge to link developers with industry and academia.

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Web site: www.openfoundry.org

ACTIVITIES

Mid-Autumn Festival Party Games

Pomelo-Peeling Contest

Here comes our annual pomelo-peeling contest!
The contestants are about to vie to see who can peel the most pomelos with their bare hands.

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