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DECISION LINE

Vol. 46, No. 2 March 2015

PRESIDENT'S LETTER

Hello DSI Membership:

Marc J. Schniederjans, University of Nebraska-Lincoln

Thank you for permitting me to be your president during this past year. I think it is important that you recognize your fellow Board members when you see them. This year the DSI Board of Directors and there offices were:

Marc Schniederjans (President)
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Morgan Swink (President Elect)
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Janelle Heineke (Treasurer)
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Constantin Blome (VP of European Division)
Stuart Orr (VP for the Asia-Pacific Division)

Much has been accomplished because your Board of Directors has given a great deal time and effort to help improve DSI. Some of the accomplishments we have initiated this year include:

- Membership enrollment efforts that results in slightly over 1100 reported in the April 2014 Board meeting to slightly over 1600 reported in the January 2015 Board meeting. We are growing again, after many years of decline.
- Under the leadership of Powell Robinson and Dana Evans

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FEATURES

SPECIAL REPORTS

DECISION LINE

DECISION LINE is published five times a year by the Decision Sciences Institute to provide a medium of communication and a forum for expression by its members, and to provide for dialogue among academic and practitioner members in the discipline. For more information about the Institute, please call 404-413-7710.

News Items: Send your news items and announcements to the editor at the address below.

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DEADLINES:	March 2015 issue	February 10th
	May 2015 issue	April 10th
	July 2015 issue	June 10th

Vision Statement

The Decision Sciences Institute is dedicated to excellence in fostering and disseminating knowledge pertinent to decision making.

Mission Statement

The Decision Sciences Institute advances the science and practice of decision making. We are an international professional association with an inclusive and cross-disciplinary philosophy. We are guided by the core values of high quality, responsiveness and professional development.

2014-2015 Decision Sciences Institute Officers

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FROM THE EDITOR

MALING EBRAHIMPOUR, EDITOR, University of South Florida St. Petersburg

Maling Ebrahimpour *is professor of management at the College of Business at the University of South Florida Saint Petersburg. He is an active researcher and has authored or co-authored over 100 articles that have been published in scientific journals and proceedings. Most of his work focuses on various issues of quality in both service and manufacturing companies. He received his PhD in business administration from the University of Nebraska-Lincoln and has served on the editorial review board of several journals, including* Journal of Quality Management, Journal of Operations Management, *and* International Journal of Production Research.

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This issue of Decision Line contains several very interesting articles written by our members and the result of the DSI election. More than 50% of the eligible voters voted and it appears that this is one of the largest number of voters that DSI had in its history.

Congratulations to our new officers and we are happy that there are very capable people con-tinue leading the changes of DSI to make it a more efficient and highly respected organization. The newly elected officers are: Funda Sahin (University of Houston), President-Elect; Jennifer Blackhurst (Iowa State University), Secretary; Kaushik Sengupta (Hofstra University), VP – Marketing; Anand Nair (Michigan State University), VP – Publications; Bob McQuaid (Pepperdine University), VP – Technology; Bob Pavur (University of North Texas), VP – Americas Division; Bhimaraya Metri (International Management Institute, India), VP – Asia Pacific Division. CONGRATULATIONS!

President Schniederjans' letter is his last as the President of DSI. Much has been den during Marc's presidency and the DSI is in a better position than before. His letter summarizes the accomplishments of DSI during his presidency. As you will see the result of the election has been included in this issue.

Mirzaei and Crivelli in their article discuss the opportunities that exist where the two areas of Protein Structure and Machin Learning intersect. One of the needs that the authors identified is the need for more aggressive involvement of the machine learning community to tackle, as an example, different aspects of protein-folding problem which can help to realize the dream of delivering the "Precise Medicine," to provide "the right treatment at the right time for a specific individual."

"Big Data in Small Bites" is the title of the article by Paul Rubin. In his article he discuss the rush to use big data may not be necessary and sample can be used. He proposes two interesting questions: "need we use all the data; and need we use it all at once?" He concludes that although there is a rush to use big data, "both the volume and the velocity of "big Data" may require us to reevaluate that approach."

I encourage those doctoral students who are preparing to enter the job market to read Varun Grover's article on how to prepare for the interview. Grover writes about how doctoral students who are in the job market can prepare for the best presentation and handle the questions from interviewers. He takes the readers through the process in three steps of preparation, actual presentation, and the question. Furthermore, he provides a "Job Talk Preparation Checklist" that is a helpful tool for all who are entering the job market.

"In the Classroom" feathers an article by Thomas Rienzo titled "Calculating Last Dates of Attendance in large Lecture Classes." Rienzo describes creation and an automated scalable spreadsheet that helps calculating the last dates of attendance. This spreadsheet should help administrators to capture information needed to Title IV financial aid from the US Department of Education.

In addition, there is information about the special issue of Decision Sciences Journal on Innovative Education. The special issue is focused on 'Identifying and Managing Critical Success Factors of Online Education.' Carol J. Latta Memorial DSI Emerging Leadership Award for Outstanding Early Career Scholar describes the process and dateline for applications and nominations to be sent to the DSI Home Office. Please nominate any DSI member who is in the early stage of the profession and has been already an active member of the DSI.

I encourage you, our reader, to share your opinions, ideas with us by writing and sending it to me at: mebrahimpour@ mail.usf.edu.

I am looking forward to reading your articles for inclusion in Decision Line.

Maling Ebrahimpour, PhD

Editor ■

BY JOHNNY (MANUS) RUNGTUSANATHAM, INTERIM EXECUTIVE DIRECTOR

CONGRATULATIONS TO NEWLY ELECTED DECISION SCIENCES INSTITUTE OFFICERS

As the Interim Executive Director, appointed by the Board of Directors for the *Decision Sciences Institute* (DSI) on February 1, 2015, I want to take this opportunity to congratulate the newly-elected 2015 officers and directors.

Many qualified individuals stood for elections to these positions. The Decision Sciences Institute is grateful and appreciates the continued involvement and support of its members.

The newly-elected officers and directors will begin their term in April 2015. The Decision Sciences Institute looks forward to their guidance and leadership.

2015 Voting Process

In an effort to make the business of the *Decision Sciences Institute* more transparent, please find a brief description of the voting process below, which involved some discrepancy regarding regional members and their votes. Moving forward, a systematic process is being designed into the membership module of the NOAH system (Home Office IS) to confirm regional memberships. This will take effect as DSI members renew their dues.

For this election, the Decision Sciences Institute contracted with Simply Voting, a web-based online voting system (https://www.simplyvoting.com/), to manage the voting process. This allowed voting to be conducted "blind" to the Home Office and in a secure fashion that prevents tampering. Once voting closed on February 19, 2015 (5:00 pm), voting results were then tabulated and verified by Simply Voting against a name list of DSI members.

Procedurally, the following steps constituted the process:

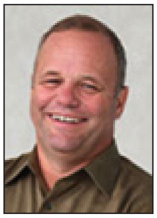
1. An electronic ballot managed by Simply Voting was sent to 1662 individuals on January 19, 2015. The 1662 individuals constitute the population of DSI members in the membership database maintained by the Home Office.
2. This ballot included the candidates for all positions, and allowed all DSI members to vote for all positions. However, voting for the VP – Americas Division and the VP – Asia Pacific Division should have been restricted to members of organizations in those respective regions. One of the candidates for the VP – Asia Pacific Division withdrew his candidacy, so there was no question regarding the election for that office. Regarding the VP – Americas, DSI contracted with Simply Voting to sort out the votes of regional members that should count for the VP – Americas Division. The following steps were conducted to identify regional members:
    a. The Home Office conducted a survey asking all 1662 members to confirm their regional affiliation (if any).
    b. The survey results were then passed to the officers of the regions asking for their verification.
    c. A finalized list with DSI member names and their regional membership affiliations was then forwarded to Simply Voting.
3. Simply Voting reported the following:
    a. 604 DSI members voted (~36% of DSI members). These 604 votes counted for electing the President-Elect, Secretary, VP – Marketing, VP – Publications, and VP – Technology positions
    b. 200 of the 604 DSI members who voted were identified as members of a region comprising the Americas Division (NEDSI, SEDSI, MWDSI, SWDSI, WDSI, and MDSI). These 200 votes were counted for electing the VP – Americas Division.

Funda Sahin *(University of Houston) President-Elect*

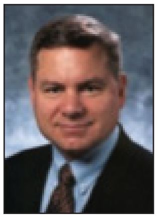
Jennifer Blackhurst
(Iowa State University)
Secretary
- *Elected unopposed since no other candidate stood for election*

Kaushik Sengupta
(Hofstra University)
VP – Marketing

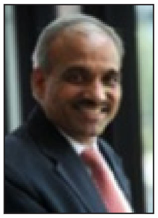
Anand Nair
(Michigan State University)
VP – Publications



Bob McQuaid
(Pepperdine University)
VP – Technology



Bob Pavur
(University of North Texas)
VP – Americas Division



Bhimaraya Metri
(International Management Institute, India)
VP – Asia Pacific Division
- *Elected by default because an opposing candidate withdrew after the ballot had been sent out*

Research Opportunities at the Intersection of Protein Structure Prediction and Machine Learning

by Shokoufeh Mirzaei, California State Polytechnic University, Pomona; and Silvia Crivelli, Lawrence Livermore Laboratory, Berkeley

Shokoufeh Mirzaei *is an assistant professor of Industrial and Manufacturing Engineering at California State Polytechnic University, Pomona and a visiting faculty at Lawrence Berkeley National Laboratory (LBNL). Her core areas of research are applied optimization, statistics, and machine learning. Currently, she conducts research in the application of machine learning techniques in biology, specifically, Protein Models Quality Assessment, in collaboration with scientist in the LBNL. She believes progress in biology and especially drug design can substantially benefit from machine learning and pattern recognition techniques to which she has dedicated her research efforts.*

Silvia Crivelli *is a computational biologist working on protein folding. She started the WeFold coopetition (collaboration and competition) experiment that brings together labs and individuals to solve one of the 100 top outstanding challenges in science. She wants to leverage the unique character of the social-media-based collaborative research community created by WeFold to develop next generation STEM researchers and to help young researchers further their professional networks and scientific expertise. She believes that progress in science will come from the rich combination of ideas that only a highly diverse community can create and that the current generation has the responsibility to provide the means to open doors to individuals from all walks of society.*

In this year's State of the Union Speech, President Barack Obama unveiled his "Precision Medicine Initiative," a proposal aimed at pushing the U.S. to the forefront of cutting edge medical treatments. This initiative will harness large genomics and epigenomics data to design drugs and treatments specifically customized for individual patients. This multidisciplinary, cross-organizational effort will bring together scientists from across disciplines to study genetic profiles, molecular and cellular analyses, and medical records. It will enable scientists to progressively pinpoint the relationship between a patient's genes and a specific disease and develop appropriate drugs and treatments. Consequently, this initiative may lead to a new era of medicine, and as President Obama argued "one that delivers the right treatment at the right time". A thorough investigation of the human genome combined with a fast and accurate prediction of protein tertiary structure is essential to the success of this effort. This is where the power of decision science tools will have a direct impact in the success of such initiatives.

The Human Genome

The human genome is the complete set of genetic information for humans. This information is encoded as DNA sequences within the 23 chromosome pairs. The DNA contains the codes required to build and maintain an organism. In fact, each chromosome holds genes with specific instructions to make proteins, which perform most life functions. Each tissue has a different function in the human body. Thus, each cell only activates a subgroup of its genes depending on its function. The activated genes, initiate a process during which the genetic codes are translated into a chain of amino acids. Guided by atomic forces among the atoms within a protein and between the protein and its aqueous environment, the protein chain folds into a specific three-dimensional structure, called the native structure, which defines its specific function in the cell. The process during which the sequence of amino acids is folded into the native structure is called protein folding..

Protein Folding

The folding process is very fast (fastest proteins fold in microseconds) and proteins are very efficient at folding in the right way. However, sometimes misfolding occurs and that might lead to neurodegenerative disease like Alzheimer's, Parkinson's or Mad Cow Disease (Selkoe 2004).

Currently, more than 6,800,000 protein sequences are available in the National Center for Biotechnology Information (NCBI) sequence database (ftp://ftp.ncbi.nlm.nih.gov/blast/db/). The NCBI maintains a comprehensive, integrated, and non-redundant set of sequences related to genomic DNA and proteins called "Reference Sequence" (RefSeq)[1] . However, protein structures are discovered at a rate far lower than the sequences. This is due to the difficulty and intricacy of the experiments by which protein structures are determined. Currently, X-ray crystallography and NMR spectroscopy are the most common meth-

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[1] http://www.ncbi.nlm.nih.gov/refseq/about/

ods for determining proteins structures. There are about 106,000 experimentally determined protein structures available, which are stored in the Protein Data Bank (PDB) (http://www.rcsb.org/pdb/).

Given that experimental approaches to determine 3D structure are so expensive and time consuming, computational approaches have been proposed to complement and guide the experimental ones. Such computational methods could allow scientists to efficiently determine a protein structure from its sequence of amino acids. Unfortunately, this problem is extremely hard as the native structure of a protein corresponds to the global minimum of an energy function that has a vast number of local minima whose number increases exponentially with the number of amino acids in the sequence. Finding this global minimum is a computationally demanding task.

Generally, there are two types of protein structure prediction methods: template-based and free modeling. This classification is based on the fact that proteins with similar sequences have similar structures. Template-based modeling methods are used when the sequence of amino acids for an unknown protein is similar to that of another protein in the PDB. In contrast, free modeling (FM) or "ab initio" methods are used when no similar sequence is found in the PDB. Using machine-learning techniques, methods that take advantage of the experimentally known structures in the PDB have identified similarities between protein structures and their sequences, and have substantially improved protein structure prediction. Nevertheless, protein structure prediction remains a challenge with no single method being able to produce consistent results.

Most protein structure prediction methods follow a 2-step approach that consists of 1) sampling and 2) selection. The first step samples the vast protein conformational space by generating a large number of 3D models called decoys. The second step ranks those samples and selects the best ones. Current template-based protein structure prediction methods are able to generate very good models. Unfortunately, they are unable to select those models in a consistent manner making it necessary to develop reliable methods to rank the protein models.

To evaluate and improve the prediction methods, a large-scale experiment was introduced two decades ago (Moult, Pedersen et al. 1995). The experiment, which is known as Critical Assessment of protein Structure Prediction (CASP), determines the quality of current protein structure prediction methods and assesses their improvement. The experiment consists of three phases: in the first phase a set of sequences corresponding to proteins that have been or are about to be experimentally determined but not yet published is gathered. This ensures that the structures are not available in the public domain at the time the predictions are made. Hence, the predictions are made blindly without the knowledge of the native structures. Then, the sequences of amino acids for those proteins are provided to the community of predictors. The second phase of CASP is to collect the structural predictions provided by different prediction groups. In this phase, each group submits a set of tertiary structure predictions for the given sequence of amino acids. Only five submissions per sequence are accepted per participating group. Thus, each group only submits their best five predicted models. The last phase is to evaluate and assess the quality of decoy structures against the experimentally known structures, which have become publicly available after the collection phase.

Evolution of Scoring Functions

In the context of protein folding, a predicted structure has a high quality when it is similar to the native structure. However, since the native structure is unknown during the prediction process, biologists have proposed a number of features to measure different native-like characteristics of a protein model. These features are combined into a scoring function, which is a ranking function that, given a protein model as input, produces a single number or score as the output. The manner in which features are combined to generate the output score is key to an accurate scoring function. Scoring functions have been proposed not only to "relatively" rank the protein models predicted for a given sequence without knowing the corresponding native structure, but also to "absolutely" rank predicted models for a given sequence when the native structure is known. The former is useful for CASP predictions whereas the latter is useful for CASP assessment. However, these scoring functions are insufficient to determine the practicality of predicted structures for biomedical application such as drug design, mutagenesis experiments, and other practical applications. Therefore, discovering quality assessment measures that can score computationally-determined protein models according to their protein-like characteristics independently of other decoys or prediction methods is crucial for biomedical purposes (Schwede, Sali et al. 2009, Benkert, Biasini et al. 2011). Hence, developing quality assessment functions has become the center of attention in recent years.

Generally, current scoring functions can be classified into four major categories: physics-based, statistical-based, consensus-based, and machine-learning-based functions (Manavalan, Lee et al. 2014). Physics-based functions calculate the potential energy of a model according to the laws of physics governing the protein folding process (Lazaridis and Karplus 1999)(Petrey and Honig 2000). The main drawback of these methods is their complexity which demands extensive computation time. Additionally, these methods are sensitive to small atomic changes. Statistical-based functions calculate protein model potentials based on the statistical information obtained from structural attributes of native protein structures. However, since statistical potential functions are established based on the aggregated data obtained from the features of native proteins, they have a limited power to dicriminate protein models accurately. Consensus-based functions are useful when the set of decoy models is similar to the native structure . However, these functions are outperformed by knowledge-based scoring functions when the majority of models in the pool have poor quality, or simply fail when the homology between the models is low. Machine learning algorithms, such as support vector machine (SVM), rank protein models by learning from the sequences and structural features of the native protein structures (Ginalski, Elofsson et al. 2003, Qiu, Sheffler et al. 2008, Wang, Tegge et al. 2009, Shi, Zhang et al. 2011).

The development of scoring and quality assessment methods for protein models can substantially benefit from application of machine learning techniques. First, because machine learning methods can extract hidden patterns within data, which is hard to be expressed using any specific statistical method or distribution. Second, they can easily and efficiently integrate several protein features into a single score function to provide a unique quality score, Third, they are cognitive and can be adapted as new models become available in the Protein Data Bank and grow toward an absolute close to perfect approximation of protein quality.

Currently, the data collected by the Prediction Center (http://predictioncenter.org) from the past 11 rounds of CASP has become a great repository of the predicted protein models and their associated quality. Hence, analyzing such data could provide initial insights regarding the association of protein model properties and their quality. This challenge has led to the emergence of a new field of research for the machine-learning community which seeks to develop techniques that estimate the absolute quality of protein models in the absence of the experimentally known native structures. Furthermore, advances to this problem will identify a group of protein characteristic that is significant in forming native-like protein structures. It is worth mentioning that the answers to this problem unveil invaluable information for biologist to design drugs and medications as well as to design new proteins with desired functions that are not currently available in nature.

Conclusion

Over the years, scoring functions have been developed to help scientist to 1) provide more accurate methods of predicting protein structures by "relatively" ranking protein models for a given sequence of amino acids and 2) assessing different prediction methods by estimating the absolute measure of similarity between a given model and the corresponding native structure. In the latter case, CASP assessors have developed different evaluation criteria and assessment methods for each category of prediction models –template-based and free modeling. However, until recently these methods were unable to provide a reliable quality assessment and assessors usually spent weeks, manually inspecting protein models in order to perform their final ranking. In the latest rounds of CASPs, the assessors have reached a consensus on a set of robust measures for the purpose of assessing the quality of protein decoys. Although, scoring functions have reached an almost perfect performance when discriminating good models from mediocre and bad ones, they are inconsistent when comparing models of similar quality. Therefore, given the complexity of the problem, scoring functions design efforts continue to be ad hoc to the best of our knowledge and quality assessment still lacks consistency. Consequently, the goal is to formulate universal scoring function and quality assessment methods that do not require human intervention and that are independent from methods of prediction.

The effort toward discovering a universal scoring function is two-fold and requires 1) finding new measures and metrics that provide better insights about the quality of protein structures and 2) finding the association of such features to protein structure quality. The latter purpose can benefit from the application of machine learning techniques to crunch the massive data with hundreds of variables in pursuit of developing "absolute" scoring functions which are capable of evaluating proteins models independently.

Finally, although the rapid advancement of high-performance computing technologies have provided an unprecedented opportunity to predict and assess protein structures faster than ever, the volume of available data and the opportunities for analysis and pattern recognition efforts have grown at a rate far higher than the experts in the field. Therefore, there is an urgent need for more aggressive involvement of the machine learning community to tackle different aspects of the protein-folding problem for instance, by developing scoring functions. All these efforts may help realize the ultimate dream of delivering "Precise Medicine;" that is to provide "the right treatment at the right time for a specific individual".

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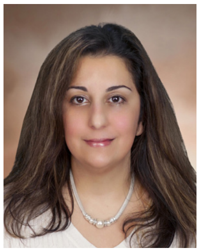
2015 Program Chairs' Message



Natasa Christodoulidou, California State University DH

We are pleased to share with you the call for papers for the Decision Sciences Conference 2015 in Seattle, Washington! Our conference is now only 10 months away and our submission deadlines are coming up very soon this spring.

The theme for this year's conference is **Decision Sciences in the 21st Century: Theoretical Impact and Practical Relevance.** We have two program pillars: (1) research and (2) education/professional development. This year we are introducing some new tracks as well as retaining many of the ones that were well received last year. The new tracks include Supply Chain Flexibility, Agility, Resilience and Strategic Management. We also have several special focus tracks: Healthcare Management, Ethics, Hospitality Management and Marketing, Public Policy, and Entrepreneurship.

Submission Deadlines:
Referreed Papers and Competitions
May 1, 2014
Abstracts and Proposals
May 15, 2014
www.decisionsciences.org

We ask that you save the dates of our conference, **November 21-24, 2015** and stay tuned for updates on exciting networking events and other relevant issues that we will keep you posted on.

How is the 2015 Annual Meeting Organized?

The program for the 2015 Annual Meeting of the Decision Sciences Institute is organized around its two pillars, plus keynote addresses, and special events.

Shawnee Vickery, Michigan State University

Pillar 1: Research

Invites full paper, abstract, and panel proposal submissions that speak to the generation of new knowledge pertinent to relevant business disciplines. Research presentations for this pillar are ideally positioned for publication consideration by Decision Sciences or other high impact business related journals. Panels for this pillar focus on identifying emerging research interests and topics.

Pillar 2: Education and Professional Development

Invites full paper, abstract, and panel proposal submissions that speak to the generation of new knowledge pertinent to the design, delivery, and evaluation of business curricula. Presentations for this pillar are ideally positioned for publication consideration by Decision Sciences Journal of Innovative Education or similar business education journals. Panels for this pillar focus on identifying leading edge issues and topics.

We look forward to seeing everyone at the DSI 2015 Annual Meeting in Seattle!

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ANALYTIC AND DATA SCIENCE

SUBHASHISH SAMADDAR, FEATURE EDITOR, **Georgia State University**

Big Data in Small Bites

by Paul A. Rubin, Ph.D., Michigan State University

Introduction by Subhashish Samadar

"Big Data and Analytics are in the air these days yet what defines 'big' data remains elusive at best. It is hard to find any area of studies or businesses that say they are not using some form of analytics and big data. However, in the halls of academics and some practitioners, questions have started to emerge regarding the scope and usefulness of big data and its role in analytic decision making. Professor Rubin's article below makes the point that big data may not always be needed. Hope you would enjoy it and join the discussion. With this article I intend to start a series of articles discussing this and other relevant topics. Please share your thoughts."

Subhashish Samaddar
Founding director of GSU's new MS in Analytics program, Subhashish (Sub) Samaddar, Ph.D., CAP, is a professor of Managerial Sciences at the J. Mack Robinson College of Business. Dr. Samaddar's research and teaching interests are in the broad area of business analytics and operations management. A winner of multiple research awards at both the national and regional levels, Dr. Samaddar has published in all premier journals in his field including in Management Science, Manufacturing and Service Operations Management, the Journal of Operations Management, European Journal of Operations Research, and Decision Sciences among others. His research specializes in analytics, optimization, operations, information technology and decision strategy.

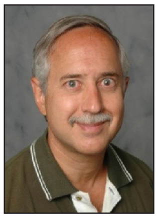
The era of "Big Data" is upon us. For some of us, that conjures thoughts of a second box of punch cards, but in contemporary usage it means sifting through giga-/tera-/peta-/exabytes of data, often collected online but also through point-of-sale systems, RFID scanners etc., to fit models that will be used in many instances to predict or classify in real time (deciding if a credit card transaction seems fraudulent, recommending the right box of chocolates to add to that Bastille Day gift, ...). "Big Data" is driving both demand and salaries [3] for "data scientists" [2] (formerly known as "statisticians"?). It is also motivating developments in software (e.g., Hadoop [7]) and even hardware (purportedly explaining Google's interest in the D-Wave "quantum computer" [4]). The pursuit of "Big Data" has drawn the attention of major players, including IBM Corporation, which defines "Big Data" in terms of "four V's": volume; variety; velocity; and veracity [5]. Lost in the "Big Data" tidal wave, though, are two key questions: need we use all the data; and need we use it all at once?

"Big Data" is not an entirely new concept. Sample sizes and computing capabilities have always been in a race, leapfrogging each other. Until recently, faster CPUs and cheaper and more plentiful memory pushed computing capacity into the lead. The collection of vasts amounts of data on the Internet has now put sample size back in front, at least for the moment. In the past, when we had more data than capacity, we used subsamples and variable reduction techniques (such as principal components analysis or stepwise regression). The tsunami of "Big Data" excitement may be causing us to lose sight of those options.

Why we need to use it all

Common arguments, either implicit or explicit, for the use of more and more data include the following:

- *We are paying to acquire and/or store it, so we should use it.* This seems obvious, but the phrase "escalation of commitment" comes to mind. There may also be an element of framing bias. Does management tend to ask "How will we use this data?" when the question perhaps should be phrased "How much of the data should we use, and how should we use it?" ("Escalation of commitment"? "Framing bias"? Clearly I spent too many years housed with



Paul A. Rubin
is Professor Emeritus of Management Science in the Eli Broad College of Business at Michigan State University. He holds degrees in mathematics (A.B., Princeton University; Ph.D., Michigan State University) and statistics (M.S., Michigan State University). Dr. Rubin's primary research interest is in the application of integer programming models and algorithms. His previous publications have appeared in IIE Transactions, Operations Research, Decision Sciences, European Journal of Operational Research, and various other journals perspicacious enough to accept them.

my school's organizational behavior faculty.)

- *Larger sample sizes yield more accurate predictions and classifications.* There is some truth to this, butperhaps not as much as the forces behind "Big Data" believe. Suppose that we are trying to predict a response variable Y, and let X be a vector of all variables belonging to the union of two sets: those that actually influence/predict Y; and those we believe influence/predict Y (and will include in our model). The response is determined by $Y = f(X) + \varepsilon$, where f gives the conditional mean of Y given X and ε is random noise. We select a functional form (linear, log-linear, . . .) to predict Y. Let $f()$ be the function from that class that best approximates $f()$, and let $\hat{f}()$ be the estimate of $\tilde{f}()$ obtained using our sample data. Prediction error is

$$Y - \hat{f}(X) \quad = \quad (Y - f(X)) + \left(f(X) - \tilde{f}(X)\right) + \left(\tilde{f}(X) - \hat{f}(X)\right)$$

where the first term is ε (the random noise), the second term is model bias and the third term is variously known as training, estimation or sampling error. Cranking up the size of the training sample reduces the training error but has no affect on noise or bias. Thus, as we expand the sample size, prediction error converges asymptotically to a non-zero lower limit.

- *Someone would have to decide what/how much to use.* This should actually not be too difficult; stratified sampling, cluster sampling etc. have been around for years and are well understood. The real difficulty may lie in convincing a non-statistical superior that a data deluge does not translate into omniscience.

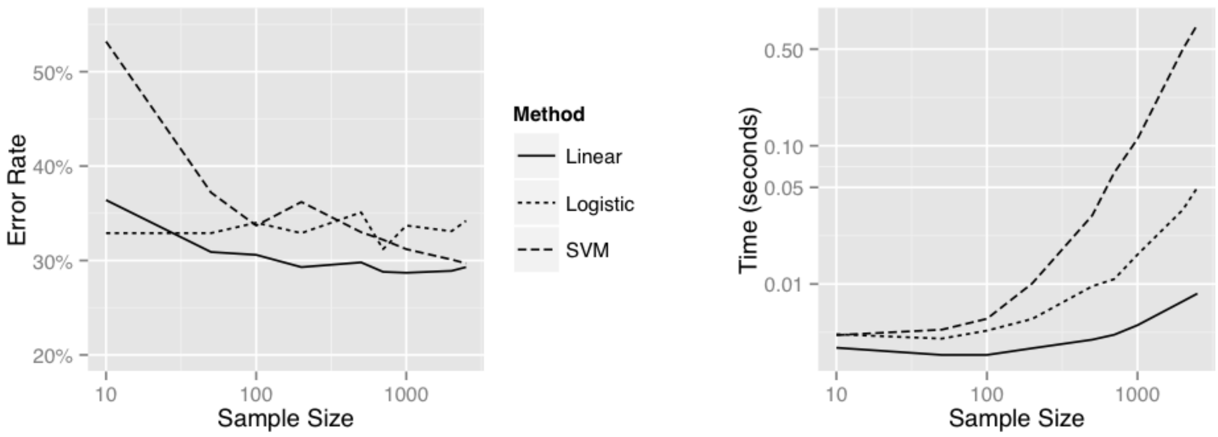
Why we do not need to use it all

Let me counter with some arguments why we might not want to use all available data.

- *Volume competes with velocity*. To adapt to rapidly changing situations, we need to be able to fit (and refit) models rapidly. Processing larger samples takes longer. A good decision arrived at in a timely manner is worth more than a "perfect" decision reached too late to be useful.

- *There is a cost/benefit trade-off*. As noted above, increasing the sample size used in fitting a model reduces prediction error, but prediction error diminishes gradually toward a non-zero asymptote. Figure 1a illustrates this for three classification models: linear regression; logistic regression; and support vector machine (SVM, [11]). I fitted the models to increasingly large samples from a simulated data source (which I coded in R [6]). The data generator deliberately differs from the fitted models in both the formula and predictors used, to simulate model bias, so the asymptotic error rate is not zero. Meanwhile, the time to fit a model (on a 3 GHz, quad-core personal computer) increases at least linearly (and for some model types much faster than linearly) as a function of sample size. Figure 1b demonstrates this, with the support vector machine in particular having rapidly increasing fitting times. (Note that the sample size scale in both halves of Figure 1 and the time scale in Figure 1b are logarithmic.) Regardless of the costs we associate with prediction errors and processing time, sooner or later the marginal gain in prediction error will be outweighed by the marginal pain of processing time.

- *Too much variety can cause strange effects*. For example, John D. Cook points out in a blog post [1] that as the number of correlated features (variables) grows, the projection of the data onto individual features can turn into "a tiny smudge near the origin". Throwing in too many



(a) Classification Accuracy

(b) Estimation Time

Figure 1. Effect of Sample Size

predictors can also result in overfitting [10] and confounding [8].

- *There is a fifth "V": value.* We need to ask whether all the data we amass has actual predictive value. In some cases, this may be a question of the source. Click-through rates for an online advertisement hosted on a site that is slow to load or frequently drops connections may say less about the ad than about the host (see, for instance, [12]). Credit card transactions at a coffee shop (in-person, low value) may not be helpful in detecting fraudulent online transactions.

Why we do not need to use it all

Even if we do use most or all of the data available to us, we may be better off fitting a number of models to smaller subsamples rather than fitting a single model using the entire sample.

- Fitting multiple distinct models to subsamples allows us to easily exploit parallel processing opportunities. Since the fitting operations are essentially independent, there should be minimal coordination and communication required between the controller thread and the threads fitting the models; thus separate models likely will use parallel capacity more efficiently than would a single model fitted to a larger sample.
- "Ensemble" learning methods [9] such as boosting and bagging are designed to combine input from multiple models. Although these often involve fitting different models to the same sample, they can also be used with one or more models fitted to disjoint subsamples.

One concern with using ensemble learners is the time and capacity required to generate predictions or classifications for new observations. If a recommender engine sees a consumer purchasing tax preparation software online, it needs to decide within milliseconds what ancillary purchases to suggest (bookkeeping software? antacid tablets?). Again, parallel processing may make this attractive, or at least less onerous, with each submodel "voting" in a separate processor or thread and a single process combining the votes. In fact, not every submodel need be consulted; we might randomly select one (or a few) of the submodels, evaluate their predictions and combine just those.

Conclusion

Many of us were taught to fit a single model to all available data, or to fit a few competing models to the entire data set and select a winner. Both the volume and the velocity of "Big Data" may require us to reevaluate that approach. Sometimes smaller is better.

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DECISION SCIENCES
JOURNAL OF INNOVATIVE EDUCATION

CALL FOR PAPERS - Special issue on ‘Identifying and Managing Critical Success Factors of Online Education’

Guest Editors: Sean Eom, College of Business, Southeast Missouri State University; and Nicholas J. Ashill, College of Business, American University of Sharjah, United Arab Emirates; and J. B. (Ben) Arbaugh, University of Wisconsin Oshkosh

Motivation and Background

We are entering a golden age of e-learning. E-learning could be at a ‘Tipping Point’ as American’s trust in the quality of e-learning grows, and the number of students who take at least one online course continues to increase. Now is the time to make e-learning more successful. The success of an e-learning system can be measured in terms of learning outcomes and learner satisfaction, two dependent constructs that have been widely accepted in the e- learning literature. Learning outcomes are measured by progress on relevant objectives set by the instructor including progress on gaining factual knowledge, learning fundamental principles, and learning to apply what is learned to improve problem solving. Learner satisfaction is measured by the degree of satisfaction with perceived outcomes of taking online courses, courses, and instructors.

- Review, critical analysis, and/or meta-analysis of past research to evaluate the current state of e-learning and to guide future directions for e-learning development
- Conceptual frameworks for e-learning
- Dimensions of e-learning systems
  - Human dimension
    - Students: Self-Motivation, Personality, Learning Styles
    - Instructors as Facilitators, Motivators, Moderators
  - Design dimension
    - Learning models (Objectivism, Constructivism, Collaborativism, Cognitive information processing, Socioculturalism)
    - Course content, structure, and infrastructure
  - Learning Management systems and Information technology
    - Technology platforms and tools
    - Security considerations
    - Collaborative meetings and discussion tools
    - Student-created instructional materials
  - Learner control and self-regulated e-learning
    - Problem based learning
    - Self-directed learning
- Impact of interactions on e-learning outcomes
  - Instructor-student
  - Student-student
  - Student-content/learning management system
- Learning outcomes and learner satisfaction
  - Development and validation of measurement instruments

Review Process and Deadlines

Manuscripts for the special issue should be submitted after the authors have carefully reviewed DSJIE’s submission guidelines at http://dsjie.org/JournalMission/tabid/84/Default.aspx. Authors submitting a manuscript should indicate that it is for the special issue on ‘Identifying and Managing Critical Success Factors of Online Education’.

Deadlines for the special issue are as follows:

June 15, 2015: Submission deadline for initial submission

September 1, 2015: First-round decisions on all submitted manuscripts

November 1, 2015: Submission deadline for invited revisions

December 15, 2015: Final decisions

For more information, please contact the editor (dsjie.editor@gmail.com). ■

DSI Celebrates First Year Anniversary at University of Houston

It is with great pleasure that the home office announce our 1st year anniversary at the University of Houston! On behalf of the Executive Committee and the Home Office Staff, we would like to thank Dean Latha Ramchand, C.T. Bauer College of Business, for her generosity, support, and hospitality over the past year.

It was not an easy task moving the DSI home office from Georgia State University to the University of Houston, but with the dedication and support of the C.T. Bauer College of Business, the partnership has proven to be a very successful venture with many accomplishments.

To celebrate the first official year, President Marc Schniederjans and the Executive Committee presented an official token of appreciation to the Dean during the executive meeting on Friday, March 6th, 2015. We plan to keep our institute and relationship growing with UH, and continue to provide our membership nothing less than the best.

With your support and leadership, we will continue to explore new heights this year. ■

From left: President Schniederjans, Dean Ramchand, President Elect Swink, and Immediate Past President Ebrahimpour

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From PRESIDENT'S LETTER, page 1

(and her staff) the DSI Home Office not only completed the move from Atlanta but now offers a variety of new social media services it has never offered the membership.

- The DSI Board approved the launch of a new DSJ: Supply Chain Management journal to augment our other fine publications. Wiley, our publisher has confirmed their support for the new journal and Ken Boyer is heading up a committee to search for the new editor.
- The DSI Board approved the creation of a college structure that will help improve membership networking. Three colleges where initially approved with themes including supply chain and operations management, information technology/information systems, and business analytics/quantitative methods. More colleges will be added as we grow into a more diverse organization.
- Under the leadership of 'Jon Jasperson and Home Office staff the NOAH information system has substantially been implemented this year to begin providing select services to support Institute and Regional meetings in 2015. Further advances in information support are planned as new informational needs are identified.

The Board has been busy on many fronts this year doing our best to bring DSI around from a state of decline to a growth oriented organization. We have had to change some traditions and people's attitudes to look at not where we were but where we are going. This is a future-oriented organization, it is DSI 2.0.

Best wishes all,

Marc J. Schniederjans
President, Decision Sciences Institute ■

Putting on the Best Job Talk You Can: Guidelines and Tips for Doctoral Students

by Varun Grover, Ph.D., Clemson University

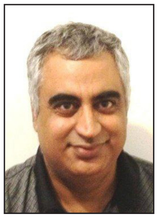
You just got the email. You have a campus visit. Of course, you are relieved – since this means that you might actually get the job. From the dozen preliminary interviews, at least one school shortlisted you into the list for their campus visit. Once the initial excitement is over, you have some apprehension. The campus visit is a different ball game. Questions run through your mind. Will they like me? Will I blow my job talk? What if I make a fool of myself? What if I can't answer their questions? Your biggest apprehension however is regarding the job talk. You know how this talk can make or break your visit. "Nail the job talk and you will nail the job" – is something you have repeatedly heard and observed at your school.

So, how should you deal with the job talk? Let's divide the talk into three stages and assess what needs to be done for each stage. The first is "preparation." The second is the "actual presentation." Finally, we have "the questions." Of course, depending on your chosen format, questions could be interspersed with the talk itself. Each stage can have its own set of guidelines and tips, but unequivocally the *preparation* stage is the most critical, as it sets you up for the other stages.

Preparation

As a doctoral student, an ongoing preparation for the job talk is getting familiar with the format, and atmosphere of a job talk, as well as the considerations for a good research presentation. Hopefully, for the latter, you have attended research presentations at your institution as well as presentations art conferences. In attending these, you have made mental notes of what a good presentation looks like. If you have presented your research at your school and/or at a conference, hopefully you received some feedback and you have a sense of where your presentation strengths and weaknesses are. Sometimes, despite sitting through innumerable presentations, you focus so much on the content, that you miss out on noting what the presenter is doing to present well. So, make a point to jot down notes on research presentations you see. Observe successful tactics. Observe dynamics with the audience. See whether there are things that you can adopt – keeping in mind that presentation tactics could be idiosyncratic. What might work for one person may not work for another. So, separating the general tactics and idiosyncratic ones may be useful. For instance, a speaker may ask the audience to hold questions until after the talk. You might feel that is a good general tactic that would help maintain the flow and timing of the presentation. On the other hand, a speaker might make his slides quite animated, with new things jumping in at every click. You might feel that this particular tactic would not work for you, as you like to view things holistically and then systematically go through them.

Getting familiar with the format and atmosphere of a job talk requires that you attend them at your institution. Here too, you will observe what works and what does not. You will see how candidates dress, the confidence they exude, the way they handle questions, the audience reac-



Varun Grover *is the William S. Lee (Duke Energy) Distinguished Professor of Information Systems at Clemson University. He has published extensively in the information systems field, with over 200 publications in major refereed journals. Ten recent articles have ranked him among the top four researchers based on number of publications in the top Information Systems journals, as well as citation impact. His h-index is 68 and he has over 20,000 citations to his work. Dr. Grover is Senior Editor (Emeritus) for MIS Quarterly, the Journal of the AIS and Database. He is recipient of numerous awards from USC, Clemson, AIS, DSI, Anbar, PriceWaterhouse, etc. for his research and teaching, and is a Fellow of the Association for Information Systems. For over 20 years, Dr. Grover has been fortunate to be integrally involved with doctoral students in various capacities. He has written a number of articles in Decision Line based on his experiences.*

tion to stylistic elements, and how they navigate out of difficult situations. Observe keenly, and presume that you will be faced with a similar environment and format – typically around 1.5 hours in a room with faculty and possibly doctoral students as your audience.

The most important preparation you can do is to set up your slide deck and get feedback from faculty. Then, practice, practice, and practice. Try to present to various audiences – your mirror, your family and friends, your fellow doctoral students, your advisor, other faculty, etc. Take their feedback seriously and adjust. As well as helping you fine-tune the content, this is an opportunity to rehearse your presentation tactics. Practice taking questions throughout or asking for questions to be held till the end. In both cases be cognizant of timing. It would reflect poor form if you set aside time for questions, but you leave no time and were forced to rush through the back-end of the presentation.

In general, it is better to know the content of your research well, and not refer to notes. This requires you to be comfortable with the research. Go through each slide in your deck and envision questions that could be asked. Be prepared for common questions – In what way does your dissertation contribute to the field? If you were to do it all over again, what would you do differently? In which journals do you expect to publish your research? What research related to your dissertation do you see yourself doing 5 years from now?

Just before you leave for the campus visit, do not hesitate to ask your contact about the talk – the room, the equipment (i.e., do you need to bring a laptop or just a memory stick), the duration, and the audience. Hopefully, you will have enough time to set-up your slides and get comfortable with the room and equipment just before the talk. And turn off your phone (not vibrate) before you start the presentation!

Actual Presentation

It is natural to be a bit nervous before the actual presentation. Nerves (within limitations) can be good to keep you alert and at the top of your game. However, keep in mind that no one in that room has invested as much time in understanding and contextualizing your research – so you are the expert!

It is usually good practice to start the talk by thanking your host institution and your key contact person. Some people like to lighten the mood by starting off with something humorous. That is fine, but limit the humor in the presentation – and avoid any humor that might be viewed as controversial (e,g., humor that requires a certain world view to appreciate).

Some general heuristics to keep in mind for a good presentation:

- The best kinds of research presentations are those that appear to be simple, but it is obvious that a lot of work and thought has gone into them.
- Slides in general should not be cluttered, should be easily readable and should make no more than three key points.
- Frame your entire presentation by providing a (i) Roadmap of the presentation, (ii) a Roadmap of your Research Program (beyond the presentation), and (ii) a Roadmap (timeline) of your Completion.
- It's usually good practice to be a bit redundant in order to reemphasize key points. Colloquially, "tell 'em what you're gonna tell 'em, tell 'em, then tell 'em what you told 'em."
- Pitch the presentation at a high level, but remember that many in the room may not be in your area, and so too much jargon without simple explanations may turn them off.
- Be engaging – use illustrations and examples when getting into complex concepts to explain your point.
- If you start strong, try to maintain the energy throughout the presentation. Be aware of whether you are "fading out" toward the end.
- Set up a time management system – perhaps your cell phone or computer clock can be noted at certain slides to see whether you are sticking to your schedule.

Job Talk Preparation Checklist

☐ Have you attended other research job talks?

☐ Do you generally note tactics in presentations that work well?

☐ Have you made research presentations? Have you obtained feedback on your own presentation skills?

☐ Are you very comfortable with your dissertation? Do you know the key literature around your dissertation well?

☐ Is your slide deck well organized, not cluttered and systematically evolves as a story?

☐ Do you have contingency slides for certain details?

☐ Have you obtained feedback to hone your slide deck?

☐ Have you repeatedly practiced your presentation in front of different audiences?

☐ Do you have a system to manage the timing of your presentation?

☐ Have you worked on common and specific questions related to your research?

☐ Have you contacted the institution regarding audience, equipment, etc.?

- Do not make disparaging comments about a method or a theory. You never know who in that room might be deeply invested in the object of your disparagement.

You can close your presentation by thanking your audience and opening up the floor. Consider having your research model on the screen if you would like to encourage questions about your dissertation, or a summative slide (e.g., your research program) on the screen to encourage broader questions.

The Questions

Questions offer the interviewing institution the opportunity to assess your competence and ability to think on your feet. The whole presentation experience also serves as a demonstration of your ability to teach in the classroom and respond to student questions.

Even if you have taken questions throughout, after you have finished your talk, it is usual to open up the floor to questions. There may be many hands that go up. It is usually good practice to take questions from faculty first over graduate students (assuming you can distinguish between the two). It is perfectly acceptable to take a few seconds to understand the question before responding – or even to ask for clarification. If the question asks for justification of what you have done – the best response would include a rationale as well as citations of others that have followed the same approach. If the question deals with your lack of consideration of some factors in your model – again the rationale and boundary conditions for your model can be described. Be sensitive to methodological questions – and try to have detailed slides on things you did (e.g., testing of assumptions for statistical tests; validity and reliability analysis for constructs) that you can readily display if the question is brought up. Finally, if you are truly stumped with a question – do not pretend to know or try to obfuscate the issue by throwing out complex concepts. Just say that you do not know – but are curious to learn more.

Phew, it's finally over and you have received the ceremonial applause. Now you can relax and (try to) enjoy the remainder of the interview process. With one real job talk under your belt, the next one should be a bit easier….. ■

From RESEARCH OPPORTUNITIES, page 7

misfolding: the examples of Alzheimer's and Parkinson's diseases." Nature cell biology **6**(11): 1054-1061.

Shi, X., et al. (2011). "A sampling-based method for ranking protein structural models by integrating multiple scores and features." Current Protein and Peptide Science **12**(6): 540-548.

Wang, Z., et al. (2009). "Evaluating the absolute quality of a single protein model using structural features and support vector machines." Proteins: Structure, Function, and Bioinformatics **75**(3): 638-647. ■

From CALCULATING LAST DATES, page 20

```
' Ask user for the row that contains headers
header_msg1 = “Macro will enter a header called Last Scored”
header_msg2 = “in header row.  Enter header row number.”
header_row = InputBox(header_msg1 & header_msg2, “Header Row”)
If col_start = “” Or header_row = “” Or row_start = “” Then
    MsgBox (“One of the required entries is blank.  Try Again”)
  Exit Sub
End If
no_of_col = Cells(header_row, Columns.Count).End(xlToLeft).Column
' Enter a header for the last date scored
Cells(header_row, no_of_col + 1) = “Last Scored”
' Get the last date column from the first row
date_col = Cells(1, Columns.Count).End(xlToLeft).Column
' Loop through the rows and columns obtaining dates for any score > 0
For i = row_start To last_row
' Reset array size based on number of date columns. Also serves to erase previous array values
  ReDim date_array(date_col - col_start)
' Loop through columns in a given row
    For j = col_start To date_col
' Enter date in row 1 for any score > 0, otherwise enter the beginning semester date
        If Cells(i, j).Value > 0 Then
          date_array(j - col_start) = Cells(1, j).Value
        Else
          date_array(j - col_start) = Cells(1, 1).Value
       End If
    Next j
' Use the max function to obtain the last date scored
  last_date = Application.Max(date_array())
' Enter the last date scored in its proper column, format as short date
  With Cells(i, no_of_col + 1)
   .Value = last_date
   .NumberFormat = “m/d/yyyy”
  End With
Next i
End Sub
```

References

Office of the Registrar. (2012). *Monitoring Enrollment*. Western Michigan Univesity.

The College Board. (2014). *Trends in Student Aid*. Retrieved December 15, 2014, from Trends in Higher Education: http://trends.collegeboard.org/student-aid

University of Oregon Office of the Registrar. (2014). L*ast Date of Attendance/Participation*. Retrieved December 15, 2014, from University of Oregon: http://registrar.uoregon.edu/faculty_staff/last-date-of-attendance ■

Calculating Last Dates of Attendance in Large Lecture Classes

by Thomas F. Rienzo, Ph. D, Western Michigan University

Colleges and universities administering Title IV financial aid from the US Department of Education must document student participation in courses in which students receive Title IV funds. These funds comprise most of the financial aid offered to higher education by the federal government, and the amounts are substantial. In 2013 Federal aid to colleges and universities exceeded $170 million (The College Board, 2014). Students must enroll in courses to be eligible for Title IV money and those who do not remain enrolled in courses, or fail courses, are evaluated for repayment of all or a portion of the grants and loans they receive on a prorated basis (Office of the Registrar, 2012). Date of last attendance in courses is a factor in repayment decisions, and has become an important record for many college administrators (University of Oregon Office of the Registrar, 2014).

Determining accurate last dates of attendance (LDA) in large lecture classes can be a formidable task. Many course management systems do not have embedded processes to determine LDA, and manually checking hundreds of students to ascertain LDA is so time consuming that it becomes impractical. Assessment of LDA in large classes becomes realistic with the establishment of: (1) a spreadsheet process that calculates LDA for individual students and (2) automation of that process to make it scalable for very large classes. A suitable spreadsheet format and associated macro are presented in this article. Attendance is often not taken in large lecture classes so an alternative indicator must be measured that indicates student engagement in courses, and is readily accessible in course management systems. Tracking grades in course assignments, quizzes, and exams satisfies both conditions, and can be an effective alternative for student attendance in courses.

Scaling with Automation

One advantage of an automated process is that it can be applied to hundreds, or even thousands of students. The ability to scale means that an LDA process does not have to concern itself only with students who must be evaluated with respect to Title IV funds. It can be applied to everyone, so at reporting time, most recent dates of engagement are available for everyone in the class. Here are the steps necessary to create an automated LDA macro in Microsoft Excel:

1. Establish a format for student records that contains all students, all graded course activities, and dates for all graded assignments.
2. Evaluate all graded activities for all students, capturing activity dates in arrays for all that have scores.
3. Calculate the last (most recent) date involving scored activities for each student.
4. Display the date of the most recent graded activity in a spreadsheet field or report.

Format Student Records

LDA measurements require student identifiers, assignment dates, and graded scores assembled in rows and columns of a spreadsheet. Large courses usually have more students than assignments, so entering students in rows and assignments/

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Homepage
http://homepages.wmich.edu/~trienzo

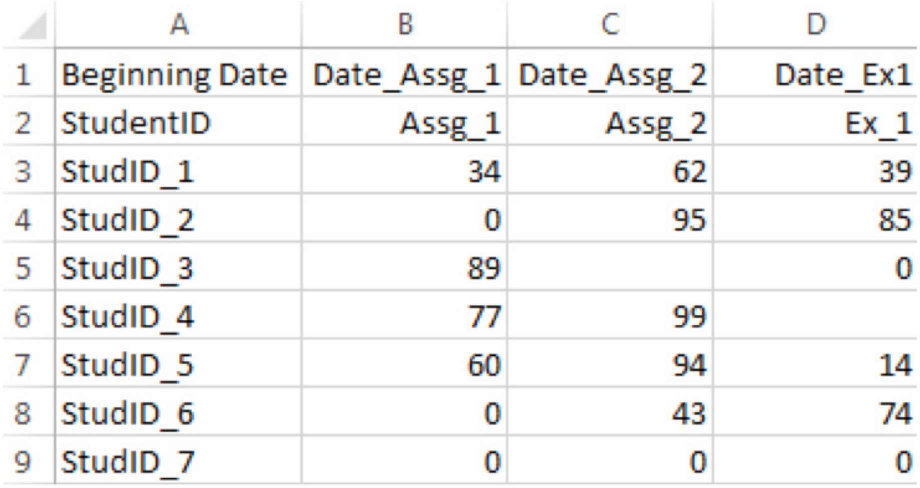
dates in columns is likely the most efficient way to arrange the data. A suitable format to prepare for automated listing of LDA is shown in Table 1.

Dates for assignments, quizzes, or exams are displayed in the first row, just above student scores. The first date in the first row (cell A1) reflects the beginning of the semester, and is not associated with any graded activity. Students who do not have any scores, or scores no greater than zero in all graded activities will show the beginning of the semester as their LDA.

There is no need to begin graded assignments in the second column. Any number of columns with student information can precede the grid of scored class assignments, but assignments, exams, and quizzes should be grouped together as shown in Table 1 (columns B, C, and D). The number of assignments, quizzes, or exams available for analysis is limited only by the number of spreadsheet columns. In Excel that limit is above 16000. The author regularly calculates LDA with 80 to 90 individually graded clicker questions, and more than 110 graded activities in a semester. Student enrollment typically exceeds 450 per semester.

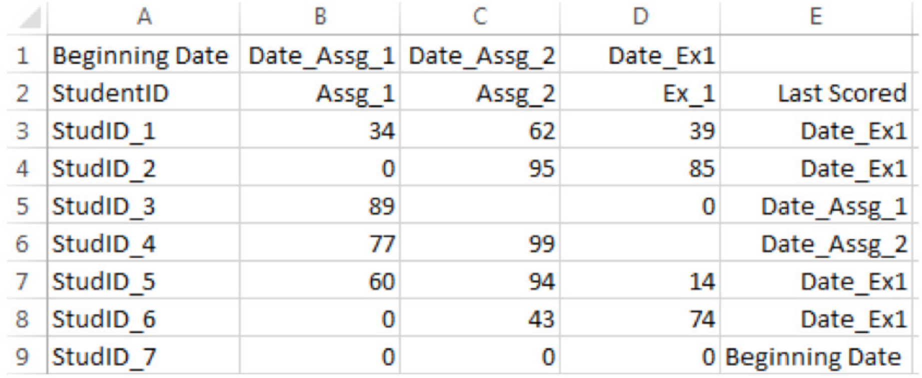
There are two items of caution concerning spreadsheet configuration:

1. Calculation of LDA based on grades means that instructors should use global grading capabilities of course management systems with care. Applying a score to an entire class will produce an attendance date for everyone on the day of the globally graded course activity whether or not students actually engaged with the activity.
2. Scored activity dates must be on the first row of the spreadsheet, and the beginning semester date must be in the first column of the first row.



	A	B	C	D
1	Beginning Date	Date_Assg_1	Date_Assg_2	Date_Ex1
2	StudentID	Assg_1	Assg_2	Ex_1
3	StudID_1	34	62	39
4	StudID_2	0	95	85
5	StudID_3	89		0
6	StudID_4	77	99	
7	StudID_5	60	94	14
8	StudID_6	0	43	74
9	StudID_7	0	0	0

Table 1. Spreadsheet Format of Student IDs, Scores, and Assignment Dates



	A	B	C	D	E
1	Beginning Date	Date_Assg_1	Date_Assg_2	Date_Ex1	
2	StudentID	Assg_1	Assg_2	Ex_1	Last Scored
3	StudID_1	34	62	39	Date_Ex1
4	StudID_2	0	95	85	Date_Ex1
5	StudID_3	89		0	Date_Assg_1
6	StudID_4	77	99		Date_Assg_2
7	StudID_5	60	94	14	Date_Ex1
8	StudID_6	0	43	74	Date_Ex1
9	StudID_7	0	0	0	Beginning Date

Table 2. Spreadsheet after LDA Macro

Capture Dates for all Graded Activities with Scores above Zero

Date capture for all graded activities is the heart of LDA determination. A date array is declared in the macro and each element of the array receives a date value for each scored column in a given row. The date value is the date shown at the top of the column when each score is evaluated, assuming the score is greater than zero. If the score is not greater than zero, the value of the array element is the first date of the semester. For example, the values of the first three date array elements when examining Stud_ID3 (row 5) in Table 1 would be Date_Assg_1, Beginning Date, and Beginning Date since only the first assignment has a score above zero. For Stud_ID6 (row 8) the value of the first three date array elements would be Beginning Date, Date_Assg_2, and Date_Ex1. The date array hold dates for every scored activity, row by row.

Calculate the Latest Date

The latest (most recent) date is calculated through the spreadsheet application max function. The highest date numbers are the most recent.

Display the Last Date of Attendance

In each row, the calculated last date of a submission with a score greater than zero (LDA) is entered in the column to the right of the scoring grid. Values of the date array are cleared before a new row (new student) is evaluated. Macro output is shown in Table 2.

A flowchart for the Excel macro calculating LDA and inserting it in the last column of each student row is shown in Figure 1. The program obtains the worksheet row and column where grades first appear, as well as the proper row to enter a header designating LDA. Excel formulae determine the number of rows to evaluate and the column that will receive the LDA list. Each cell with a score is examined, and an appropriate date is placed in a corresponding date array element. Code assumes dates are listed in the first row. There are two loops in the program. The first captures all rows (students) in the course, and the second moves through all graded columns in a given row (assignments). As the column loop is completed, a max function calculates the highest (most recent) date, and that date is entered in the column immediately following the scoring grid.

Benefits of Spreadsheet Automation of LDA

The spreadsheet macro can be used with all course management systems since all systems can export a grid of students and activity scores suitable for spreadsheet import. The automated spreadsheet is also versatile. Variables and functions permit the user to declare the first column of the scoring grid, and the first row with student scores. Those variables are used in calculations to determine numbers of rows and columns needed to encompass all students and all scores. Declaring the user supplied data as variant data types in the macro allows them to accept empty spaces as well as numbers, which provides a path to exit the macro if the user cancels an input box. Canceling an input box inserts a null string into the variable associated with it.

The scalability of the macro allows it to work with any number of students and any number of graded activities. Re-dimensioning the date array insures the proper number of elements, and clears date array values at the start of each new row. Creation of an LDA column as the right-most column in the worksheet means letter grades can be computed just before listing LDA, producing a convenient format for reporting.

The complete Excel Macro, with comments, follows. It can be typed into an Excel module creating the macro *FindLastDate*. The macro can then be run through the Developer ribbon in Excel.

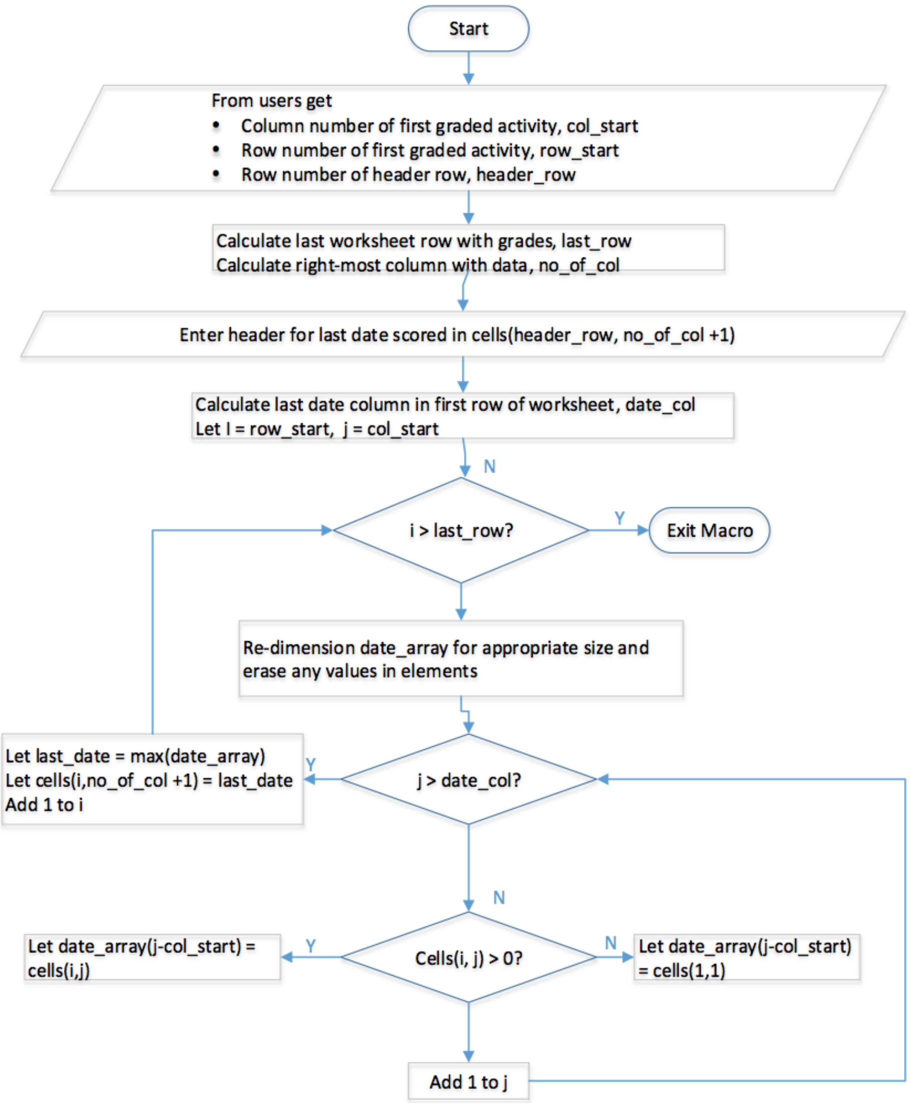


Figure 1. Flowchart for LDA Calculation

Excel Macro FindLastDate

```
Option Explicit

Dim i, j, last_row, no_of_col, date_col As Integer

Dim col_start, row_start, header_row As Variant

Dim last_date, date_array() As Long

Dim header_msg1, header_msg2 As String

‘ This macro will enter the last date in which a student received a score for an assignment.

‘ First line must contain dates for assignments.

‘ First column of first line should contain a date for the beginning of the semester.

‘ Macro gets the last row involved in calculations from the first column

‘ If there are no scores > 0, the beginning semester date is entered.

Sub FindLastDate()

‘ Ask user to enter column in which grades first appear. Macro determines last occupied row in the first column.

col_start = InputBox(“Enter the column number of the first dated assignment in the worksheet”, “First dated column”, 2)

last_row = Cells(Rows.Count, 1).End(xlUp).Row

‘ Ask user to enter row in which grades first appear.

row_start = InputBox(“Enter the row number of the first scored.”, “First row scored”, 3)
```

See CALCULATING LAST DATES, page 17

Carol J. Latta Memorial DSI Emerging Leadership Award for Outstanding Early Career Scholar

The **Carol J. Latta Memorial DSI Emerging Leadership Award for Outstanding Early Career Scholarship** will be awarded annually at the DSI Annual Meeting to an early career scholar in the Decision Sciences field who has served the Institute and its goals. The recipient will receive a plaque and a token financial award, which is funded by DSI and the Carol J. Latta Memorial Fund.

To be eligible for consideration, the applicant must be nominated by a faculty member or academic administrator. Nominators must submit a nomination letter describing the basis for the recommendation along with the candidate's curriculum vita. Recommendations may be sent electronically to info@decisionsciences.org with Carol Latta Memorial Award in the subject line. Paper nominations may be sent to:

Carol Latta Memorial Award, Decision Sciences Institute, ATTN: Ms. Dana Evans, C.T. Bauer College of Business, 334 Melcher Hall, Suite 325, Houston, Texas 77204-6021. All nominations must be received by October 19, 2015.

Award Criteria

This award shall go to an emerging scholar in the decision sciences disciplines who has earned his or her terminal degree (e.g. PhD, DBA, etc.) in the previous five (5) years. Evidence of excellence in research, teaching, and/or service to DSI may be provided as an appendix to the recommendation letter (limited to five pages, Please do not include full journal articles.). Such evidence may include documentation regarding Institute-related professional service (DSI committees, reviewing, session chair, track chair, etc.), teaching performance (teaching award, new course development, etc.), and scholarly research (publications in Decision Sciences, Decision Sciences Journal of Innovative Education, and other highly-regarded journals in the decision sciences field and presentations at DSI meetings). The awardee must be a member of the Institute in good standing.

Please share this email with your junior faculty members and consider their recommendation. ■

From 2015 ANNUAL MEETING COORDINATORS, page 10

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INSTITUTE CALENDAR

■ MARCH 2015

March 20 - 22

The **2015 Annual Meeting of the Northeastern DSI Region will be held in Cambridge, MA**

March 31 - April 3

The **45th Annual meeting for WDSI will be held in Lahaina, Hawaii** at the Westin Maui Resort and Spa

■ OCTOBER 2015

October 25

All papers and proposals must be submitted electronically on or before this date for the 2015 NEDSI conference in March

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November 21 - 24

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