Writing Samples

Adrienne Sabilia

A new method for materials simulation

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The ability to predict the properties of materials before they are fabricated, or to explore their behavior under conditions which are impractical to replicate under laboratory conditions (eg extreme temperatures

or pressures) is critical for next generation materials design. Improving the predictive power of materials modelling guides planning and design, saves money, and can accelerate discovery.

Unlike the conventional “ball and stick” picture, the electrons within molecules are mobile; they fluctuate, redistribute themselves and are distorted by their complex environments. This behavior leads to a wide range of interactions, such as electron fluctuations (polarization) and charge distortion (dispersion) which influence how matter behaves. A good way of handling these effects, (incorporating quantum mechanical effects), without prohibitive computational expense, hasn’t yet been developed. As a result, these effects are normally neglected in conventional simulations of materials, and predictive power is limited as a result.

As an added problem, simulating molecules is even more difficult when dealing with outside influences, such as when the molecule is in a solution, encapsulated (such as when used to aid drug delivery), tagged with other molecules, or in contact with a cell surface. Coping with such a wide range of conditions presents fundamental challenges for current methodologies which tend to be designed to cope with a single, average, environment rather than adapt to changing circumstances.

IBM researchers, in conjunction with the Hartree Centre have developed a fundamentally new strategy for capturing these electronic effects in molecules, which can predict the weird properties of water – from the freezing point to the critical point (when water’s liquid and vapor states can coexist) and beyond. The approach – called “electronic coarse graining” – represents the electron cloud bound to a molecule as a single charged object tethered to the molecular frame by a spring. The simplicity of the “electronic coarse graining” approach captures the full spectrum of intermolecular forces, including those that arise from dispersion and polarization, which are typically not included in conventional models.

A particularly challenging and important area for this type of research is in the life sciences and biotechnology space, where the development pipeline for new drugs and compounds is often long and costly – and molecular-level insight is priceless. Here, it is essential to understand the structure and simulations of elements at the molecular scale in a variety of complex and changing environments, as the molecular structure of drug design is critical to their effectiveness.

This work lays the foundation for much more predictive, and reliable materials modelling involving fewer assumptions, and taking into account a much more complete set of molecular forces. The method will be extended first in life sciences and simple biomolecules and eventually on to short proteins and self-assembling structures. All of these circumstances are relevant to the drug discovery cycle from early design concepts, understanding mode of action at the molecular scale, through to the development of a new medicine.

Brainiacs: Applying Watson for Genomics to better understand brain tumors

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This spring I was invited to a global meeting about cancer research – how tumor data should be gathered, integrated and interpreted. It brought together specialists from medicine, biology, chemistry, mathematics and computer science for an extensive multi-disciplinary exploration. On the long trans-Atlantic flight back, to distract myself, I casually pulled out a movie from the in-flight entertainment with an intriguing title, "Collateral Beauty." To my great surprise, the movie touched on cancer- it was about the devastating effect on the hapless family of a glioblastoma multiforme (GBM) victim. A gut-wrenching account.

GBM strikes indiscriminately and more frequently than one would imagine[1]. About a hundred thousand cases of brain tumors are diagnosed a year in the US, and a quarter of these are gliomas, or tumors of the supportive tissue of the brain. They account for 75 percent of all malignant tumors, and nearly 50 percent of the gliomas are GBMs. GBMs are usually highly malignant and grow aggressively, invading surrounding tissues. Our team in IBM Research set out to explore the potential for applying machine learning and data science to better understand and predict this disease.

Researchers prepare tissue samples for whole genome sequencing at The Rockefeller University, where clinical researcher Robert Darnell, MD, PhD, led a study with the New York Genome Center and IBM to analyze complex genomic data from state-of-the-art DNA sequencing of whole genomes. The findings were published in the July 11, 2017 issue of Neurology® Genetics, an official journal of the American Academy of Neurology. (Photo Credit: Epic Creative)

Would analyzing more genes give us a more complete view of the patient? In this case, is more really 'more'? That's the question we investigated in our paper published in *Neurology Genetics* this month: one of the results of our collaborative effort with New York Genome Center and other specialists [2]. Current commercially available genomic testing (called "assays") target a small panel of a patient's genes. We extended this analysis to a patient's entire genome, as well as other omic-assays, such as proteomics (the study of proteins) that included whole genome expression (i.e., RNA or ribonucleic acid) data. We found that this indeed results in identifying more variants of their individual genome that can be potentially targeted for therapy by an oncologist.

Next we asked, does a machine-based (algorithm) analysis of this multi-modal, whole genome data hold a candle to a crack team of human bioinformaticians and cancer oncologists, in terms of accuracy and quality of analytics? We used a research version of Watson for Genomics at the time and demonstrated that it does! It was able to cut the time for accurate genomic data interpretation from 160 expert human hours to 10 minutes, opening the door for the possibility of scaling this highly specialized analytics.

Currently we are extending this work to a larger set of GBM patients and extending to other cancers, while we continuously improve the underpinning algorithms. Now we are also setting our sights on

understanding the genomic basis of other complex phenomena such as resistance and response to therapy and immunotherapy.

Monitoring Parkinson's disease with sensors and analytics to improve clinical trials

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One year ago, IBM and Pfizer announced a partnership, Project BlueSky, aiming to develop a system to improve how clinical trials are conducted for Parkinson's disease (PD) drugs in development. Over the last 12 months, the interdisciplinary team from both companies has made great strides in building and deploying new technology to automatically assess the symptoms of PD using sensors and analytics.

PD is a neurodegenerative disease affecting over a million people in the United States and which has rapidly growing social and economic impacts [1]. Bradykinesia (slowness of movement), rigidity (stiffness and resistance to passive movement), tremor, and gait and balance difficulties are all symptoms of the disease's impact on the body. There is no cure, and treatment is based on managing symptoms, primarily, but not exclusively, in the form of dopamine replacement.

The current evaluative process for PD is "episodic assessment," requiring the patient to come to a clinic and be tested on the Movement Disorder Society's Unified Parkinson's Disease Rating Scale (or MDS-UPDRS3). The exam includes the biases of both the examiner and subject (e.g., subject may perform up 30 percent better in clinic compared to the home setting [2].

The goal of the BlueSky project is to develop a system to passively capture data from people with PD continuously in their daily life. This data collection would provide a real-time estimate of their motor function that is analogous to scores obtained during a standard neurological exam. Other systems have been developed elsewhere based on sensors or mobile technologies, but the work has mainly focused on prompting subjects to perform scripted tasks, an aspect that repeatedly burdens patients and reduces compliance.

The team has already evaluated numerous types of sensors/devices, selected a few models for

evaluation and conducted a study in healthy volunteers. Healthy volunteers were studied first both to provide baseline data and to harden and refine the technology before assessing it on PD subject.
To evaluate the new technologies, the team outfitted two facilities in the IBM T.J. Watson Research Center and in Pfizer's Andover research facility. Healthy volunteers were recruited from a pool of employees at both IBM and Pfizer sites. Volunteers participated in two one-hour sessions of performing tasks based on standardized neurological exams; replicating normal activities of daily living (ADLs), such as dressing, eating and opening doors.
Our data collection process is administered by a trained examiner, and the subject's performance is scored on the MDS-UPDRS3, a battery of motor tasks designed to isolate and assess the four principal motor signs of PD. The tasks include walking, sitting, reaching, and repetitive finger and foot tapping.
The team is working under the hypothesis that complex human movement in everyday life can be broken down into movement primitives that can be mapped to the different tasks of the MDS-UPDRS3 test. For example, one primitive is "pronation and supination", which can be described as rotation of the wrist and forearm from a position with the palm facing down to a position with palm facing up. This movement will occur in ADLs such as turning a door knob, twisting off a bottle cap, and buttoning a shirt. When detected in ADLs, the quality of these movement primitives can then be scored to produce a continuous, dynamic assessment of the motor function of the patient.
Towards this goal, the team developed a system for integrating and analyzing multiple streams of sensor data collected from the study volunteers executing MDS-UPDRS3 exam tasks and scripted ADLs. In this work, the team has already demonstrated that the data collected from MDS-UPDRS3 tasks can be used to train machine learning classifiers to automatically identify movement primitives as the human subjects perform the scripted ADLs.
The ultimate outcome of the work will be a system that can be deployed to several hundred PD subjects in a phase 3 clinical trial. Our aim is that the system we build should provide a continuous assessment of a patient with minimal impact to their lives. This goal of continuous monitoring aligns with overall goals in the field toward personalized, closed-loop medicine. While initial efforts of the BlueSky focus on PD, the hope is that similar technologies can be employed to other diseases in the future.
Spotting Diabetic Retinopathy by analyzing medical images pixel by pixel
View this post online: https://www.ibm.com/blogs/research/2017/04/spotting-diabetic-retinopathy/
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Medical images are a rich source of data for clinicians in their diagnosis and treatment of diseases. In fact, specialized fundus photography can help pinpoint tiny pathologies in the eyes of diabetics, revealing signs of diabetic retinopathy (DR), one of the world's leading causes of blindness.
In the vast majority of these cases, early detection is the key to a patient's survival and treatment outcome. Yet it is estimated that half of Australians with diabetes do not undergo the recommended frequency of screening. even though early intervention can reduce the risk of blindness by 95 percent (CERA). And this is not only a challenge in Australia. Eighty percent of blindness worldwide is preventable if detected and treated early (WHO).
A new vision for preventable blindness
While education is a major part of encouraging regular screening, ensuring easy access for all Australians is also a key factor. Picking up subtle signs of DR in images is often a manual and subjective process for clinicians. Accuracy of the diagnosis heavily depends on their level of expertise, which can be hard to come by, particularly in rural or remote communities. We believe we can help with this challenge.
Scientists at IBM Research-Australia are studying how new cognitive technologies could support clinicians in streamlining their analysis of images, as well as enable greater access to health services for everyone, regardless of their location.
Last week, my team and I presented new research findings at the 2017 IEEE International Symposium on Biomedical Imaging (ISBI), using deep learning and visual analytics technology for the early detection of DR.
Our new method uses deep learning algorithms combined with pathology insights to analyze real-world images of both the left and right eyes of patients from datasets collected by EyePACS. The key to identifying DR is looking for tiny signs of hemorrhages and micro-aneurysms, which signal to a doctor the presence and severity of the disease. The algorithm analyzes images pixel by pixel and patch by patch and, based on the visual characteristics, learns patterns associated with a particular pathology and disease. It takes a lot of training and feedback for the algorithms to identify, for example, mild diabetic retinopathy vs. moderate, but they get better over time as they're trained on more samples.
The number of pathologies and where they are distributed in the eye informs the clinician of the severity

level of the disease. At ISBI, we presented a novel method for classifying severity across the five levels of the international scale for DR: none, mild, moderate, severe and proliferative.
Our technology combines two various analytics approaches into one hybrid method, wherein a convolutional neural networks (CNN)-based method for DR classification is integrated with a dictionary-based learning that incorporates DR-specific pathologies. This hybrid analysis resulted in a great improvement in classification accuracy[1]. Our method takes approximately twenty seconds to analyze the image and achieves an accuracy score of 86 percent in classifying the disease across the five severity levels.
We also showed a new method for the accurate segmentation of the fovea in retinal color fundus images. Fovea is responsible for sharp central vision. Location of retina lesions and pathologies with respect to the fovea impacts their clinical relevance. Our technology allows for a pixel-wise segmentation of the fovea. It does not require prior knowledge of the location of other retinal structures such as optic disc or retina vasculature. This is an advantage over other published methods, which can either localize only the center of the fovea or need a priori information about major structures in the image[2].
These same methods can also be applied to other eye diseases, so we will continue to extend our research to support the early detection of all preventable causes of blindness worldwide.
Our ongoing challenge is improving accuracy and providing deeper insight into severity levels for clinicians. In addition, it is also very important to us to validate our technologies with new data sources. We want to make sure that our methods do not only work with one source of data, but many different types of databases.

Healthcare research: IBM uncovers new way to stimulate the body to fight disease
View this post online: https://www.ibm.com/blogs/research/2017/03/new-research-ibm-uncovers-new-way-stimulate-body-fight-disease/
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Using nanomaterials to carry drug molecules to specific cells in the body is a relatively new field in healthcare research. But it's an important one.
For example, in order to target therapies to tumors, scientists have developed techniques to attach drug molecules (or vaccines) to nanomaterials like graphene sheets, a single-atom-thick sheet of carbon that is stronger than steel and as stiff as diamond. These "Trojan horse" nanotherapies can bring drugs directly to tumors, where they can be released onto cancer cells to, in theory, fight the disease.
A movie on the molecular scale shows how an uncoated graphene nanosheet interacts with an E. coli outer cell membrane.
The Soft Matter Science department in IBM Research's Healthcare and Life Sciences group is working to develop new techniques and approaches to understanding this increasingly important field for disease research.
Scientists know that unless you attach "coating molecules" such as polyethyelne glycol (a linear polymer) to graphene sheets, their bare surfaces and sharp edges can inadvertently damage surrounding cells. Attaching polymers to graphene sheets makes them more biocompatible.
What we didn't know is that these polymer-coated graphene sheets have an inadvertent effect on the human immune system. Our team recently discovered that polymer-coated nanomaterials trigger a dramatic reaction in the body's cells — one that we previously didn't see.
Cells can communicate with each other, sending signals to other types of cells. In a recent healthcare research paper published in Nature Communications, we discovered that these polymer-coated graphene sheets trigger an emergency response in the body's immune system. Simply put, your cells sense that there's a foreign body (the nanomaterial) and release "signal flares" (in the form of proteins called cytokines). These signal flares attract the body's immune cells — like helper T cells (which relay the signal forward) and killer T cells (which, as their name suggests, kill infected cells) to the location of the graphene sheets. Simulations on IBM's Blue Gene supercomputer showed that the polymers "glue" the nanomaterials to cell surfaces, which amplifies the initial signaling process. The healthcare research also suggests that these signals are broadcast within six hours of the nanodrugs being encountered.
Polymer-coated graphene sheets aren't necessarily harmful to human beings, which is partially why scientists hadn't discovered this accidental impact until now. Your cells are basically crying wolf whenever they detect polymer-covered nanomaterials nearby; immune cells simply respond to the call and travel to the sites of polymer-coated cells.
We've essentially uncovered a new way to trigger the body's immune cells to spring into action, which is

not an easy task. Without causing physical damage, polymer-coated graphene sheets incite cells into shooting off signal flares that bring the teeth of the immune system to bear at whatever location in the body the nanodrugs are delivered.

This discovery could represent an incredible development in precision medicine. If these nanomaterials were targeted at, say, tumors or virus-infected cells, one could, in principle, stimulate the immune system to attack cancer and infections at their source.

Immunotherapies like this might also be coupled to the delivery of traditional drugs, which we already know can be attached to graphene surfaces. Coupling both the body's own natural immune system with nano or traditional pharmaceuticals could form the basis for new ways in which human diseases are fought.

IBM 5 in 5: With AI, our words will be a window into our mental health

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As a neuroscientist, I want to understand the brain. Beyond just the physical structures of neurons and the synapses, but how it works. How is it that we think? How is it that two pounds of protein and water can produce this amazing, complex organ that literally drives humanity? Ultimately, behavior is what the brain is for. We, in the scientific and medical community, are studying behavior with the same types of computational approaches that we use to study the physical attributes and workings of the brain.

Nearly 20 percent of individuals in the United States alone will experience a mental health condition sometime in their life. Ranging from the neurological (Huntington's, Alzheimer's, Parkinson's etc) to mental (depression or psychosis) the global cost of treating mental disorders are greater than the cost of diabetes, respiratory disorders or cancer combined.

How can we help the doctors and patients who are impacted by these diseases? Could we, using computational biology, analytics and machine learning, build tools to quickly and simply analyze language and predict the onset of these diseases to allow for earlier intervention, better allocation of resources or better treatment planning?

We think so. In a study with Columbia University psychiatrists, we were able to predict, with 100 percent accuracy, who among a population of at-risk adolescents would develop their first episode of psychosis within two years. In other research with our Pfizer colleagues, we're using only about 1 minute of speech from Parkinson's patients to better track, predict and monitor the disease. We're already seeing results of nearly 80 percent accuracy. In five years, we hope to advance the study of using words as windows into our mental health.

Some days I think I am more philosopher than scientist, but I am often reminded that those roles, like those of the neurons and behavior in the brain, are two halves of the same function. The field of neuroscience is moving quickly – we know so much, but still have much more to uncover.

What is the prediction?

In five years, what we say and write will be used as indicators of our mental health and physical wellbeing. Patterns in our speech and writing analyzed by cognitive systems will provide tell-tale signs of early-stage mental disease that prompt us to seek treatment.

Why will this change the world?

Today, analysis of language is done in a labor-intensive process of manually interviewing and recording multiple lengthy sessions with a patient. There is no way to quantify or codify these sessions, resulting in a massive "big data" problem. A tool that could, in near real-time, analyze and codify a sample of the patient's speech and provide an analysis would drastically shorten the time it took for doctors and caregivers to predict and diagnose patients. For all conditions, the earlier a diagnosis is made, the higher likelihood of a successful treatment and management of the disease.

What is the underlying technology?
IBM is building an automated speech analysis application that runs off a mobile device. By taking approximately one minute of speech input, the system uses text-to-speech, advanced analytics, machine learning, natural language processing technologies and computational biology to provide a real-time, overview of the patient's mental health.

IBM Research Takes Watson to Hollywood with the First "Cognitive Movie Trailer"
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Attributed Author – John Smith
Ghost writer – Adrienne Sabilia
How do you create a movie trailer about an artificially enhanced human?
You turn to the real thing – artificial intelligence.
20th Century Fox has partnered with IBM Research to develop the first-ever "cognitive movie trailer" for its upcoming suspense/horror film, "Morgan". Fox wanted to explore using artificial intelligence (AI) to create a horror movie trailer that would keep audiences on the edge of their seats.
Movies, especially horror movies, are incredibly subjective. Think about the scariest movie you know (for me, it's the 1976 movie, "The Omen"). I can almost guarantee that if you ask the person next to you, they'll have a different answer. There are patterns and types of emotions in horror movies that resonate differently with each viewer, and the intricacies and interrelation of these are what an AI system would have to identify and understand in order to create a compelling movie trailer. Our team was faced with the challenge of not only teaching a system to understand, "what is scary", but then to create a trailer that would be considered "frightening and suspenseful" by a majority of viewers.
As with any AI system, the first step was training it to understand a subject area. Using machine learning techniques and experimental Watson APIs, our Research team trained a system on the trailers of 100 horror movies by segmenting out each scene from the trailers. Once each trailer was segmented into "moments", the system completed the following;
1) A visual analysis and identification of the people, objects and scenery. Each scene was tagged with an emotion from a broad bank of 24 different emotions and labels from across 22,000 scene categories, such as eerie, frightening and loving;
2) An audio analysis of the ambient sounds (such as the character's tone of voice and the musical score), to understand the sentiments associated with each of those scenes;
3) An analysis of each scene's composition (such the location of the shot, the image framing and the lighting), to categorize the types of locations and shots that traditionally make up suspense/horror movie trailers.
The analysis was performed on each area separately and in combination with each other using statistical approaches. The system now "understands" the types of scenes that categorically fit into the structure of a suspense/horror movie trailer.
Then, it was time for the real test. We fed the system the full-length feature film, "Morgan". After the system "watched" the movie, it identified 10 moments that would be the best candidates for a trailer. In this case, these happened to reflect tender or suspenseful moments. If we were working with a different movie, perhaps "The Omen", it might have selected different types of scenes. If we were working with a comedy, it would have a different set of parameters to select different types of moments.

It's important to note that there is no "ground truth" with creative projects like this one. Neither our team, or the Fox team, knew exactly what we were looking for before we started the process. Based on our training and testing of the system, we knew that tender and suspenseful scenes would be short-listed, but we didn't know which ones the system would pick to create a complete trailer. As most creative projects go, we thought, "we'll know it when we see it."

Our system could select the moments, but it's not an editor. We partnered with a resident IBM filmmaker to arrange and edit each of the moments together into a comprehensive trailer. You'll see his expertise in the addition of black title cards, the musical overlay and the order of moments in the trailer.

Not surprisingly, our system chose some moments in the movie that were not included in other "Morgan" trailers. The system allowed us to look at moments in the movie in different ways –moments that might not have traditionally made the cut, were now short-listed as candidates. On the other hand, when we reviewed all the scenes that our system selected, one didn't seem to fit with the bigger story we were trying to tell –so we decided not to use it. Even Watson sometimes ends up with footage on the cutting room floor!

Traditionally, creating a movie trailer is a labor-intensive, completely manual process. Teams have to sort through hours of footage and manually select each and every potential candidate moment. This process is expensive and time consuming –taking anywhere between 10 and 30 days to complete.

From a 90-minute movie, our system provided our filmmaker a total of six minutes of footage. From the moment our system watched "Morgan" for the first time, to the moment our filmmaker finished the final editing, the entire process took about 24 hours.

Reducing the time of a process from weeks to hours –that is the true power of AI.

The combination of machine intelligence and human expertise is a powerful one. This research investigation is simply the first of many into what we hope will be a promising area of machine and human creativity. We don't have the only solution for this challenge, but we're excited about pushing the possibilities of how AI can augment the expertise and creativity of individuals.

AI is being put to work across a variety of industries; helping scientists discover promising treatment pathways to fight diseases or helping law experts discover connections between cases. Film making is just one more example of how cognitive computing systems can help people make new discoveries.

IBM and University of Alberta Publish New Data on Machine Learning Algorithms to Help Predict Schizophrenia

Pioneering research in "computational psychiatry" uses AI to explore disease prediction and assessment

YORKTOWN, N. Y. and EDMONTON, CA - 21 Jul 2017: IBM (NYSE: IBM) scientists and the University of Alberta in Edmonton, Canada, have published new data in Nature's partner journal, Schizophrenia[1], demonstrating that AI and machine learning algorithms helped predict instances of schizophrenia with 74% accuracy. This retrospective analysis also showed the technology predicted the severity of specific symptoms in schizophrenia patients with significant correlation, based on correlations between activity observed across different regions of the brain. This pioneering research could also help scientists identify more reliable objective neuroimaging biomarkers that could be used to predict schizophrenia and its severity.

Schizophrenia is a chronic and debilitating neurological disorder that affects 7 or 8 out of every 1,000 people. Those with schizophrenia can experience hallucinations, delusions or thought disorders, along with cognitive impairments, such as an inability to pay attention and physical impairments, such as movement disorders[2].

“This unique, innovative multidisciplinary approach opens new insights and advances our understanding of the neurobiology of schizophrenia, which may help to improve the treatment and management of the disease,” says Dr. Serdar Dursun, a Professor of Psychiatry & Neuroscience with the University of Alberta. “We’ve discovered a number of significant abnormal connections in the brain that can be explored in future studies, and AI-created models bring us one step closer to finding objective neuroimaging-based patterns that are diagnostic and prognostic markers of schizophrenia.”

In the paper, researchers analyzed de-identified brain functional Magnetic Resonance Imaging (fMRI) data from the open data set, Function Biomedical Informatics Research Network (fBIRN) for patients with schizophrenia and schizoaffective disorders, as well as a healthy control group. fMRI measures brain activity through blood flow changes in particular areas of the brain. Specifically, the fBIRN data set reflects research done on brain networks at different levels of resolution, from data gathered while study participants conducted a common auditory test. Examining scans from 95 participants, researchers used machine learning techniques to develop a model of schizophrenia that identifies the connections in the brain most associated with the illness.

CAPTION: Here, we see the regions of the brain that showed a statistically significant difference between patients with schizophrenia and patients without it. For example, arrow 1 identifies the precentral gyrus, or the motor cortex, and arrow 5 marks the precuneus, which involves processing visual information.

The results of the IBM and University of Alberta research demonstrated that, even on more challenging neuroimaging data collected from multiple sites (different machines, across different groups of subjects etc.) the machine learning algorithm was able to discriminate between patients with schizophrenia and the control group with 74% accuracy using the correlations in activity across different areas of the brain.

Additionally, the research showed that functional network connectivity could also help determine the severity of several symptoms after they have manifested in the patient, including inattentiveness, bizarre behavior and formal thought disorder, as well as alogia, (poverty of speech) and lack of motivation. The prediction of symptom severity could lead to a more quantitative, measurement-based characterization of schizophrenia; viewing the disease on a spectrum, as opposed to a binary label of diagnosis or non-diagnosis. This objective, data-driven approach to severity analysis could eventually help clinicians identify treatment plans that are customized to the individual.

“The ultimate goal of this research effort is to identify and develop objective, data-driven measures for characterizing mental states, and apply them to psychiatric and neurological disorders” said Ajay Royyuru, Vice President of Healthcare & Life Sciences, IBM Research. “We also hope to offer new insights into how AI and machine learning can be used to analyze psychiatric and neurological disorders to aid psychiatrists in their assessment and treatment of patients.”

The Research Domain Criteria (RDoC) initiative of NIMH emphasizes the importance of objective measurements in psychiatry. This field, often referred to as “computational psychiatry”, aims to use modern technology and data driven approaches to improve evidence-based medical decision making in psychiatry, a field that often relies upon subjective evaluation approaches.

As part of the ongoing partnership, researchers will continue to investigate areas and connections in the brain that hold significant links to schizophrenia. Work will continue on improving the algorithms by conducting machine learning analysis on larger datasets, and by exploring ways to extend these techniques to other psychiatric disorders such as depression or post-traumatic stress disorder.

IBM and Sage Bionetworks announce winners of first phase of DREAM Digital Mammography Challenge

Challenge is aimed at helping to refine cancer detection algorithms so they can be used in routine clinical practice

ARMONK, N.Y. - 02 Jun 2017: IBM (NYSE: IBM) and Sage Bionetworks announced today that the winners of the first phase of its DREAM Digital Mammography (DM) Challenge have developed algorithms that had 5% fewer false-positive errors in breast cancer screenings than recently published state of the art computerized methods[1]. This 5 percent improvement could potentially lead to less anxiety and unnecessary procedures for an estimated two million women per year in the United States and could help reduce costs associated with follow-up exams and biopsies.

More than 120 independent teams of data experts from inside and outside the medical imaging field have participated in the challenge, which focused on developing predictive algorithms that reduce false-positive mammograms while maintaining or improving cancer detection. The goal is to enhance the predictive accuracy of algorithms so that they can be used in routine clinical practice.

In the first phase of the challenge, participants completed two tasks: They (i) developed a predictive algorithm that can analyze digital mammography images, (ii) and developed a predictive algorithm that can analyze both digital mammography images and clinical information.

Winning Teams

Yaroslav Nikulin, an engineer from the French imaging company Therapixel, and his team received top honors for their work on the first task and tied for first place in the second task. In the first task, they developed an algorithm with a predictive accuracy of 80.3 percent, which is 5 percent more accurate than the runner up. In the second task, Nikulin and his team developed an algorithm that was 80.4 percent accurate.

Tied for first place in the second task was a team led by Yuanfang Guan, Assistant Professor in the Department of Computational Medicine and Bioinformatics at the University of Michigan, Ann Arbor. The group developed an algorithm with a predictive accuracy of 77.5 percent and outperformed the runner-up by more than 2 percent. Though the difference in accuracy between Guan's and Nikulin's teams was 2.9 percent, their performance was indistinguishable in the other metrics used to score the algorithms. Both winning teams used "Deep Learning," one of the most advanced artificial intelligence techniques capable of analyzing and interpreting images.

Reducing False Positives

Mammograms are widely considered the most accessible and cost-effective breast cancer screening method. However, the American Cancer Society and the United States Preventive Services Task Force recently issued changes to recommendations for when women should start having mammograms and how often they should get them. The changes are due, in part, to the large number of false-positive mammograms. One in 10 women undergoing screening mammography is recalled for a diagnostic workup, though fewer than 5 percent of the recalled women will eventually be found to have cancer. Recalled patients often experience stress and additional medical costs, and some require interventions, including unnecessary biopsies. New algorithms may eventually be used by doctors to help them customize screening regimens for patients and identify women who would benefit from more or less frequent screening.

About the Challenge

Participating teams used hundreds of thousands of de-identified mammograms and clinical trial data provided by Kaiser Permanente Washington and the Icahn School of Medicine at Mount Sinai to create algorithms that can determine a woman's cancer status in the 12 months following her mammogram. Eight teams with the best algorithms will now move on to the community phase of the challenge, where they will be invited to add outside expert collaborators. They will also share their source code publicly, including other challenge participants, in an attempt to foster cooperative learning. In the community phase, finalists will work together to develop an algorithm that can fully match the accuracy of an expert radiologist.

"I am extremely pleased with the results of the competitive phase of the DM Challenge," said Gustavo Stolovitzky, Director at IBM Research and Founder of the DREAM Challenges. "By providing powerful computational resources and making available what is, to the best of our knowledge, the largest public mammography dataset ever released, we empowered hundreds of data scientists to contribute to the solution in the fight against breast cancer. Moreover, the code and methods generated during the DM Challenge are now available for anybody interested in building on these results to help solve this

important public health problem."

"The innovation in this challenge stems not only from its final output—a set of robust models to aid clinicians in detecting breast cancer—but also the structure of the challenge itself. This challenge embodies a new paradigm for data sharing and cloud-hosted collaboration to tackle important questions in biomedicine," said Dr. Justin Guinney of Sage Bionetworks. "By working together as a community of researchers and using the best tools of science and technology, we have advanced set the framework for clinicians in the field of breast cancer detection."

If by the end of the community phase, the top eight teams—including Nikulin's, Guan's, and six others—can develop an algorithm that matches the expert radiologist performance of about 87.9 percent accuracy, they will receive a prize of up to $1 million.

The DM Challenge was born out of the White House's Cancer Moonshot initiative and is funded in part by the Laura and John Arnold Foundation. It was designed by an organizing committee that includes IBM, Sage Bionetworks, Kaiser Permanente Washington, the Icahn School of Medicine at Mount Sinai, and the U.S. Food and Drug Administration. The challenge relied on the technological advances of Sage Bionetworks and IBM—Sage provided Synapse, a collaborative platform to host the challenge, as well as science and engineering expertise; IBM research teams in the United States, Israel, and Australia built the infrastructure for the challenge within the IBM Watson Health SoftLayer cloud and contributed further engineering and data science expertise.

IBM Research, Sutter Health Collaborate to Train Research Models That Could Be Used for Identifying Heart Failure Earlier

ARMONK, N.Y. - 15 May 2017: A team of scientists at IBM (NYSE: IBM) Research, in collaboration with scientists from Sutter Health, recently completed research developing methods to help predict heart failure based on hidden clues in Electronic Health Records (EHRs). Over the last three years, using the latest advances in artificial intelligence (AI) like natural language processing, machine learning and big data analytics, the team trained models to help predict heart failure.

Today, doctors will typically document signs and symptoms of heart failure in the patient record and also order diagnostic tests that help indicate the possibility that a person may experience heart failure. Despite best efforts, a patient is usually diagnosed with heart failure after an acute event that involves a hospitalization where the disease has advanced with possibly irreversible and progressive organ damage.

The research uncovered important insights about the practical tradeoffs and types of data needed to train models, and developed possible new application methods that could allow future models to be more easily adopted by medical professionals. For example, the research showed that only six of the 28 original risk factors contained within the Framingham Heart Failure Signs and Symptoms ($FHFSS^2$) were consistently found to be predictors of a future diagnosis of heart failure.

In addition, other team findings showed that other data types routinely collected in EHRs (such as disease diagnoses, medication prescriptions and lab tests) when combined with FHFSS could be helpful predictors of a patient's onset of heart failure.

Practical implications of the research were documented in a November 2016 paper "Early Detection of Heart Failure Using Electronic Health Records" and an editorial "Learning About Machine Learning: The Promise and Pitfalls of Big Data and the Electronic Health Record"" in Circulation: Cardiovascular Quality and Outcomes.

All three parties will continue to collaborate to improve accuracy, clinical relevance and to test models for use in clinical care. In addition, the work may have potential application to other diseases. The confluence of the availability of big data and advances in cognitive computing could have dramatic advances in earlier disease detection.