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Internal Quarterly Newsletter

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Management speaks



Dr. Eric Stawiski Vice President, Bioinformatics

Dear MedGenome Colleagues,

I am the Vice President of Bioinformatics at MedGenome, Foster City, California. I have not had the opportunity to meet all of you, so I would like to send you a brief introduction about my background and what I do here at MedGenome.

I have a PhD in Computational Biology with over 15 years of bioinformatics industry experience in Services, Diagnostics and Research and Development with companies including InforMax, Monogram Biosciences and Genentech. Prior to joining MedGenome in 2018, I spent 8 years at Genentech where I led a NGS Bioinformatics Group. We carried out many research projects related to medical genetics, cancer genomics and the development of genomics technologies. With a focus on research throughout my career, I have approximately 40 peer-reviewed publications related to bioinformatics or genomics, including those in the prestigious

journals of Nature, Nature Genetics, Nature Biotechnology and Cancer Cell. A passion for using genomics and bioinformatics to make discoveries that could ultimately help patients is what drives me in my work at MedGenome and I am excited to partner with you in this endeavor.

Here at MedGenome, I have two primary responsibilities, the first of which is to oversee US services-related bioinformatics projects. Over the past few months we have been experiencing a sizeable increase in the number of sequencing and bioinformatics projects from US-based clients. This can partly be attributed to some of the new genomics technologies we are offering, including single cell sequencing. We can now use genomics to describe individual cells as part of a larger batch of cells at the transcriptome, T-Cell and B-Cell receptor levels. As you might imagine, this takes a large, focused bioinformatics effort to make sense of the large amount of data. We look forward to expanding our single cell technology offerings and the accompanying bioinformatics in the near future, which will include the description of individual cells at their epigenetic level. In addition, we are putting in place a series of software infrastructure upgrades that will help us scale to the next level for US commercial projects.

My other key responsibility at MedGenome is to develop the data strategy of the company. As a genomics-based company, we have access to a plethora of data. In my opinion, the greatest opportunity (and challenges) of this data is not just its mere generation but is in its interpretation. This can only be carried out through strategic partnership with the bioinformatics team at MedGenome. We need to develop and refine bioinformatics capabilities to utilize this data in an insightful and productive way. There are many qualities of our data that make it particularly unique and exciting. Most of our data originates from India and combined with our research and collaboration network across India, we are uniquely situated to become the leaders in genetic data from South Asia. In the past, the majority of genetics based research has been carried out on European populations. At MedGenome, there is an incredible opportunity to advance the future of medical research by studying the Indian population. To support this effort, we plan to carry out extensive analysis of our data resources and to publicize key findings that highlight the potential of our data through scientific meetings, presentations and publications. Our long-term strategy is to expand our current data assets to enable the study of the genetics of specific diseases at a larger scale. This is an exciting time to be a bioinformatics scientist at MedGenome as we have the opportunity to use our unique data assets to greatly advance the field of medical genetics. I look forward to collaborating with you to make this a reality.

Sincerely, Eric Stawiski

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Most talked about

MedGenome in news

Business Standard

Festing for a chromosomal disorder during pregnancy is advisable (Health Notes)

IANS December 01, 2018 Last Updated at 11:42 IST

It may sound like code language or a password. But no, 22q11.2 is the name of one of the most common chromosomal disorders after Down syndrome.

What is 22q11.2? It's caused by a loss or deletion of a small part of chromosome 22 at position q11.2. Hence the name 22q11.2 deletion syndrome.

friendly-version?article_id=118120100190_1

The disorder has variable presentation. It may affect different parts of the body, mostly the heart, kidney, mouth and brain, along with the immune and endocrine system, leading to multiple deformities. With incidence of one in every 2,000 births, it occurs spontaneously in most cases while it is inherited in 5-10 per cent of cases, with a 50 per cent chance of transmitting the disorder. However, due to unfamiliarity and lack of understanding most cases are still identified after birth, during childhood or even during adulthood.

Here is a case study: Like any expectant parent, Juhi was excited when she learnt about her pregnancy. However, she suffered a miscarriage as her foetus was affected with Down syndrome. Juhi didn't lose hope and conceived again after few months. This time, for precaution, she consulted a geneticist who advised her to undergo a noninvasive pre-natal test (NIPT) which not only detects Down syndrome but also few other chromosomal disorders.

To her dismay, this time as well the foetus was detected with a chromosomal disorder -- the 22q11.2 deletion syndrome, also known as DiGeorge syndrome. Though she was initially upset, she was thankful to have information early to make an informed decision.

Today most expectant parents are aware of Down syndrome, all thanks to the awareness created about it. However, there are many other abnormalities which haven't been spoken about, nor heard of, as they are relatively rare. To add to the difficulty, there is not much known of the disorder or of its treatment. Therefore, we often hear stories of parents running from pillar to post in diagnosing the disorder of their child or seeking funds for the treatment of their child.

So, what is the solution? It is evident that there is no cure for such disorders and hence management is only the way to improve the quality of life of the patient.

Prevention encompasses a lot of things :

* Being aware of your genetic predisposition to certain diseases.

* Knowing your family history.

* Matching your genes with your husband/wife before planning a baby.

MedGenome takes over Centre for Genetic Health Care



MedGenome, India's premier genomics based research and diagnostics company, has announced that as part of its growth plans, it has taken over the management and operations of the Centre For Genetic Health Care (CGHC) in Mumbai. It will henceforth be called MedGenome- Centre For Genetic Health Care (CCHC). CGHC, a leading genetic centre, accredited by NABL and CAP and offering cytogenetic and FISH tests in pediatrics, prenatal, reproductive genetics and haematological oncology segments, has been at the forefront for providing Genetic counselling services. With this take over, it will be able to provide patients with a wide range of molecular tests across all the specialties like Reproductive, Neurology, Nephrology, Oncology, Cardiology, ENT, Endocrinology, Ophthalmology, rare diseases etc. This will empower clinicians with validated and actionable clinical information to make effective treatment decisions for their patients. This will also bring a lot of synergy providing a unique opportunity for doctors and patient to leverage each other strengths. MedGenome-CGHC will now have cross functional team comprising of experienced medical geneticits, scientists and bioinformatics etc, who can leverage knowledge and depth on patient scenarios with large amount of curated content for enhanced reporting.

2) लर्टः एक धीढ़ी से दूसरी में जाता है केंसर, देश में केंसर के हर साल करीब 10 लाख नए मामले।

एक अंग में दो जगह कैंसर की वजह आनुवांशिक

उत्तिर एंड जेपोर्टितस जीरकंषतः : माता-रिता से मिलता है। इसलिए रिसे मिलता है। इसलिए रिसे के रा हुआ हैं उसले कर्वा को मो जेतेटिक टेस्टिंग जरूरी है। शादी से प्रस्त भी करानी चाहिए। हालाकि सरकारी अस्पतालां में जेनेटिक स्थ्वीनिंग उत्तरब्धा नहीं है। नेश्वस्ट जेनेश्वन सिखरींसा कीमत काफी कम हुई है।





कैंसर खराब जीवनसैती की वजह से होता है। 👌 'ह में पुरुषों में पए जाने वाले तत्वबाकू-गुटरवा एकसाथ चबाने से भी गयूट्रेशन

Chetana Belage

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पहली स्टेज में इलाज आसान

ant, said, "I an already 38 years old and my fiance is 32. I oticed that my future er-in-law's sister has a liborder. My parents are about this. We decided

WHAT IS CARRIER SCREENING TEST?

It provides vital information of Carrier status to couples and the risks of passing down any recession tas two couples of an advantal green to be recluded. The record where a parson has two couples of an advantal green to bere risks of the recluded. It works couples an opportunity for reproductive choices, recluing pre-implantation genetic disposis, prevalat disposis and heigh prepare for the newtown. Tata Boy wides timely diagnosis of genetic disorders austantativity impove the quality of life.

Through a blood or saliva sample, a lab can check for genetic mutations associated with diseases and conditions at any private lab like MediSenome. WHAT CAN BE SCREENED? Thatassemia ciklu and anadomic di W

WHAT CAN BE SCREENED? mia, sickle-cell anaemic and HIV can als

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awarehoes anout carrier screenings should begin in adolescence HI years, say doctors. "Colleges " should to talk to their students do about genetic abnormalities and how screenings and counselling we have screening and the state of the student of the screening we have a Sandhya and Rajesh Maik who to go for the carrier screening test to parary that they do not have to have been state of the screening test for the screening screening screening test for the screening scre

In 2018, on business side we concluded the Series C funding and have been successful in closing partnership deals with hospitals and diagnostic labs across the country. In addition, we have expanded our presence in Mumbai by taking over Centre for Genetic Health Care and launched three genomic centres in Chennai, Coimbatore and Kolkata respectively. This has helped us in reaching wider markets and larger pool of patients thus realising our objective of making genetic testing more accessible to the public. On research from, we had some important papers published on new Monogenic Form of Diabetes, Non-invasive Prenatal Testing, personalized cancer vaccine approach to treat Lynch Syndrome, discovering genetic mutation causing rare colorectal disorder and identification of a treatable mutation linked to lung cancer. On product side we have added couple of new tests for haemophila, myeloma, breast cancer, leukaemia to name a few, while we have line up of launching new tests for rare diseases in 2019. Though there has been a spur in the number of companies offering genetic tests, thi waverness and adaptability has been low. We hope in the waverness and adaptability has been low. We hope in the upublic and private partnerships for its wider adoption. - **Dr VL Ramprased**, COO, MedGrenome

Testing for a chromosomal disorder during pregnancy is advisable - Business Standard

https://www.business-standard.com/article/news-ians/testing-for-a-chromosomal-disorder-during-pregnancy-is-advisable-health-notes-118120100190_1.html

2 Cancer story in Rajasthan Patrika

- 3
- Forget Kundalis, couples go for 'Carrier counselling'

http://www.newindianexpress.com/cities/bengaluru/2019/jan/04/forget-kundalis-couples-go-for-carrier-counselling-1920654.html

- 4 MedGenome takes over centre for Genetic healthcare Biospectrum
- 5) Dr. Ramprasad's quote in 'Biospectrum' on the challenges and achievements made by MedGenome in 2018

MedGenome connect

ACTIA



Winner Of Genetic Genius Quiz Receving Exome Test Voucher @ ICNC Conference, Mumbai

The period between September and December 2018 was quite engrossing, and yet exciting for team ACTIA. Also called as the quarter of events, this period saw our participation in many national and regional conferences. Some of them included Neuropedicon at Delhi, Kawasaki Conference at Chandigarh, ISPGHAN and ICNC at Mumbai, MYOCON at Chennai, and SIAMG at Vellore. This was coupled with numerous disease-specific CMEs having attedence of many potential doctors.

Overall, participation was in 8 conferences and 12 CMEs/RTMs, with an access to more than 2000 doctors across India – an objective closely chased by ACTIA to cement its presence in the rare disease space.

Connect with KOLs has never been better than what it was during the quarter of events. Creation of new KOLs in newer therapy areas like Endocrinology, Nephrology and Ophthalmology played a pivotal role in growth of ACTIA during this period.

Being the last lap in FY 2018-19, Actia will be at its best in doctor coverage, brand promotion, business generation, and customer connect to ensure this year ends on a high, and MedGenome becomes a name to count on by larger doctor base.

PRIMA

The period between 1st Dec 2018 to 30th Dec 2018 was quite exciting and full of events for Team PRIMA. We participated in 6 important national across India which included thefollowing:

- 1. Cancer survivors meet at GD Birla Sabhaghar, Kolkata attended by mostly survivors and cancer patients.
- 2. ICGCW 2018 conference at ACTREC Mumbai the conference was organized with topics focusing on Genetic Counselling and Molecular Genomics
- 3. Marrow Matters Conference on Haematology and PaediatricOncology at Bangalore



Sales team Representing at ICGCW event at Mumbai

- 4. Conference on Flowcytometry at Berhampur Orissa, Dr. Shruti Presenting in Workshop on Flow Cytometry
- 5. CRABECON conference on Oncology at Jammu
- 6. PHOCON paediatric conference of haematological malignancies at Bangalore

Our team of experts, i.e. Dr. Ramprasad, Dr. Vidya, Dr. Sakthivel and Dr. Shruti made our participation remarkable with their involvement. The visibility and awareness on PRIMA and its offerings was boosted further by our sales team across cities in India. The major therapies touch-based through these engagement programs were Oncology and Haematology.

MedGenome connect

CLARIA



Knowledge-sharing session underway in RTM @ Apollo Hosital, Kolkata

CLARIA riding high on event participation and promotion of cytogenetics testing

The last lap of the calendar year 2018-19 was full of activities and new initiatives for CLARIA. We participated in 1 major conference, i.e. SIAMG at CMC (Vellore) along with 6 key CMEs that ensured our targeted reach to 750+ clinicians. The Business Team ensured that the awareness on CLARIA offerings was driven strongly among participating Gynecologists, Fetal Medicine Specialists, IVF specialists and Geneticists, as a follow-up to these events.

The press conference followed by symposium on prenatal genetics at Mumbai, chaired by Dr. Hema Purandarey,

Dr. Ramprasad and Dr. Priya Kadam invited lot of interest among clinicians. A wave of new enthusiasm was felt in Business Team while sharing this information with the doctor in-clinic.

CLARIA will be at its best in promotion and business scale-up in coming 90 days, this will also be ensured by improved promotion in-clinic and also through participation in industry events like AICOG 2019. Enhanced focus on cytogenetic testing will propel growth for CLARIA in this last lap of the financial year.

Making a difference

Genetic testing helps in treatment of a two-year-old boy with magnesium deficiency



Two- year-old Amar (name changed) was suffering from epilepsy and has been having seizures since he was a month-old baby. His parents then consulted Dr.Vivek Jain, Paediatric Neurologist at Santokba Durlabhji Memorial Hospital and Medical Research institute, Jaipur. Dr.Vivek tried various anti-epileptic medicines but to his surprise none of them worked. He then approached MedGenome labs, Bangalore for conducting Amar's genetic test.

The analysis of the test revealed that Amar had magnesium deficiency and suffered from a rare genetic disorder, Hypomagnesemia. It is a rare autosomal recessive disorder characterized by very low serum magnesium levels caused by

a mutation in the gene TRPM6. Autosomal recessive disorder means two copies of an abnormal gene, one maternal and one paternal, must be present for the disease or trait to develop.

Magnesium is required for efficient parathyroid function and parathyroid hormone production, which is responsible for maintaining blood calcium levels. In some Hypomagnesemia cases, severe magnesium deficiency leads to failure of the parathyroid gland, causing low calcium levels in the blood or hypocalcemia. The disease typically manifests during the first months of life with generalized convulsions or signs of increased neuromuscular excitability, such as muscle spasms or tetany.

Hypomagnesemia can occur in elderly as a result of decreased intake, increased renal or gastrointestinal losses and altered intracellular-extracellular distribution, diuretic use, alcohol use, and chronic diarrhoea. However, in Amar's case it was due to a genetic mutation.

Based on the genetic report Dr. Vivek treated him with magnesium which helped to manage the symptoms that wasn't previously controlled by other seizure medication. Hence genetic testing helped in identifying the mutation and the disease to decide the prognosis for the patient. In fact, early diagnosis and ideal treatment prevented irreversible neurological complications which may have resulted, if treatment was delayed.

From our US office

Our recent symposium on "Genomics based biomarker discovery in cancer" was co-sponsored by Paragon Genomics, Illumina and Takara. The symposium provided deep insights into cancer immunotherapy research and the latest trends. The symposium was attended by more than 40 leading research scholars from different institutions.

Detailed Video Presentations are also available in our Website – MedGenome Sponsored Scientific Sessions: https://www.medgenome.com/research/

We have also recently published our research progress in cancer immunotherapy in the prestigious journal "Frontiers in Immunology".



in Immunology Cancer Immunity and Immunotherapy

To read more, visit our publications section on the website: https://www.medgenome.com/publications/

MedGenome also hosted a webinar recently on "Tumor Intrinsic and Extrinsic Factors Determining Success of Immunotherapy"

For More Details and Video, please click on: https://www.youtube.com/watch?v=cM1yKBomPKY&f eature=youtu.be





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Sneak peek into the world of science

MedGenome's OncoPeptTUME identifies Immunogenic Features of Prognosis in Human Cancers

By Dr. Malini Manoharan - Bioinformatics Scientist II



Cancer immunologists scooped the 2018 medicine noble prize for pioneering treatments that unleash the body's own immune system to attack cancer cells. It represents a completely new principle which unlike the previous strategies that target the cancer cells, rather targets the brakes — the checkpoints — of the host immune system.

Immunotherapy based on check point inhibitors has shown astounding clinical success with countess patients with varied tumor types showing a pronounced clinical response, however, many more patients show a decreased or no clinical benefit. Understanding the complexity and diversity of the tumor microenvironment in the context of its immune composition can largely improve patient stratification. To this end, MedGenome has developed

IMMUNE BOOST

Several methods are showing promise in helping immune sentinels called T cells to attack cancer.

CHECKPOINT INHIBITOR DRUGS

'Checkpoint' proteins block T-cell activity. Inhibitor drugs can release the brakes on T cells at different stages.



The CTLA-4 checkpoint protein prevents dendritic cells from priming T cells to recognize tumours. Inhibitor drugs block the checkpoint.

The PD-1 checkpoint protein prevents T cells from attacking cancer cells. The inhibitor drug allows T cells to act.

onature

Figure 1: Role of checkpoint inhibitors in immunotherapy.



OncoPeptTUME, a genomic solution that utilizes its highly cell-type specific proprietary minimal gene expression signature to characterize the composition of currently 8 different immune cells. The expression of genes for a given signature is transformed to produce a cell-type specific immune score that is used to quantitate the relative proportion of cell types present in the tumor microenvironment (Figure 2).



Figure 2: Creation and validation of minimal gene expression signature profile (MGESP) for eight different immune cells. Workflow of the OncopeptTUME platform.

Pan cancer analysis of the TCGA data using OncoPeptTUME revealed immunogenic features that impact prognosis in human cancers. Our analysis revealed that CD8+ T cells expressing higher levels of anergic and exhaustion markers, which are hallmarks of dysfunctional T-cells were enriched in the deceased group compared to the alive group. The analysis published recently (Manoharan et al., 2018) reveals critical determinants of long-term survival pointing to an integrated approach that can be designed for selecting patients who will benefit from cancer immunotherapy treatment.

Manoharan Malini, Mandloi Nitin, Priyadarshini Sushri, Patil Ashwini, Gupta Rohit, Iyer Laxman, Gupta Ravi, Chaudhuri Amitabha (2018). A Computational Approach Identifies Immunogenic Features of Prognosis in Human Cancers. Front. Immunol., 9.

Sneak peek into the world of science

Machine learning in genetics and genomic medicine

By Praveen Raj Somarajan - Associate Director



Recent technological advances have increased the understanding of genome biology to an incredible degree. However, the complexity and sheer amount of information contained in DNA and chromatin remain roadblocks to complete understanding of all functions and interactions of the genome. Connecting genotype to phenotype, predicting regulatory function, and classifying mutation types are all the areas in which harnessing the vast genomic information from a large pool of individuals can lead to new biological insights. However, working in this large data space is challenging when conventional methods are used. The field of machine learning, therefore, promises to enable computers to assist humans in making sense of such large, complex data sets.

Machine learning is a branch of Artificial Intelligence (AI) based on the idea that systems can learn from data, identify patterns and make decisions with minimal human intervention [1]. Learning can be classified as either supervised or unsupervised. In

supervised learning, the objective is to predict a desired output value (e.g. phenotype) inferred from input data (e.g. genetic profile). The prediction task is called classification if outputs are categorical (e.g., pathogenic-benign, or susceptible-moderate-resistant), and regression if outputs are continuous. In unsupervised learning, the objective is to discover homogenous groups in data (e.g. group patients with similar biochemical profile) and associations among input variables (Hastie et al., 2009).



Fig 1 (a) A canonical example of a supervised machine learning application. A set of features with known class labels (e.g. variant significance pathogenic-benign) or target value (e.g. HbA1c measurement) is given to the learning procedure as input ("training data"). The learning algorithm produces a model that can then be subsequently used, with a prediction algorithm, to determine the label of an unlabelled data ("test data"). The model can be rebuilt with new data over time to improve accuracy and generalize to new set of features in the data. (b) Types of machine learning

Machine learning techniques such as deep learning enables the algorithm to make use of automatic feature learning where the algorithm learns how to combine multiple features of the input data into a more abstract set of features from which to conduct further learning. This multi-layered approach to learning patterns in the input data allows such systems to make quite complex predictions when trained on large datasets.

Machine learning methods have been applied to a broad range of areas within genetics and genomics. It is perhaps most useful for the interpretation of large genomic data sets and has been used to annotate a wide variety of genomic sequence elements. For example, machine learning methods can be used to 'learn' how to recognize the locations of transcription start sites (TSSs) in a genome sequence [2]. Algorithms can similarly be trained to identify splice sites [3], promoters [4], enhancers [5] or positioned nucleosomes [6]. Gene expression data can be used to learn to distinguish between different disease phenotypes and, in the process, to identify potentially valuable disease biomarkers. Chromatin data can be used, for example, to annotate the genome in an unsupervised manner, thereby potentially enabling the identification of new classes of functional elements. Machine learning applications have also been extensively used to assign functional annotations to genes. Such annotations most frequently take the form of Gene Ontology term assignments [7][8].

Many researchers have worked on different machine learning algorithms for disease diagnosis. Several examples of deep learning in oncology are listed in the section that follows. Though this list is by no means complete, it gives an indication of the long-ranging impact of deep learning on the medical diagnosis today and in the near future.

Deep Learning plays a vital role in the early detection of cancer. Researchers from Oregon State University were able to use deep learning for the extraction of meaningful features from gene expression data, which in turn enabled the classification of breast cancer cells [9]. They have used the technology to extract genes considered useful for cancer prediction, as well as potentially useful cancer biomarkers, for the detection of breast cancer.

A research paper published in Nature by Stanford University researchers has shown that their convolutional neural network (CNN) achieves performance on par with all tested experts when classifying skin cancer [10]. Andre Esteva *et al.* used 129,450 clinical images of skin disease to train a deep convolutional neural network to classify skin lesions. The result is an algorithm that can classify lesions from photographic images similar to those taken with a mobile phone. The accuracy of the system in detecting malignant melanomas and carcinomas matched that of trained dermatologists.

Researchers from China have used deep learning for segmenting brain tumors in MRI images, where it provided more stable results as compared to manually segmenting the brain tumors by physicians, which is prone to motion and vision errors [11]. A team led by Dr. Qi Zhang of Shanghai University found that deep learning can accurately differentiate between benign and malignant breast tumors on ultrasound shear-wave elastography (SWE), yielding more than 93% accuracy on the elastogram images of more than 200 patients [12].

In an effort to accelerate cancer research, Oak Ridge National Laboratory (ORNL) researchers are applying deep learning towards automating information collected from cancer pathology reports that are documented across a nationwide network of cancer registry programs [13].

Deep learning can be used for tracking tumor development. Google research team has used pathology images to train their deep learning algorithm Inception (aka GoogLeNet) to identify breast cancer tumors that have spread to adjacent lymph nodes [14]. The algorithm reached a localization score of 89%, exceeding the 73% accuracy rate for pathologists.

Prognosis provides an estimate of how serious or advanced the stage of cancer, and hence the chances of survival. Researchers in South Korea utilized deep learning to develop a prediction model for the prognosis of patients suffering from gastric cancer and undergoing treatment (i.e. gastrectomy). They found that deep learning showed superior survival predictive powers compared to other prediction models [15].

The aforementioned are a few recent advancements in Oncology. Deep learning techniques are also being applied in other disease areas such as Diabetes [16][17], Ophthalmology [18][19], Cardiovascular disease[20], Liver disease early detection and prognosis is one of several important healthcare areas where deep learning technology has been applied. ML promises to transform medical research which could lead to optimization of day-to-day clinical workflow while improving risk assessment and potential outcomes.

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Employee connect - Testimonials

Mridul



I aspire to apply emerging latest technologies to our projects. Also, my plans for 2019 include bringing the two research manuscripts to publication before first quarter. I am looking forward to be a part of novel research initiatives by MedGenome.

The year 2018 brought to me the global frontier of bioinformatics in the form of single cell sequencing projects and I was thrilled to work on it and happy to deliver successfully. The experience and knowledge of the field gained at NGBT Jaipur was priceless. Gave my first ever poster presentation there.



Buvanesh





My memorable event of the year was when the National Human Resources Development Network – Hosur Chapter was awarded as the Best Emerging Chapter during the National Conference of NHRDN conducted in Hyderabad during August 2018. I am proud to be associated as an executive committee member with the NHRDN Hosur Chapter as this was the 5th time in a span of 6 years that we are being bestowed this award for exemplary contribution to the HR fraternity in the region. The lcing on the cake was, meeting Prof. T V Rao, who is being credited with pioneering the new HR Movement along with Dr. Udai Pareek in India.

Soumitra



Comprehensive analysis of the 'Familial genetic disease study (FGDS)' that will enable to understand the mutation spectrum, frequency and genetics of rare monogenic diseases in the Indian population.

Launched 'Ophthatome - knowledgebase for ophthalmic diseases research' in Association for Research in Vision and Ophthalmology (ARVO), 2018, held at Honolulu, USA.





Ankur



Do well both professionally & personally (Just got married :))

Rejoined MedGenome and been part of several new pipeline projects.

Sushri Priyadarshini



Looking forward to more IPs for MedGenome through collaborative projects between informatics and lab wing.

MedGenome's OncoPept[™] got Best Overall Genomics Solution in MedTech Breakthrough Awards, 2018. Felt good to be part of the team.









Rakesh Kumar



Tajuddin Baidya



K Ranjith Reddy



Rojashree J



Gnana Prakash Visvanathan



C S Mudasir Naazar



Balraj Rani



Amar Baswaraj Murge



Manoj Kumar Tiwari





Simeon



Shashank Singh



Employee connect

Cross word puzzle



Across

- 1. Has its own DNA
- 5. Mean, green protein
- 10. Hot polymerase
- 12. Keeps general information safe
- 13. Development DNA
- 14. Tiny DNA difference
- 16. Mosquito sickness
- 17. Dolly and Bonnie
- 19. Body's detox
- 20. Mullis multiplier
- 23. Research fungus
- 24. Knowledge miner
- 27. Microbe gang
- 28. Body rhythm
- 29. Dense DNA
- 30. Blob organism

Down

- 2. RNA reading
- 3.23 chromosomes
- 4. Protein factory
- 6. Mendel's veggies
- 7. Computers+biology
- 8. Colored gene grid
- 9. Bead on a string
- 11. Protein recipe
- 15. DNA's shape
- 18. End DNA
- 21. Chopped-out DNA
- 22. Evolution dad
- 25. Furry research tool
- 26. Disease simulator

Kindly mail your answers by 15th Feb 2019 to editor@MedGenome.com. The first two people to answer the puzzles correct will be featured in the next edition of our newsletter.



Photo feature

CELEBRATIONS





























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