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# STOMATA 1.3

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## Molecule of the month (May 2016)

### Zika Virus

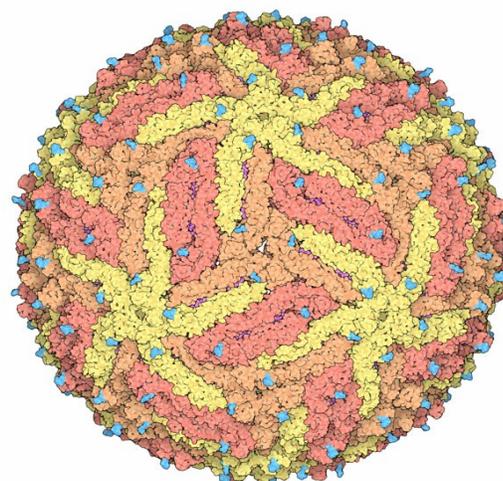
*Cryo-electron microscopy reveals the structure of Zika virus*

Zika virus was discovered in 1947, in an infected monkey in the Zika Forest of Uganda. By all expectations, it would have remained a virological oddity like other obscure tropical viruses transmitted by mosquitoes. However, study of Zika virus has gained new importance because of the recent spread of the virus in many countries around the globe and its connection to birth defects and a rare neurological disease.

### Studying Zika Virus

Cryo-electron microscopy has been used to reveal for the first time the near-atomic structure of Zika virus (PDB entry [5ire](#)). The virus was isolated from an infected patient and grown in larger quantities in cell culture. The

structure was then determined by aligning over 10,000 images of the virus, building a detailed cryo-EM map that shows the folding of the two proteins on the surface of the virus: envelope (E) protein and membrane (M) protein. You can take a look at the map at the EMDataBank website ([EMD-8116](#)).



## From the editors . . .

As I write this opening letter, Wagnaghat is experiencing one of those great early fall days with a clear blue sky and crisp air. And the campus is stirring with the kind of life that only students can bring to a place. Heartiest welcome to the 1st yearies of the

Biotechnology and Bioinformatics Department! Our intention in this issue is to offer a heartfelt “thankyou” for the generosity of the course of last semester, Jan16 to June16. It has been a great journey to learning and establishing ourselves as avid

learners of the values that biology and computer science teaches us.

Cheers to the beginning of new year! Happy Reading!

**Mansi and Shubham**  
(Coordinators)

# MAD SCIENTIST



The Synapse Club of JUIT organised a fun-filled event titled "Mad Scientist" from 10th to 12th March 2016. This event was open to all students of all branches wherein they participated in pairs and hurdled through a series of Biotech laboratory based tasks. The first round consisted of making the highest number of cotton plugs under a stipulated time. After an exciting tie-breaker, quali-

fiers proceeded to the second round wherein they had to accurately measure a substance using digital weighing balance. On the second day, the qualifiers were demonstrated how a micro-pipette functions and were then evaluated on the basis of the same. On the concluding day of the event, they were asked to perform an advanced DNA isolation technique after

which the top scorers were finally announced. The winners took away a cash prize but none went empty handed. You see, by the end of the event all participants had received a basic training of becoming a MAD Scientist

The winners of this competition were Sudhanshu Sharma and Divesh Kashmmiri

*The ones who are  
crazy enough to  
think they can  
change the world,  
are the ones who  
do!*

# DECLAMATION

On 16th February 2016, under the able guidance of Dr. Hemant Sood, a declamation contest was conducted on the topics "Science in India", "Patriotism in the 21st century" and "Terrorism in India". Ten participants competed in

this final round. They were judged by a panel of three judges- Dr. Harish Changothra, Dr. Jata Shankar and Dr. Chittaranjan Rout. It was a sight to watch as the young charismatic speakers voiced out their opinions and mesmerised the audience with their great oratory skills. After the exuberant expression of

ideas and thoughts, top 3 positions were announced.

Abhishek Rana was adjudged the winner of the Declamation contest while Shimul Garg and Neharika were declared as the first and second runner ups. The event reached its conclusion with the air still shimmering of confidence and thoughts reverberating from ideas



*Tough times never  
last but tough  
people do...*

# FORENSIC IDOL

Synapse, conducted its own version of Sherlock when it organized "Forensic Idol", a unique investigative venture, on 8th May 2016 within the University campus. The program was aimed at solving a crime mystery crafted with clues, Ariddles, decode ng and aimed to stimulate the logical and

analytical mind of the participants. The participants teamed up in groups of two, on a quest to decipher the plot and unravel the mysteries that lay ahead. The three hour long event undertook major aspects of the mystery including explanation of the storyline, showing pictures of the crime scene, collecting the

clues and evidences, taking help of research techniques and finally interviewing the suspects to draw up their conclusions. Inquisitiveness galore throughout and concluded the journey, rewarding its tidal frontiers Rahul Paramjeet & Deepak Chuggani with accolades. The event ended with a newly sprouted up zeal and mettle for mystery and competitions.

## WORKSHOP ON STATISTICAL TECHNIQUES IN BIOLOGICAL AND MEDICAL SCIENCE (STBMS) 2016



A very first time in the history of JUIT an event was organized jointly by two departments as a workshop on STBMS, which was conducted in JUIT from 13 -18 June, 2016. The main focus of the workshop was the applications of Statistics, Probability, Mathematics and Computations which solved real life problems in Biological and Biomedical Science. Essentially the theme was BioStatistics, the branch of statistics

responsible for the proper interpretation of scientific data generated in the biology, public health and other health sciences. Interactive lectures and lab sessions by experts were conducted to discuss the various statistical tools, techniques and their applications. The speakers were Dr. Ashish Sen Gupta (ISI), Dr. A. K. Aggarwal (PGIMER), Dr. Amar Nath Gill (PU), Dr. Suresh Sharma (PU), Dr. Athar Ali Khan (AMU), Dr. Parminder Singh (GNDU) – all noted personalities in the field of Statistics. The Topics covered by our guest speakers were Descriptive and inferential Statistics, Correlation and Regression: Predictors Testing, MLR, Multicollinearity, Variance inflation factor (VIF),

Logistic regression, Case studies on Biological and Biomedical Data and etc. The workshop proved to be highly beneficial not just to the Biologists, Biotechnologists, Biomedical Scientists but also to students from all these streams as it gave them an insight into Statistical Analysis which would help in their academic and research activities. The uninterrupted flow of the event is attributed to the hard work of its Coordinators, Dr. Tiratha Raj Singh and Dr. Narendra Kumar, who left no stone unturned in making the workshop successful.

*"The consequences of failure should be so dire, so unthinkable, that they make you do whatever it needs to succeed"*

## NATIONAL SYMPOSIUM ON COMPUTATIONAL SYSTEMS

With great zest and sincere efforts of Dr. Tiratha Raj Singh, the Department of Biotechnology and Bioinformatics of JUIT conducted National Symposium on Computational Systems Biology from 18 to 20 March, 2016. The Programme sponsored by Department of biotechnology (Ministry of Science and Technology) and was jointly organized with National Network for Mathematical and Computational Biology (NNMCB). The theme was based upon current research scenario of Systems Biology, the goal of which was to provide a system-level understanding of biological systems by unveiling their structures, dynamics and

control methods. The eminent Speakers were, Dr. Alok Bhattacharya(JNU), Dr. Debasis Mohanty(NII), Dr. G.P.S. Raghava (IMTECH), Dr. Somdatta Sinha (IISER), Dr. Suresh Sharma(PU), Dr. Debasis Das(IGIB), Dr. Vinod Scaria(IGIB), and Dr. Vikram Singh(CUHP). They delivered lectures on Biological Networks, Protein protein interactions, Signal transduction Pathways, Metabolic Pathways, Computational models for biological systems and other similar topics which peaked interests. The organizing committee consisted of Dr. Rajinder Singh Chauhan (Chairman), Dr. Tiratha Raj Singh (Convener), Dr. Somdatta Sinha, , Dr. C. Rout, Dr. Har-

ish Changotra, Dr. Jata Shankar, Dr. Ragothaman Yennamalli, Dr. Jayashree Ramanna and Dr. M. Udayabhanu. All other faculty members also supported the event wholeheartedly. The event was quite dynamic with active participation from JUITians, especially in Poster Presentation. The series of lectures successfully initiated students into the interdisciplinary field of Computational Biology and also provided the young minds an exposure to new upcoming technologies. It was the first of its kind event in the history of the department of BT and BI.



# CRISPR Gene Editing

Ever thought of getting powers and becoming a superhero? Getting bit by a spider to become Spider-man? Who hasn't? Well gone are the days when this thought was nothing but fiction. With the use of CRISPR gene editing techniques soon a universe might emerge where this possibility might become a reality! Bacteria and archaea have evolved adaptive immune defences, termed clustered regularly interspaced short palindromic repeats (CRISPR) that use short RNA to direct degradation of foreign nucleic acids.

These CRISPR-associated (Cas) systems, especially type II can be used in-vitro along with custom guide RNA (gRNA) to make precise targeted changes to the genome of living cells.

Moreover, multiple guide sequences can be encoded into a single CRISPR array

to enable simultaneous editing of several sites within the mammalian genome which demonstrates its easy programmability and wide applicability. The inactivation of both domains enables Cas9 to function as a retargetable DNA binding

protein which can be used to turn off a gene reversibly.

CRISPR is also more efficient than two other genome engineering techniques called zinc finger nuclease (ZFN) and transcription activator-like effector nucleases (TALENs). ZFN and TALENs can recognize longer DNA sequences but custom-designed ZFN or TALEN protein has to be created each time which is more tedious than creating RNA guide sequence for CRISPR.



CRISPR has revolutionized the world of gene editing. It has allowed scientists to conduct advanced research into diseases, research live cells, and it's not expensive or overly compli-

cated. But one thing it has always lacked is specificity. In some respects, it is the sledgehammer, not the sword; the cleaver, not the scalpel.

Improving the specificity, Harvard University researchers have developed a new method of using CRISPR to alter single letters in the DNA code. This opens up the possibility of reversing mutations (and the diseases that stem from them) caused by the changing of only one letter, which represents nearly two thirds of all genetic mutations.

In an article in the journal Nature, the researchers described the new method, which doesn't need to cut both strands of the DNA double-helix to alter the genetic code. It can directly convert a single letter of DNA to another, without deleting and inserting a bunch of random letters.

Specifically, the researchers decided to glue two proteins to a type of Cas9 enzyme that doesn't cause double-stranded breaks in DNA. The two proteins allowed the Cas9 to directly convert one specific letter in the four-letter genetic code, while preventing the cell from undoing the change. Thus, allowing high precision gene editing.

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