

ACLS International Summer School 2017 List of Participants				
Name	University	Department	Research Area	Research Interests
Kento Aoyama	Tokyo Tech	Computer Science (Artificial Intelligence)	High performance computing of containerized bioinformatics application	1. Parallel/distributed computing 2. Virtualization technology 3. Data-processing workflow
Yasunobu Asawa	Tokyo Tech	Life Science and Technology (Graduate Major of Human Centered Science and Biomedical Engineering)	Discovery of cancer drugs using organic chemistry	1. Organic chemistry 2. Computer science 3. Inhibiting proteins
Yeonjong Choi	Tokyo Tech	Computer Science (Artificial Intelligence)	Text-dependent speaker verification	1. Machine learning 2. Digital signal processing 3. Neural science
Ruoming He	Tokyo Tech	Computer Science (Artificial Intelligence)	Drug-target interaction prediction	1. Drug structure 2. Data mining
Yicong Huang	Tokyo Tech	Computer Science (Computer Science)	Molecular dynamics simulation of membrane peamination with peptide	1. Molecular dynamics simulation 2. Data analysis 3. Machine learning
Atsushi Izutani	Tokyo Tech	Life Science and Technology (Graduate Major of Human Centered Science and Biomedical Engineering)	Protein Chemistry	1. Antibody 2. Imaging system of cancer cells 3. Molecular simulation
Yeongdae Kim	Tokyo Tech	Information Processing	Human machine interface	1. Neural network 2. Bio-signal 3. Wearable device
Norwich Mungkalaton	Tokyo Tech	Computational Intelligence and Systems Science	Complex System	1. Protein-ligand binding 2. Microtubules simulation 3. Mathematical modeling
Masaru Nakao	Tokyo Tech	Life Science and Technology	Development of single cell analysis for epigenome	1. Epigenetics
Teerapat Anananuchatkul	Tokyo Tech	Bioengineering	Construction of a stapled peptide library and screening of functional peptide ligands for protein interaction	1. Protein protein interaction 2. Peptide phage display 3. Peptide protein interaction
Hiroki Ueda	Tokyo Tech	Life Science and Technology (Graduate Major of Human Centered Science and Biomedical Engineering)	Chemical Biology	1. Drug 2. Organic chemistry 3. Computational chemistry
Hikaru Watanabe	Tokyo Tech	Life Science and Technology	Microbiogy	1. Bioinformatics 2. Microbiology 3. Statistics
Hiroataka Yajima	Tokyo Tech	Life Science and Technology	Methanol utilization by escherichia coli	1. Metabolic engineering 2. Microbiology 3. Synthetic biology
Yusuke Yanagita	Tokyo Tech	Computer Science (Artificial Intelligence)	Neural networks	1. Neuroscience 2. Evolution game 3. Embryology
Takanobu Yasuda	Tokyo Tech	Life Science and Technology (Graduate Major of Human Centered Science and Biomedical Engineering)	Conversion of natural antibody to Q-body by using nucleotide binding site	1. Antibody 2. Nucleotide binding site 3. Fluorescence
Hiroshi Yoda	Tokyo Tech	Computer Science (Artificial Intelligence)	Machine learning assisted materials discovery	1. Machine learning 2. Tree search 3. Docking algorithm
Venkatraman Anandalakshmi	NTU	Biological Sciences	Drug discovery for Corneal dystrophy	1. Metagenomics 2. Drug discovery 3. Aggregation disorders
Yao Chen	NTU	Biological Sciences	Genome reorganization during chemoresistance	1. Chromosome conformation 2. Epigenetics 3. Chemoresistance
Edwin Sandanaraj	NTU	Biological Sciences	Targeting brain tumors through precision medicine strategies	1. Bioinformatics 2. Pattern learning 3. Patient database analysis
Ankur Sharma	NTU	Biological Sciences	Gene regulation in hepatocytes	1. Epigenetic gene regulation 2. 3D chromatin organisation 3. High-throughput data analysis
Mengmeng Zhu	Purdue	PULSe (Purdue University interdisciplinary Life Science)	Protein structure modeling using machine learning	1. Deep learning 2. Protein structure
Antoine Creugny	Strasbourg	Molecular Biology / Virology	Viral microRNA biogenesis / RNA interference	1. Non-coding RNA 2. RNA interference 3. Gene regulation
Farah Bouhedda	Strasbourg	Biological science / Biotechnology	Fluorescent RNA aptamers	1. Non-coding RNAs 2. Microfluidics 3. Fluorescence imaging
Tevfik Umut Dincer	UCLA	Bioinformatics	Computational inference of gene regulatory regions	1. Machine learning for biomedical applications 2. Massively Parallel Reporter Assays (MPRAs) 3. Epigenetics
Artur Tomasz Jaroszewicz	UCLA	Bioinformatics	Epigenomic regulation, Chromosome organization	1. Epigenomics 2. Splicing regulation 3. Chromosome interaction
Adriana C Sperlea	UCLA	Bioinformatics	Improving interpretability of non-coding human genome	1. Epigenetics 2. Comparative genomics 3. Machine learning
Xiangkun (Elvis) Cao	Cornell	Sibley School of Mechanical and Aerospace Engineering	FeverPhone: Point of care diagnosis of acute febrile illness using a mobile device	1. Mobile health 2. Point-of-care diagnostics 3. Microfluidics
Ariah Klages-Mundt	Cornell	Center for Applied Mathematics	Cascades and learning on networks	1. Data-driven models 2. Network science 3. Data mining