

SYSTEMS BIOLOGY & (TRANSCRIPT)OMICS ANALYTICS

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Bioinformatics Institute, A*STAR
Singapore Institute of Food & Biotechnology Innovation, A*STAR
Affiliated Principal Investigator, SynCTI, NUS
Associate Editor, Genomics (Elsevier)
Academic Editor, Scientific Reports (Nature Research)
Hon Secretary, Society for Synthetic Biology (Singapore)

26 Apr 2021



OUR TEAM (BII & SIFBI)



Mohamed Helmy

PhD, MSc (Keio University, Japan)
Senior Bioinformatics Specialist, BII

2017-2018, Head of Bioinformatics, BenchSci
2013-2017, Postdoc, University of Toronto
2012-2013, Postdoc, Kyoto University

Systems Biology, Network Biology
Bioinformatics, Proteomics



Kumar Selvarajoo

PhD (NTU), MEng & ACGI (Imperial College, UK)
Senior Principal Investigator

2017- present, BioTrans, SIFBI, BII
2014-2016, Associate Professor, Keio University, Japan
2006-2014, Assistant Professor, Keio University, Japan
2004-2006, Project Leader, BII, A*STAR

Systems Biology, Bioinformatics, Transcriptomics, Network Modeling, Data Analytics



Bui Thuy Tien

BEng (NTU), ASEAN Scholar
Research Officer, BII

2017-2018, IBN, A*STAR

Bioinformatics, Transcriptomics, Machine Learning, Data Analytics



Derek Smith

DPhil, BSc (University of York, UK)
Research Scientist, SIFBI

2012-2015: Research Scientist, BII
2008-2012, Bioinformatics Scientist, Codexis Laboratories Singapore Pte Ltd
2005-2008: Senior Post-Doc, BII, A*STAR

Bioinformatics, Molecular Modelling, Enzyme Engineering, Directed Evolution



Jasmeet Khanijou Kaur

PhD (NUS), MSc (King's College, UK), BSc (NUS)
Research Fellow, SIFBI

2019-2021, Research Fellow, NEA

Analytical Chemistry, Proteomics, Metabolomics, Systems Biology



WHAT COMPUTATIONAL SYSTEMS BIOLOGY CAN DO?

Systems Biology = Life Sciences + Engineering/Computer Science/Mathematics

- I) **Metabolic/Signaling Network Modelling**
- II) **Cellular Automata (Space-Time) Modelling**
- III) **Data Analytics For Gene Expression Response**
- IV) **Molecular Dynamics Modeling**
- V) **Machine Learning Modeling**

Discovering differential activation machinery of the Toll-like receptor 4 signaling pathways in MyD88 knockouts

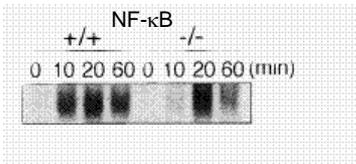
Kumar Selvarajoo*

Cell Interaction Group, Bioinformatics Institute, 138671, Singapore

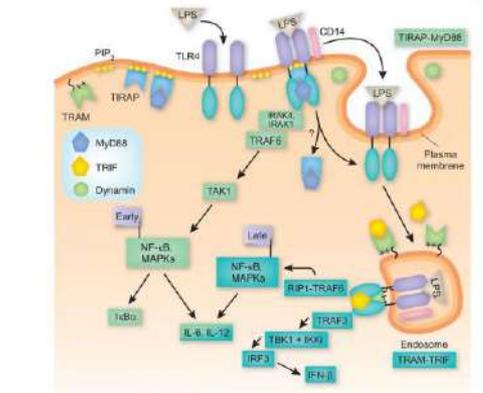
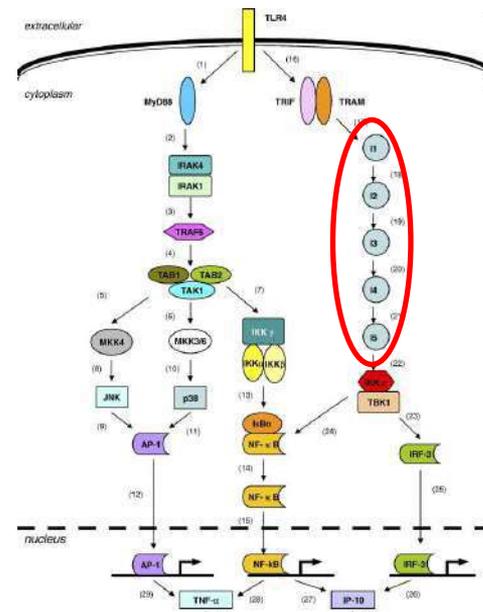
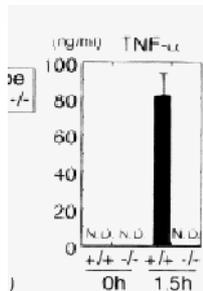
Received 6 December 2005; accepted 17 January 2006

Available online 26 January 2006

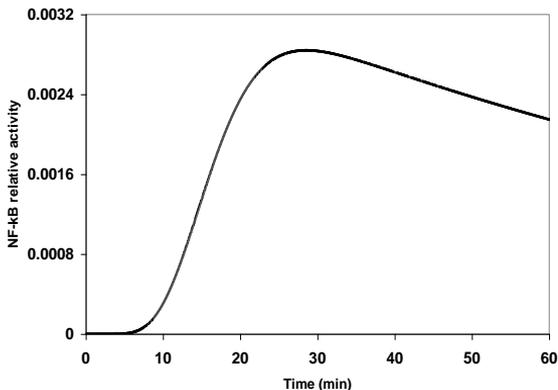
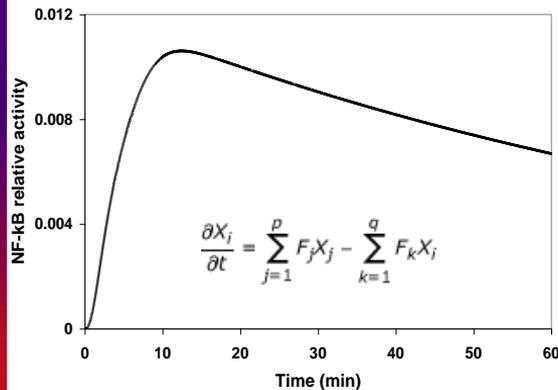
Edited by Gianni Cesareni



NF-κB activity & TNF expression under LPS stimulus wildtype (+/+) and MyD88 KO (-/-)
Kawai et al (1999) Immunity



Colin Watts (2008) Nature Immunology
Kagan et al (2008) Nature Immunology

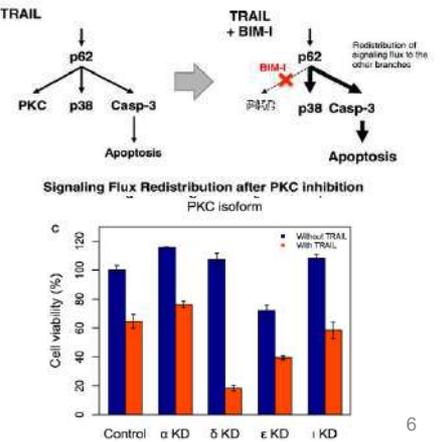
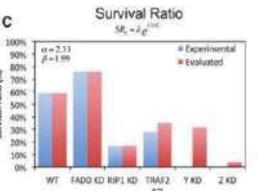
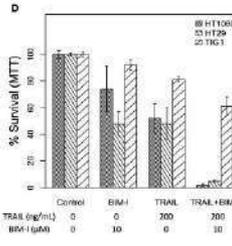
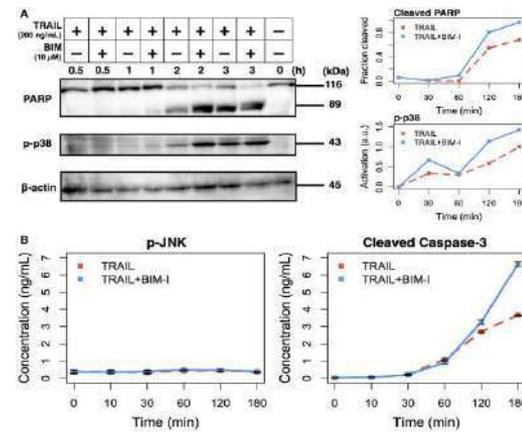
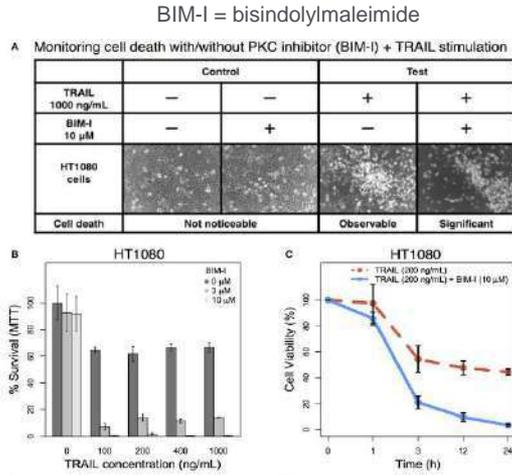
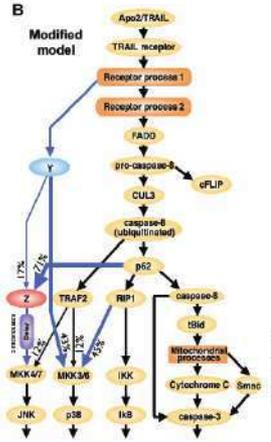
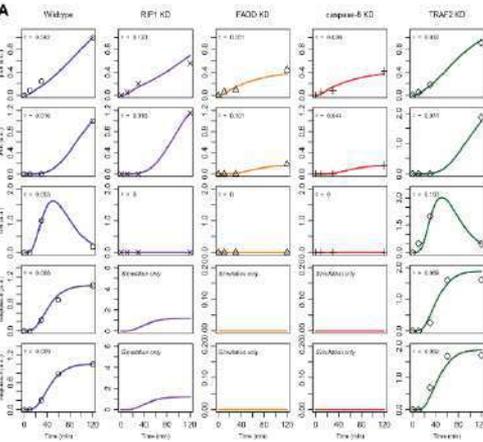
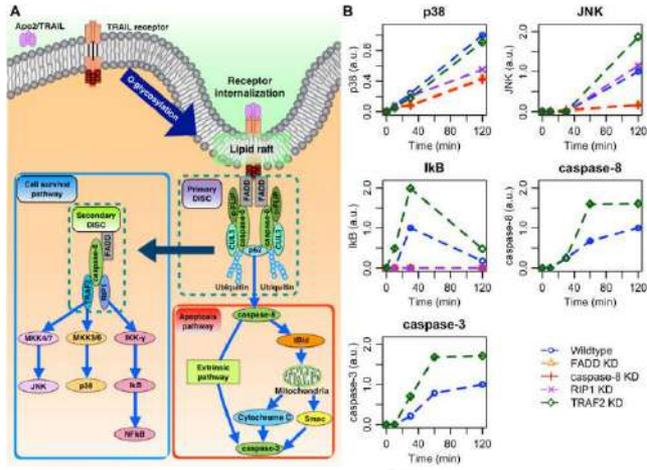


MODELING PROTEIN SIGNALING NETWORKS IN CANCER

Identifying Crucial Signaling Target For Cancer Apoptosis: **95% Cell Death**

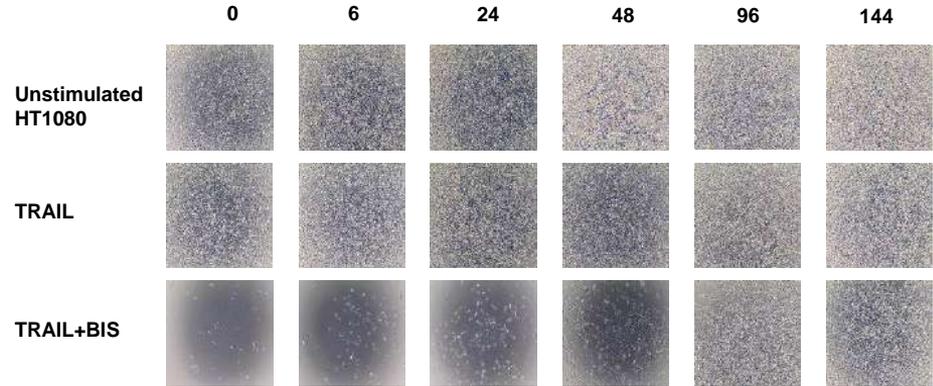


NG LIVES

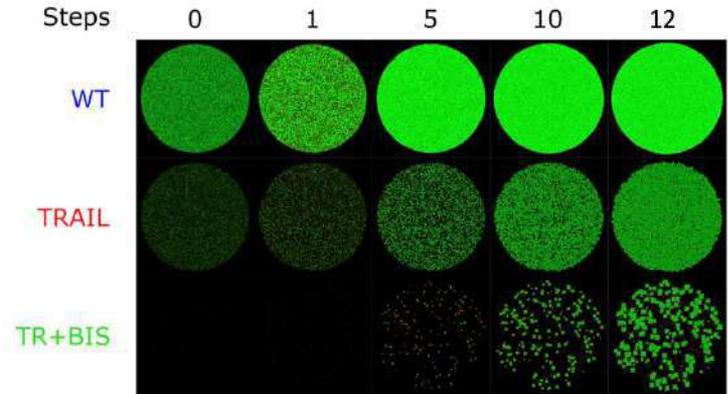
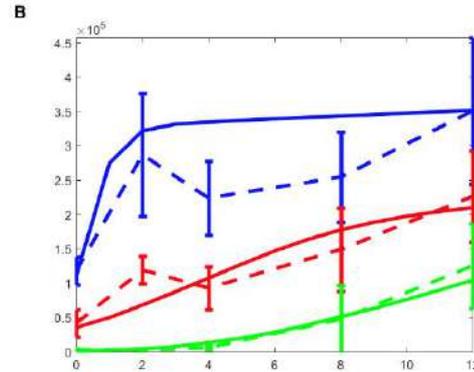
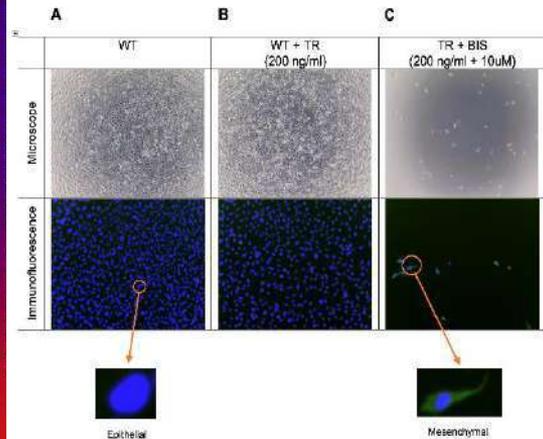


CELLULAR AUTOMATA SIMULATIONS FOR CANCER PROLIFERATIONS

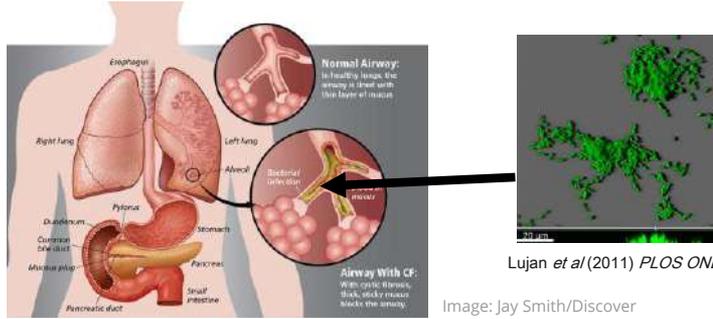
- Any E cell with less than 4 live neighbors become M cell on the next generation.
- Any M cell with more than 8 live neighbors become E cell on the next generation.
- Any dead/empty cell with 2 to 6 live neighbors (E or M) becomes live cell (E or M) as by division.
- Any M cell is able to move randomly to an empty cell on to the next generation.
- Any M cell that is unable to move becomes an E cell on to the next generation.



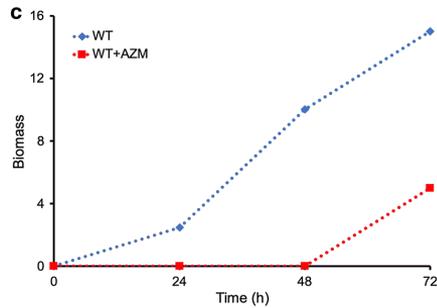
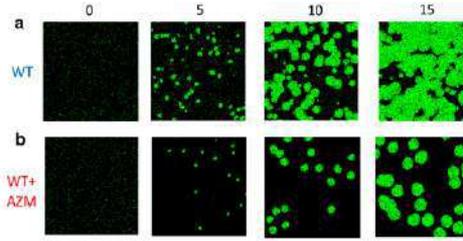
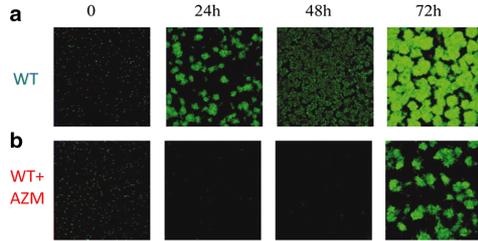
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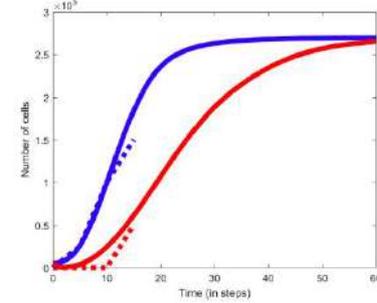
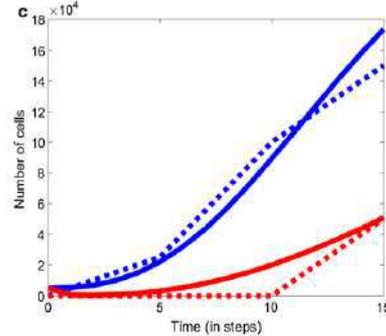
PSEUDOMONAS AERUGINOSA CELL PROLIFERATIONS



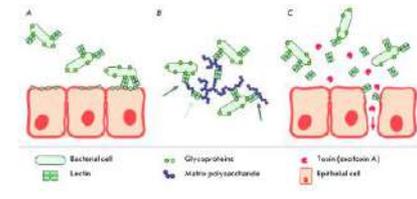
- pathogenic Gram-negative bacteria
- facilitates chronic infections in human by its rapid ability to form biofilms
- well-known for its intrinsic and acquired antibiotic resistance
- when infected in human, can cause death especially for patients with cystic fibrosis



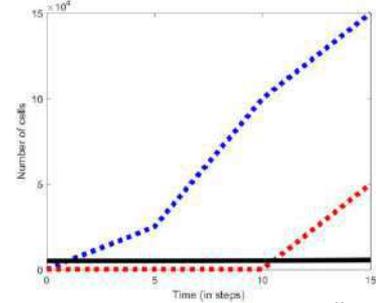
Gillis & Iglewski (2004) *J Clin Microbiol*



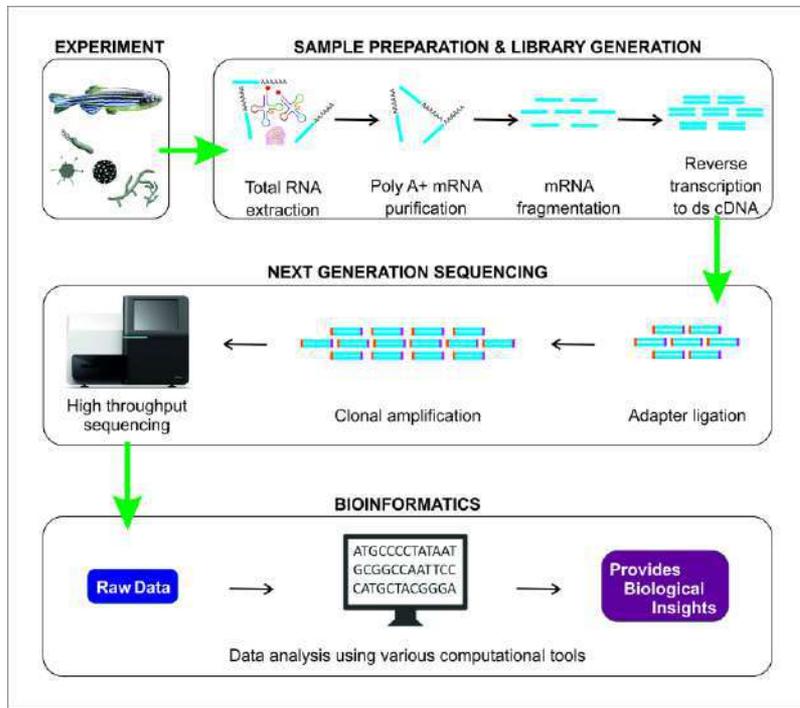
Deveaux & Selvarajoo (2019) *BMC Res Notes*



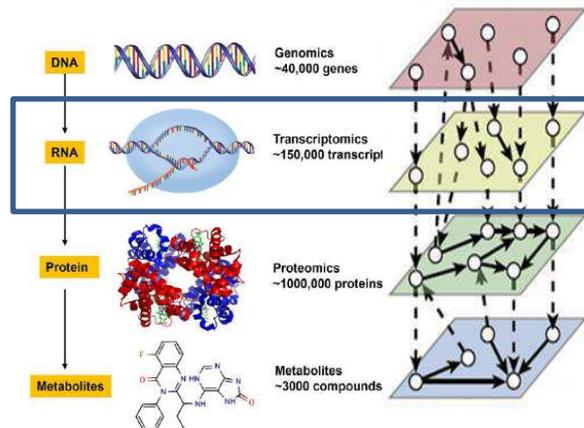
Grishin et al (2015) *Acta Naturae*



GENE EXPRESSION ANALYSIS, BIOINFORMATICS & DATA ANALYTICS



Sudhagar, et al (2018) *Int. J. Mol. Sci.*



Gene names

Raw read counts; Replicates of the same condition should be placed together

	a1 / t0	b1 / t0	c1 / t0	a2 / t1	b2 / t1	c2 / t1
15S_rRNA	12	0	8	17	6	1
21S_rRNA	195	180	113	268	93	125
HRA1	2	3	0	0	1	0
ICR1	98	148	197	84	161	540
LSR1	142	54	70	170	33	69
NME1	10	5	1	9	4	9
NTS1-2	3399	139	219	3362	106	241
PWR1	0	0	0	0	2	0

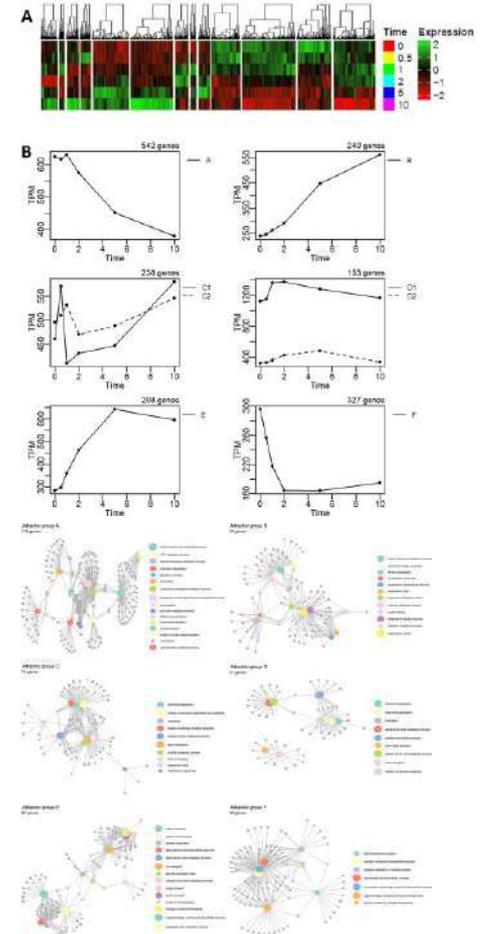
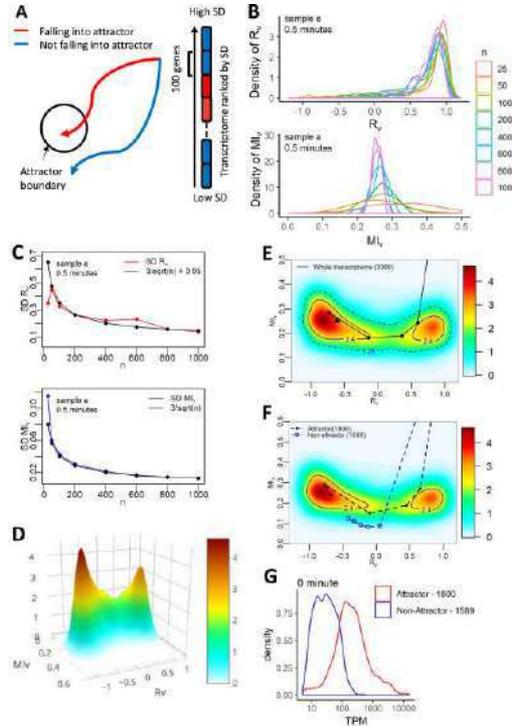
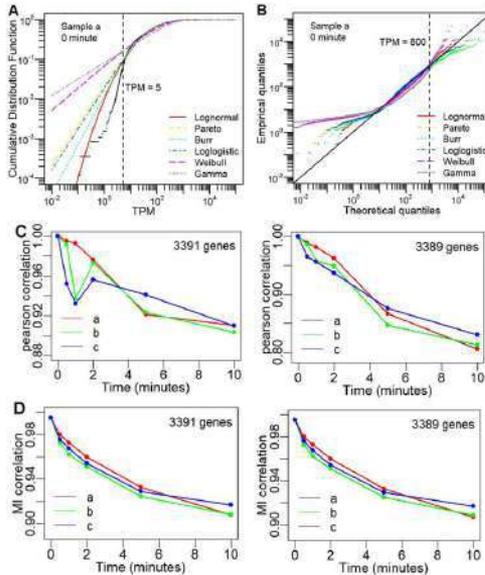
TRANSCRIPTOME-WIDE STATISTICAL ANALYSIS OF *E. COLI* DATA ANALYTICS

Understanding high-throughput gene expression response of *E. Coli* under aerobiosis

332 uncharacterized genes were revealed using Multi-dimensional statistics



ANAEROBIC TO AEROBIC TRANSITION



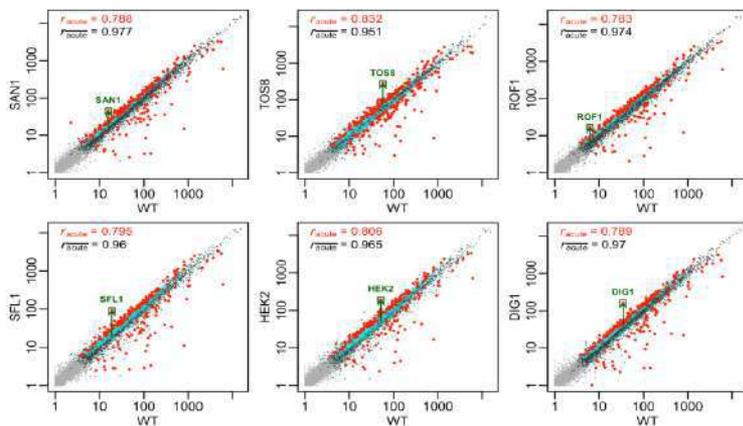
BIOFILMS ARE HIGHLY ROBUST

STRONG TRANSCRIPTOME-WIDE INVARIANCE BETWEEN DIFFERENT YEAST BIOFILM STRAINS

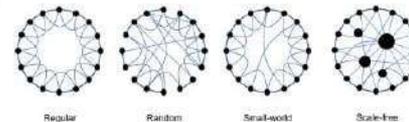
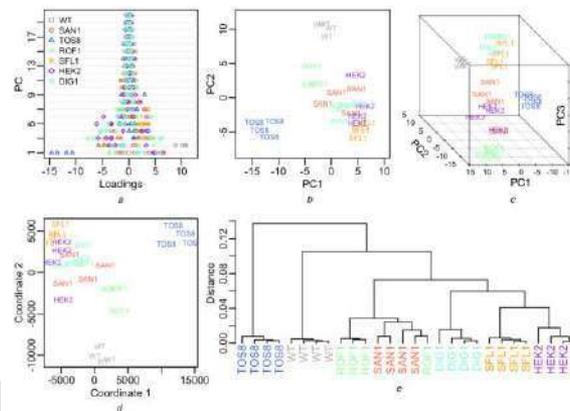
Overexpression screen identified 6 biofilm regulatory genes (Cromie GA, et al 2017, G3, GEO Accession: GSE98079)



Low to middle expressed genes are very highly correlated (even when small sampling of genes was performed) between the different genotypes, an indication of biological *sync*

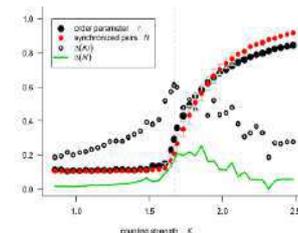
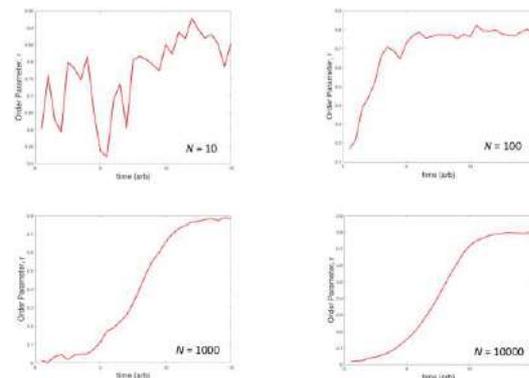


Piras, Chiow & Selvarajoo (2019) *IET Eng. Biol.*



$$\frac{d\theta_k}{dt} = \omega_k + \frac{K}{N} \sum_{j=1}^N \sin(\theta_j - \theta_k)$$

$$r(t) = \left| \frac{1}{N} \sum_{j=1}^N e^{i\theta_j(t)} \right|$$



Kitzbichler et al (2009) *Plos Comp Biol* 11

Selvarajoo (2019) *IET Eng. Biol.*

ABIOTRANS

A Biostatistical Tool for Transcriptomics Analysis



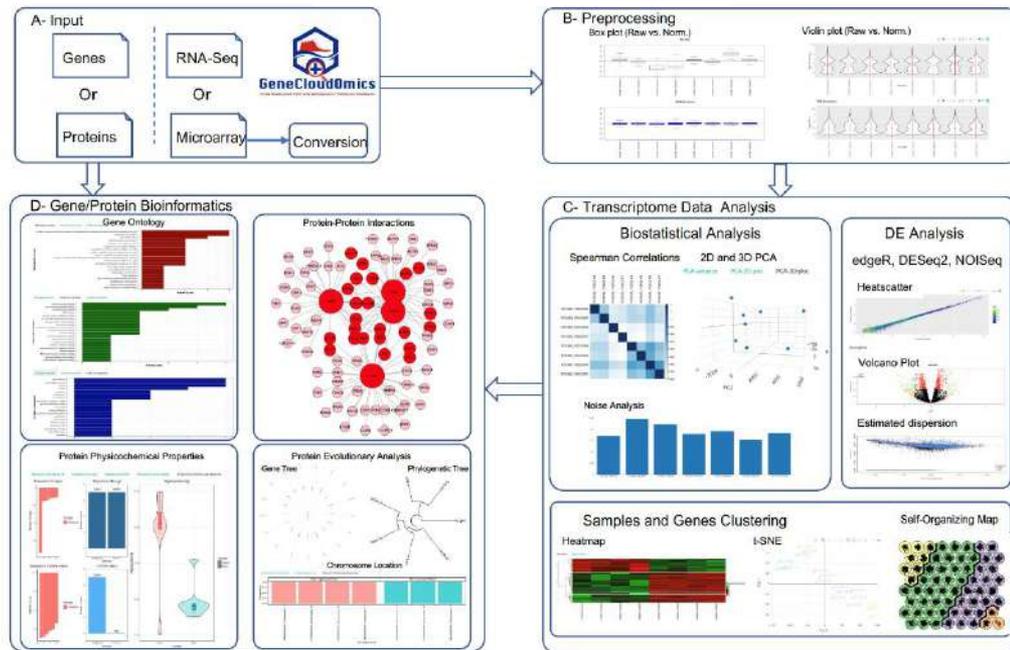
GENECLOUDOMICS

A Web Server for Transcriptome data Analysis and Visualization

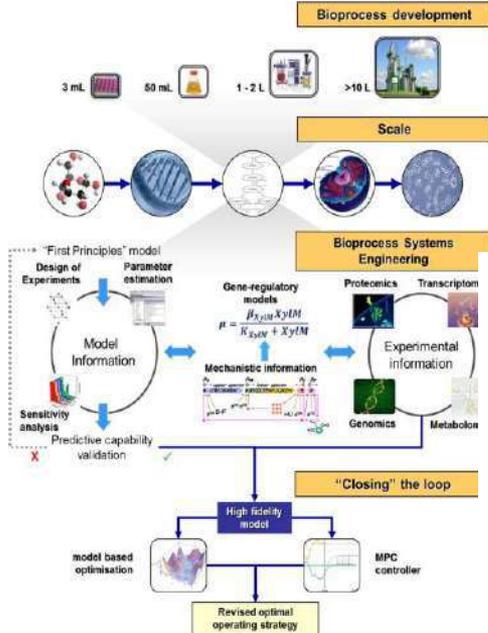


GeneCloudOmics

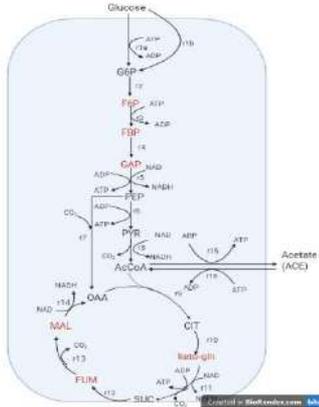
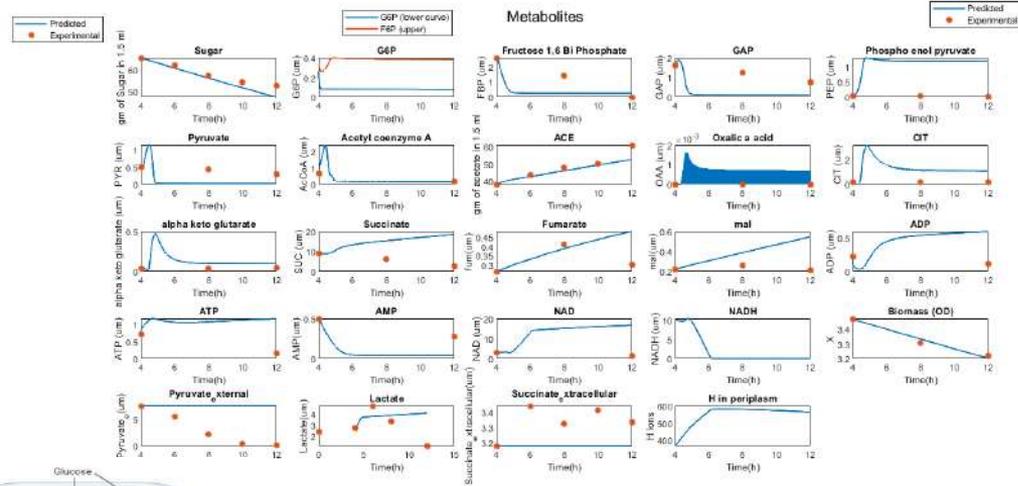
A Data Analytic Cloud Platform for Gene Expression Analysis and Visualization



BIOREACTOR MODELLING FOR VIRIDIFLOROL PRODUCTION



Koutinas, et al (2013) *Comput Struct Biotechnol J.*



Prasanth Mainali
SINGA PhD scholar,
SIFBI



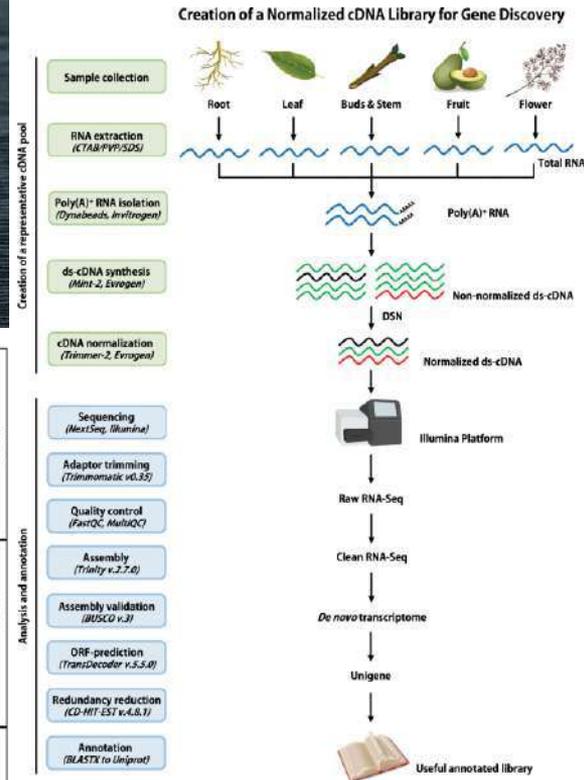
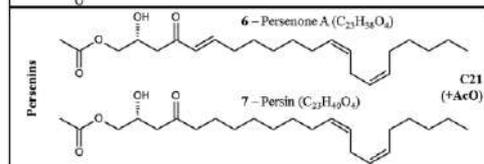
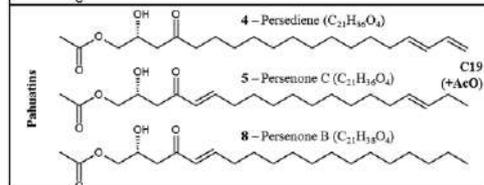
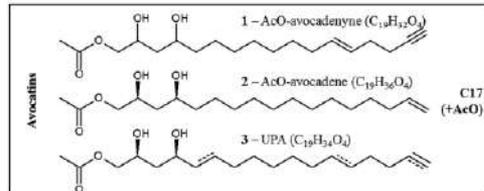
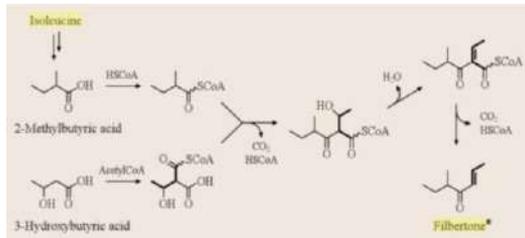
Yvonne Chow
SIFBI



Poh Chueh Loo
Biomedical & SynCTI, NUS

ENGINEERING MICROBES TO PRODUCE AGRO PRODUCTS

However, the biosynthetic pathways that produces avocadene and filberton are unknown

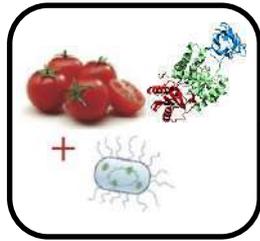
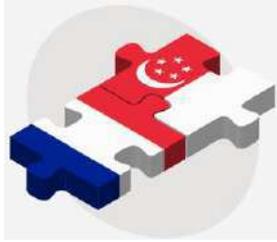


Chen Xixian
SIFBI

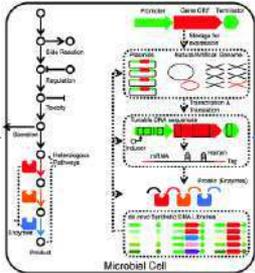




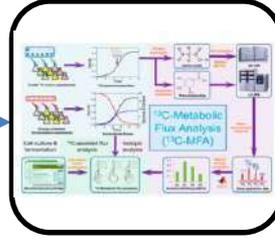
SYNTHETIC BIOLOGY & METABOLIC ENGINEERING FOR INDUSTRIAL SCALING: THE INTRA-CREATE GRANT



Food Compound Selection



Synthetic Biology or Metabolic Engineering



Systems Biology for Compound Pathway Optimization



Bioprocess Optimization



Industrial Scaling of Compound





Food Protein from Algae – Integrated Bioprocess Approach to Sustainable Living (SIFBI, BII, ICES & Sophie’s Bionutrients)

SINGAPORE FOOD STORY (SFS) R&D PROGRAMME 1ST ALTERNATIVE PROTEIN SEED CHALLENGE



Seafood Shell Waste

- 1.5 million tonnes in Southeast Asia alone
- **30 by 30 goal: increased local seafood production**

70% pure soluble protein

- suitable for food, milk products
- **30 by 30 goal: novel food supply**

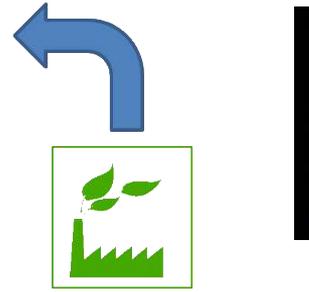
CHITIN



Uncommon re-use, resistant to biodegradation i.e. STABLE feedstock!

GLUCOSAMINE

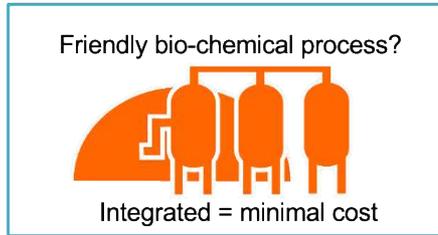
Dual clean source of carbon and nitrogen



Drop-in technology for microalgae protein factory

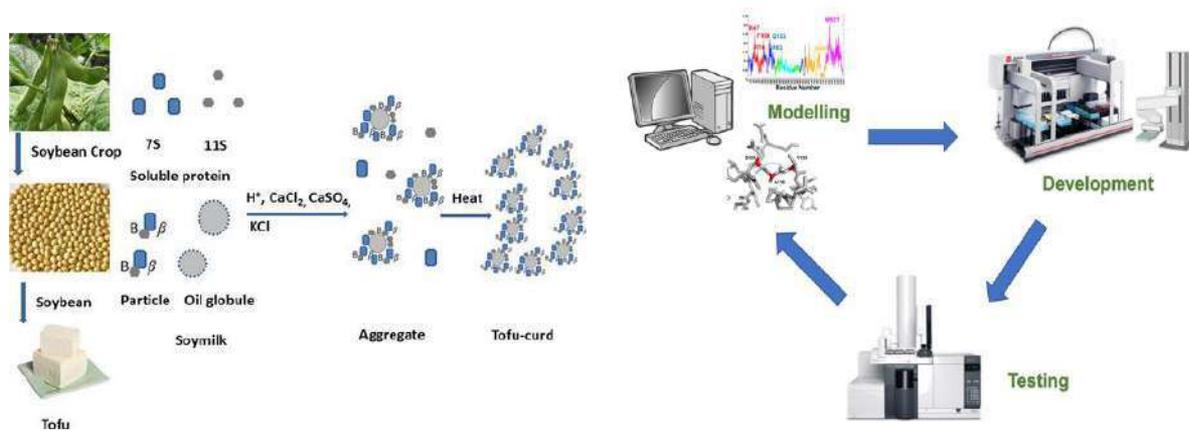


Seafood factories/restaurants (7ton/m) in Singapore

Proof-of-Concept: A multidisciplinary screening platform for functional proteins for alternative foods (SIFBI & BII)

SINGAPORE FOOD STORY (SFS) R&D PROGRAMME 1ST ALTERNATIVE PROTEIN SEED CHALLENGE



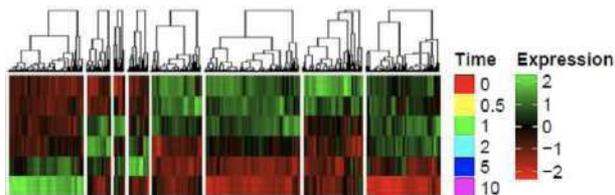
Zhao, et al (2019) *IFST*

BIOINFORMATICS AND SYSTEMS BIOLOGY

Our team expertise include; metabolic network modeling, transcriptomics & metabolomics data science, protein sequence and structure modeling, machine learning

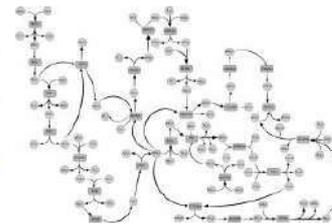
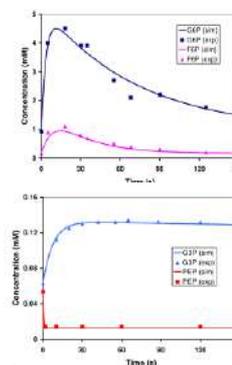
TRANSCRIPTOMICS & DATA SCIENCE

Thuy Tien



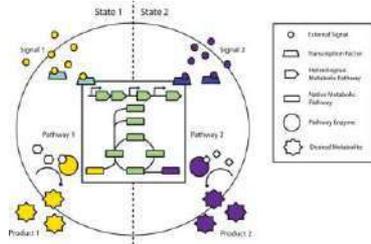
SIGNALING & METABOLIC MODELING

Helmy



BUILD

MODEL

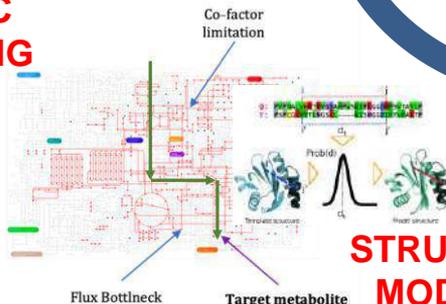


DESIGN

LEARN

SYNBIO & METABOLIC ENGINEERING

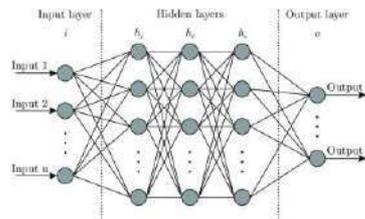
Jasmeet



TEST

STRUCTURAL MODELING

Derek



MACHINE LEARNING

Helmy



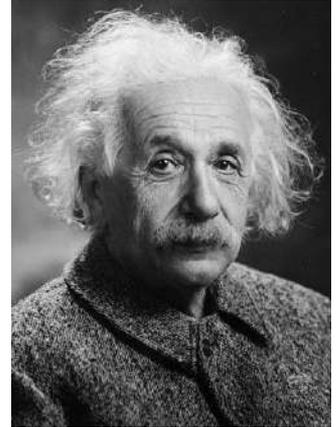


CREATING GROWTH, ENHANCING LIVES



THANK YOU

www.a-star.edu.sg



“Everything should be made as simple as possible. But not simpler”

Albert Einstein