



EFTHYMIOS MOTAKIS

STATISTICIAN/COMPUTATIONAL
BIOLOGIST



Cardiovascular
Research Institute (CVRI)

PERSONAL

Name	Efthymios Motakis
Birthday	4th January 1977 (42)
Relationship	Married
Nationality	Greek
Born	Chania, Crete, GR
Languages	Greek, English

CONTACT

Mobile	+65 9388 0421
Email	mdcfmo@nus.edu.sg
Skype	emotakis1

WORK

Experience	10+ years
Currently	Senior Research Fellow

EDUCATION

PhD	Statistics, Computational Biology
Master	Statistics/Biostatistics
Degree	Statistics

TIMELINE

- 2019** Senior Research Fellow
Cardiovascular Research
Institute. National University
of Singapore. SG
- 2016** Senior Postdoctoral Fellow
RIKEN. Center for Life Science
Technologies. Yokohama
Japan
- 2012** Postdoctoral Fellow
Bioinformatics Institute, A*STAR
Singapore,
Singapore
- 2007** Ph.D. in Statistics
University of Bristol
United Kingdom
- 2002** M.Sc. in Statistics
Athens University of Economics
and Business
Athens, Greece
KU Leuven, Belgium
- 1999** B.Sc. Statistics
Athens University of Economics
and Business
Athens,
Greece

ABOUT ME

I am a Senior Research Fellow at the Cardiovascular Research Institute of the National University of Singapore.

I have several years of professional experience in Computational Biology, Bioinformatics and Statistics.

Currently, I am mainly working on single-cell transcriptomics of cardiac regeneration and reprogramming, on the dynamics and characterization of cardiac cell populations and on the prediction of Heart Failure biomarkers with plasma proteomics. I am a member of the Human Cell Atlas consortium.

REFERENCES

Roger Foo
Professor at Cardiovascular Research
Institute. National University of Singapore.
E foosyr@gis.a-star.edu.sg

Allstair Forrest
Professor at Harry Perkins Institute of
Medical Research
The University of Western Australia.
E alistair.forrest@perkins.uwa.edu.au

Plero Carninci
Deputy Director of the RIKEN Center for
Integrative Medical Sciences
RIKEN Yokohama. Japan.
E carninci@riken.jp

TEACHING & SUPERVISION

Co-supervisor of the Phd candidate Ms Sharmelee Selvaraji (School for Integrative Sciences & Engineering, NUS) studying the epigenetic signatures of neuroinflammation in a chronic hypo perfusion model.

MAIN PROJECTS

Characterization of cardiac non-myocyte populations in TAC and Sham mouse hearts.

Characterisation of the cardiomyocyte transdifferentiation dynamics in mice.

CONFESS monitors cell cycle and predicts cell cycle regulators in proliferating cells.

Molecular mechanisms of induced atrioventricular malformations in chicken embryos.

WGS and GWAS of Heart Failure from three diverse Asian populations in Singapore (ATTRACT).

Estimation of Heart Failure biomarkers with plasma proteomics and cardiac single-cell RNA-seq.

ONLINE PROFILE



Twitter
www.twitter.com/ArisStefanosSn



LinkedIn
www.linkedin.com/in/efthymios-motakis-74707656/



RESEARCH TOPICS

Single Cell Transcriptomics
scRNA-seq, C1-CAGE

Bulk-cell transcriptomics
RNA-seq, CAGE

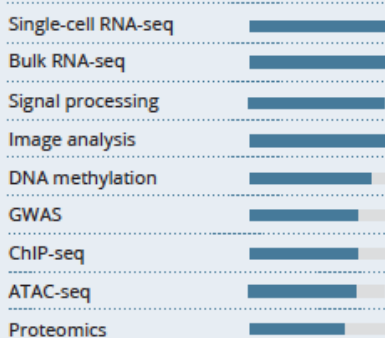
Bulk-cell transcriptomics
Microarrays, Wavelets

Chromatin organization in
heart failure

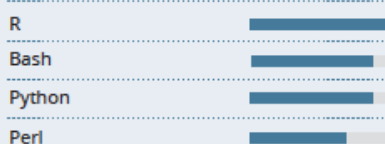
Signal processing in Molec-
ular Dynamics simulations

Cancer stratification

DATA ANALYSIS SKILLS



PROGRAMMING SKILLS



PUBLICATIONS

C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution.
Kouno T et al. Nature Communications, 10 (1):360 (2019).

CONFESS: Fluorescence-based single-cell ordering in R
Motakis E and Low DH. bioRxiv (2018).

Single-cell transcriptomes of fluorescent, ubiquitination-based cell cycle indicator cells
Böttcher M et al. BioRxiv 088500 (2015).

Retinoic acid potentiates inflammatory cytokines in human mast cells: identification of mast cells as prominent constituents of the skin retinoid network.
Babina M et al. Mol Cell Endocrinol, 406:49-59 (2015).

A promoter-level mammalian expression atlas.
Forrest AR et al. Nature, 507(7493):462-70 (2014).

Mast cell transcriptome elucidation: what are the implications for allergic disease in the clinic and where do we go next?
Babina M et al. Expert Rev Clin Immunol, 10(8):977-80 (2014).

Redefinition of the human mast cell transcriptome by deep-CAGE sequencing.
Motakis E et al. Blood, 123(17):e58-67 (2014).

Variance stabilization and normalization for one-color microarray data using a data-driven multiscale approach.
Motakis E et al. Bioinformatics, 22(20):2547-53 (2006).

Impact of adenoviral transduction with SREBP1c or AMPK on pancreatic islet gene expression profile: analysis with oligonucleotide microarrays.
Diraison F et al. Diabetes, 53 Suppl 3:S84-91 (2004).

Robust CTCF-based chromatin architecture underpins epigenetic changes in the heart failure stress-gene response.
Lee DP et al. Circulation, 139(16):1937-1956 (2019).

deltaGseg: macrostate estimation via molecular dynamics simulations and multiscale time series analysis.
Low DH, Motakis E. Bioinformatics, 29(19):2501-2 (2013).

Macrostate identification from biomolecular simulations through time series analysis.
Zhou W et al. J. Chem. Inf. Model, 52(9):2319-24 (2012).

Transposon insertional mutagenesis in mice identifies human breast cancer susceptibility genes and signatures for stratification.
Chen L et al. PNAS, 114 (11) E2215-E2224 (2017).

Sense-antisense gene-pairs in breastcancer and associated pathological pathways.
Grinchuk OV et al. Oncotarget, 8;6(39):42197-221 (2015).

A robust tool for discriminative analysis and feature selection in paired samples impacts the identification of the genes essential for reprogramming lung tissue to adenocarcinoma.
Toh SH et al. BMC Genomics, 12 Suppl 3:S24 (2011).

Complex sense-antisense architecture of TNFAIP1/POLDIP2 on 17q11.2 represents a novel transcriptional structural-functional gene module involved in breast cancer progression.
Grinchuk OV et al. BMC Genomics, 11 Suppl 1:S9 (2010).

Data-driven approach to predict survival of cancer patients: estimation of microarray genes' prediction significance by Cox proportional hazard regression model.
Motakis E et al. IEEE Eng Med Biol Mag, 28(4):58-66 (2009).

LEGEND



1st Author



Shared 1st Author



Corresponding Author

GRANTS

NUHS Seed Fund 2019 - A multi-platform computational pipeline for the accurate prediction of cell cycle regulation applied to proliferating human cardiomyocytes.

HOBBIES

guitar

basketball, comics, photography, books, baking, traveling, reading