

Mahmoud Ahmed

Postdoc - Cancer Genomics

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RESEARCH INTERESTS

- Rare variant prioritisation
 - Biological Network Perturbations
 - Repurposing of cancer drugs for novel targets
 - OMICS data integration
 - Open source scientific software
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EDUCATION

- **PhD.** Gyeongsang National University, South Korea March 2021
Project: Hierarchical regulation of autophagy genes
 - **MS.** Gyeongsang National University, South Korea March 2018
Project: Autophagy genes involvement in cell differentiation
 - **MBBCh.** Cairo University, Egypt Sep 2014
Three years of preclinical studies. Three years of clinical rotations. One year of internship.
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RESEARCH EXPERIENCE

Postdoctoral Fellow. The Institute of Cancer Research, London Feb 2023 – Present

- Developed annotation and prioritisation pipelines (*genomictools*) to identify and interpret pathogenic variants
- Identified risk genes in cohorts and families with childhood kidney cancer
- Quantified the contributions of known cancer predisposition genes in adult glioma datasets
- Coordinated the harmonization and joint analysis of datasets with external collaborators

Senior Researcher. Gyeongsang National University, South Korea Feb 2021 – Jan 2023

- Developed an open-source pipeline for repurposing cancer drugs for novel targets (*LINPSAPP*) and tools to integrate functional data (*target, segmentr*)
 - Led a cross functional team investigating regulators of anti-metastatic genes
 - Studied the role of autophagy in development and disease
 - Supervised summer medical students; introduced tools of computational research
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TECHNICAL SKILLS

- **Data Processing:** RNA-Seq, ChIP-Seq, WES, WGS, and Genotyping Arrays
- **Analysis Workflows:** Small & structural variant analysis, Burden analysis, and Case-control association studies. Differential gene expression and Biological network perturbations
- **Languages & Scripting:** R (Advanced), Python, Bash, Nextflow (scalable pipeline development), Markdown, and LaTeX
- **Software Management:** Git, Conda and Docker/Singularity containers
- **Infrastructure & Compute:** High-Performance Computing (HPC) clusters, Genomics England (GEL), DNA-Nexus, and Trusted Research Environments (TREs)

OPEN SOURCE SOFTWARE

Nextflow Pipelines

- **genomictools:** A suite of Nextflow pipelines engineered for scalable genomic data workflows. Features specialized modules for:
 - Calling copy number and structural variants from arrays, exome, and longreads data
 - Annotating variants using VEP, SpliceAI, Pangolin, AlphaGenome, ATsnp, and DeepMVP
 - Filtering and prioritising pathogenic variants
 - Studying familial segregation and linkage of genetic markers
 - Identify and assign individuals to genetic ancestry
 - Perform association and gene burden analysis in large cohorts
 - Integrate genomic data with gene expression, and somatic variants

R/Bioconductor Packages

- **pcr:** An R package for quality assessment, analysis and testing of qPCR data (CRAN)
- **target:** An R Package to predict combined function of transcription factors (Bioconductor)
- **colocr:** An R package for conducting co-localization analysis on fluorescence images (CRAN)
- **segmentr:** Perform chromatin segmentation in R by calling ChromHMM (Bioconductor)

Interactive Web Applications

- **LINPSAPP:** A database for cancer cell-specific perturbations of biological networks (Shinyapp)
 - **TARGETAPP:** A web app to predict combined function of transcription factors (Shinyapp)
 - **miRCancerdb:** A database for microRNA-gene/protein expression in cancer (Shinyapp)
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PATENT

- Ahmed, M, Kim, DR. (2025). Method for analyzing cancer cell-specific therapeutic agents using biological network perturbation (Patent No. 10-2834015). Korean Intellectual Property Office.
 - A framework for integrating causal biological networks and perturbation data
 - A prepackaged analysis and public database with the potential to be extended
 - A proof of work study of Nilotinib and AT-9283 as cell cycle regulators in melanoma

PUBLICATIONS

Pathogenic Variants Filtering and Prioratization

- Identifying rare variants in Wilms Tumour cohorts and families. *In preparation*. Reports findings from the FACT and St Jude cohorts exome and genome sequenced of Wilms cases
- Contribution of cancer predisposition genes in adult glioma. *In preparation*. Quantifies the contribution of known cancer genes in three large dataset: inhouse, GEL and TCGA
- Correcting the underestimate of copy number alterations in rare childhood cancer. *In preparation*. Reports the contribution of rare copy number variants in cancer genes in a large dataset of Wilms genotyped and sequenced cases

Task specialization in evolving cancer cells

- Ahmed M, Kim DR. Life history dynamics of evolving tumors: insights into task specialization, trade-offs, and tumor heterogeneity. *Cancer Cell Int*. 2024 Nov 6;24(1):364.
- Ahmed M, Pham TM, Kim HJ, Kim DR. Cancer cells forgo translating mRNA transcribed from genes of nonspecialized tasks. *FEBS Open Bio*. 2024 May;14(5):793-802.
- Ahmed M, Kim DR. Disruption of cancer cell functions by task-specific drug perturbations. *Front Pharmacol*. 2022 Aug 4;13:934843.

Transcriptional regulation of RKIP in cancer

- Lai TH, Ahmed M, Hwang JS, Bahar ME, Pham TM, Yang J, Kim W, Maulidi RF, Lee DK, Kim DH, Kim HJ, Kim DR. Manipulating RKIP reverses the metastatic potential of breast cancer cells. *Front Oncol*. 2023 Jul 4;13:1189350.
 - Lai TH, Ahmed M, Hwang JS, Zada S, Pham TM, Elashkar O, Kim DR. Transcriptional Repression of Raf Kinase Inhibitory Protein Gene by Metadherin during Cancer Progression. *Int J Mol Sci*. 2021 Mar 17;22(6):3052
 - Ahmed M, Lai TH, Zada S, Hwang JS, Pham TM, Yun M, Kim DR. Functional Linkage of RKIP to the Epithelial to Mesenchymal Transition and Autophagy during the Development of Prostate Cancer. *Cancers (Basel)*. 2018 Aug 16;10(8):273.
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- Hahm JR, Ahmed M, Kim DR. RKIP phosphorylation-dependent ERK1 activation stimulates adipogenic lipid accumulation in 3T3-L1 preadipocytes overexpressing LC3. *Biochem Biophys Res Commun*. 2016 Sep 9;478(1):12-17.

Perturbing biological networks in cancer cell lines

- Ahmed M, Kim DR. LINPS: a database for cancer-cell-specific perturbations of biological networks. *Database (Oxford)*. 2021 Aug 20;2021:baab048.
- Ahmed M, Lai TH, Kim W, Kim DR. A Functional Network Model of the Metastasis Suppressor PEBP1/RKIP and Its Regulators in Breast Cancer Cells. *Cancers (Basel)*. 2021 Dec 3;13(23):6098.
- Pham TM, Ahmed M, Lai TH, Bahar ME, Hwang JS, Maulidi RF, Ngo QN, Kim DR. Regulation of Cell Cycle Progression through RB Phosphorylation by Nilotinib and AT-9283 in Human Melanoma A375P Cells. *Int J Mol Sci*. 2024 Mar 3;25(5):2956. doi: 10.3390/ijms25052956.

Regulation of autophagy in development and disease

Autophagy and adipocyte differentiation

- Ahmed M, Lai TH, Pham TM, Zada S, Elashkar O, Hwang JS, Kim DR. Hierarchical regulation of autophagy during adipocyte differentiation. *PLoS One*. 2022 Jan 26;17(1):e0250865.
- Ahmed M, Lai TH, Kim DR. A Small Fraction of Progenitors Differentiate Into Mature Adipocytes by Escaping the Constraints on the Cell Structure. *Front Cell Dev Biol*. 2021 Oct 11;9:753042.
- Ahmed M, Lai TH, Hwang JS, Zada S, Pham TM, Kim DR. Transcriptional Regulation of Autophagy Genes via Stage-Specific Activation of CEBPB and PPARG during Adipogenesis: A Systematic Study Using Public Gene Expression and Transcription Factor Binding Datasets. *Cells*. 2019 Oct 25;8(11):1321.
- Ahmed M, Nguyen HQ, Hwang JS, Zada S, Lai TH, Kang SS, Kim DR. Systematic characterization of autophagy-related genes during the adipocyte differentiation using public-access data. *Oncotarget*. 2018 Feb 15;9(21):15526-15541.

Autophagy and cancer

- Ahmed M, Hwang JS, Lai TH, Zada S, Nguyen HQ, Pham TM, Yun M, Kim DR. Co-Expression Network Analysis of AMPK and Autophagy Gene Products during Adipocyte Differentiation. *Int J Mol Sci*. 2018 Jun 19;19(6):1808.

Tools for studying gene expression and regulation

- Ahmed M, Kim DR. Validating a re-implementation of an algorithm to integrate transcriptome and ChIP-seq data. *PeerJ*. 2023 Oct 20;11:e16318.
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- Ahmed M, Kim DR. target: an R package to predict combined function of transcription factors. *F1000Research* 2022, 10:344
 - Ahmed, M, Elashkar O, Lee JY, Jeong EA, Kim KE, Roh GS, and Kim DR. Tissue-Specific Gene Expression in Obese Hyperglycemic Mice. 2022. *All Life* 15 (1): 555–61.
 - Ahmed M, Min DS, Kim DR. Integrating binding and expression data to predict transcription factors combined function. *BMC Genomics*. 2020 Sep 7;21(1):610.
 - Ahmed M, Kim DR. cRegulome: an R package for accessing microRNA and transcription factor-gene expression correlations in cancer. *PeerJ*. 2019 Mar 8;7:e6509
 - Ahmed M, Lai TH, Kim DR. colocr: an R package for conducting co-localization analysis on fluorescence microscopy images. *PeerJ*. 2019 Jul 4;7:e7255.
 - Ahmed M, Min DS, Kim DR. Curated gene expression dataset of differentiating 3T3-L1 adipocytes under pharmacological and genetic perturbations. *Adipocyte*. 2020 Dec;9(1):600–608.
 - Ahmed M, Kim DR. Modelling the gene expression and the DNA-binding in the 3T3-L1 differentiating adipocytes. *Adipocyte*. 2019 Dec;8(1):401–411.
 - Ahmed M, Kim DR. pcr: an R package for quality assessment, analysis and testing of qPCR data. *PeerJ*. 2018 Mar 16;6:e4473.
 - Ahmed M, Nguyen H, Lai T, Kim DR. miRCancerdb: a database for correlation analysis between microRNA and gene expression in cancer. *BMC Res Notes*. 2018 Feb 7;11(1):103.

Editorial and book chapters

- Ahmed M, Kim HJ, Kim DR. Maximizing the utility of public data. *Front Genet*. 2023 Mar 31;14:1106631.
- Ahmed, M, & Kim, DR. Anti-cancer effect of RKIP via modulating autophagy during metastasis. In *Prognostic and Therapeutic Applications of RKIP in Cancer*. 2020 (pp. 277–293).

CONFERENCE PRESENTATIONS

- LINPS: a database for cancer cell-specific perturbations of biological networks. *BiocAsia* (2021)
 - Chromatin Segmentation Analysis in R. *BioC* (2021)
 - Hierarchical Regulation of Autophagy During Adipocyte Differentiation. *KSBMB* (2021)
 - target: An R package to Predict Combined Function of Transcription Factors. *BiocAsia* (2020)
 - Integrating binding and expression data to predict transcription factors combined function. *KSBMB* (2019)
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ACADEMIC SERVICE

- **Guest Editor:** Frontiers in Pharmacology. Research topic: “Opportunities and Challenges in Reusing Public Genomics Data” (2021)
- **Organizing Committee Member & Host:** BioConductor Asia Conference (2021 & 2022)
- **Grant & Sponsorship Coordinator:** BioConductor International Conference (2021-2023)

TEACHING & SUPERVISION EXPERIENCE

- **Supervisor,** Evaluating Clinical Evidence Training. NHI Service, South Korea (2022)
- **Instructor,** Conducting meta-analysis in R. Gyeongsang National University (2022)
- **Instructor,** Introduction to data analysis in R - Gyeongsang National University (2022)
- **Workshop Facilitator,** Integrating gene expression and biological knowledge for drug discovery and repurposing. ISCB Academy (2021)
- **Supervisor,** A training on reproducible computational research. MRC in Korea (2018)

AWARDS/FELLOWSHIPS/SCHOLARSHIPS

- **Research Fellowship.** Human Resource Development in Bio-medicine Center 2021 - 2023
- **Young Scientist Program Award.** KSBMB/FAOBMB 2020 & 2021
- **Young Pioneer Research Award.** Gyeongsang National University 2018 & 2019
- **Brain Korea 21 Plus Scholarship.** MS & PhD Courses. South Korea 2016 - 2021

REFERENCES

- **Richard Houlston** | The Institute of Cancer Research, London | richard.houlston@icr.ac.uk
- **Deok Ryong Kim** | Gyeongsang National University, South Korea | drkim@gnu.ac.kr