

Yongsoo Kim, Ph.D.

Assistant professor in oncogenomics

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I am always interested in how informatics technologies (especially machine learning) can make our life better, especially in the treatment of cancer patients. To this end, I exposed myself to both biology and computer science during my training. During Ph.D. training, I had participated in systems biology lab and machine learning group, working on identifying better ways to model biological networks. After Ph.D., I continued my academic career in cancer genomics as a postdoctoral fellow at the NKI, where I worked as a part of the group of prof. dr. Wilbert Zwart, a molecular biologist, and the group of prof. dr. Lodewyk Wessels, a computational scientist. As of 1st of October 2018, I started as an assistant professor in oncogenomics, at Cancer Center Amsterdam (CCA), UMC Amsterdam, Location VUmc. At the current position, I am delighted with having many interactions with clinicians, pathologists, and oncologists who see patients, getting more stimulation towards translational research.

Education Background

- 2018.10- **Assistant professor**, Cancer Centre Amsterdam (CCA), Department of Pathology, University Medical Center (UMC) Amsterdam, Location Vrij University Medical Center (VUmc)
- 2015.1-2018.9 **Postdoctoral Fellow**, The Netherlands Cancer Institute (the NKI), Plesmanlaan 121, 1066 DX Amsterdam, The Netherlands.
- 2013.9-2014.12 **Postdoctoral Fellow**, Systems Biology Lab, Deagu Gyeongbuk Institute of Science & Technology (DGIST), Daegu, South Korea.
- 2007.3-2013.8 **Ph.D.**, School of Interdisciplinary Bioscience and Bioengineering, POSTECH, Pohang, Korea (www.postech.ac.kr).
*Participating two laboratories: Machine Learning Lab (advisor: Prof. Seungjin Choi) & Systems Biology Lab (advisor: Prof. Daehee Hwang).
Thesis title: "Probabilistic Inference in Context-specific Dynamic Networks"
(Committee member: Prof. Seungjin Choi, Prof. Daehee Hwang, Prof. Chi-Hyuck Jun, Prof. Sung Ho Ryu, and Prof. Seong Jin Kim).
- 2003.3-2007.2 **B.S.**, Department of Computer Science and Engineering, POSTECH, Pohang, Korea, 790-784.
Senior project (2006 fall): Development of transcription factor binding site marking program (advisor: Prof. Seungjin Choi)
- * The School of Interdisciplinary Bioscience and Bioengineering (I-BIO) offers a unique chance to pursue interdisciplinary projects that involving more than two laboratories.

Peer-reviewed journal publications (selected)

1. M. G. M. Roemer, T. van de Brug, E. Bosch, D. Berry, N. Hijmering, P. Stathi, K. Weijers, J. Doorduijn, J. Bromberg, M. van de Wiel, B. Ylstra, D. de Jong, **Y. Kim**[†], Multi-scale spatial modeling of immune cell distributions enables survival prediction in primary central nervous system lymphoma. *iScience*. **26**, 107331 (2023).
2. Y. Im, **Y. Kim**[†], A Comprehensive Overview of RNA Deconvolution Methods and Their Application. *Mol Cells*. **46**, 99–105 (2023).
3. B. Andrade Barbosa, S. D. van Asten, J. W. Oh, A. Farina-Sarasqueta, J. Verheij, F. Dijk, H. W. M. van Laarhoven, B. Ylstra, J. J. Garcia Vallejo, M. A. van de Wiel, **Y. Kim**[†], Bayesian log-normal deconvolution for enhanced in silico microdissection of bulk gene expression data. *Nat Commun*. **12**, 6106 (2021).
4. **Y. Kim**, T. Bismeyer, W. Zwart, L. F. A. Wessels, D. J. Vis, Genomic data integration by WON-PARAFAC identifies interpretable factors for predicting drug-sensitivity in vivo. *Nat Commun*. **10**, 1–12 (2019).
5. S. Stelloo, E. Nevedomskaya*, **Y. Kim***, K. Schuurman, E. Valle-Encinas, J. Lobo, O. Krijgsman, D. S. Peeper, S. L. Chang, F. Y.-C. Feng, L. F. A. Wessels, R. Henrique, C. Jerónimo, A. M. Bergman, W. Zwart, Integrative epigenetic taxonomy of primary prostate cancer. *Nature Communications*. **9**, 4900 (2018).
6. T. M. Severson*, **Y. Kim***, S. E. P. Joosten, K. Schuurman, P. van der Groep, C. B. Moelans, N. D. ter Hoeve, Q. F. Manson, J. W. Martens, C. H. M. van Deurzen, E. Barbe, I. Hedenfalk, P. Bult, V. T. H. B. M. Smit, S. C. Linn, P. J. van Diest, L. Wessels, W. Zwart, Characterizing steroid hormone receptor chromatin binding landscapes in male and female breast cancer. *Nat Commun*. **9**, 482 (2018).
7. **Y. Kim**, J.-H. Jang, S. Choi, D. Hwang, TEMPI: probabilistic modeling time-evolving differential PPI networks with multiPle information. *Bioinformatics*. **30**, i453–i460 (2014).
8. Y. Kim, S. Han, S. Choi, D. Hwang, Inference of dynamic networks using time-course data. *Briefings in Bioinformatics*. **15**, 212–228 (2014).
9. **Y. Kim**, T.-K. Kim, Y. Kim, J. Yoo, S. You, I. Lee, G. Carlson, L. Hood, S. Choi, D. Hwang, Principal network analysis: identification of subnetworks representing major dynamics using gene expression data. *Bioinformatics*. **27**, 391–398 (2011).

* Equal contributions, †Corresponding authors

Grants

2018-2023	"Computational approaches for enhancing knowledge discovery using digital cancer genomic biobank"	€300,000	Amsterdam UMC
2019-2020	"Molecular markers for upfront identification of 1p/19p-codeleted oligodendroglioma patients with long, 'treatment-naïve' postoperative survival"	€100,000	Amsterdam UMC (Co-PI)
2019-2020	"A computational framework to model cellular interplays in the tumor microenvironment of B cell lymphoma"	\$99,080	Leukemia Reserach Foundation
2020-2021	"A computational framework to address within-tumour heterogeneity of pancreatic ductal adenocarcinoma "	€149.687	Cancer Center Amsterdam (CCA2019-9-62)
2022-2025	"A comprehensive multi-layer characterization of intra-tumoral heterogeneity in pancreatic ductal adenocarcinom"	€605,463	Dutch Cancer Society (KWF-13774)
2023-2026	"An affordable RNA profiling-based tumor microenvironment characterization for the optimal care of cervical cancer patients"	€410.873	Health Holland
2023-2027	"Establishing a Reproducible and Accessible Bioinformatics Framework to determine Tumor microenvironment and heterogeneity"	€300.000	NWO