Biographical Sketch

1a. Personal details

- **Name:** Yongsoo Kim, Ph.D.
- **Current position:** Assistant Professor in Multiomics Data Science, Department of Pathology, Amsterdam University Medical Center (UMC)
- Personal website: anoyaro84.github.io
- **Email:** yo.kim@amsterdamumc.nl
- **Orcid:** https://orcid.org/0000-0002-2995-2131

1b. Education/training

- **Doctorate/PhD** (MSc combined)
  - **University/College of Higher Education:** POSTECH (Pohang University of Science and Technology), Pohang, Korea
  - **Date:** March 2007–August 2013
  - **Studies:** School of Interdisciplinary Bioscience and Bioengineering
  - **Title of thesis:** "Probabilistic Inference in Context-specific Dynamic Networks"

- **Bachelor's ('BS')**
  - **University/College of Higher Education:** POSTECH (Pohang University of Science and Technology), Pohang, Korea
  - **Date:** March 2003–February 2007
  - **Studies:** Department of Computer Science and Engineering

2. Positions and Honors

I. Positions and employment

- **2018.10–Present:** Assistant Professor, Cancer Center 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 (NKI), Amsterdam, The Netherlands
- **2013.9–2014.12:** Postdoctoral Fellow, Systems Biology Lab, Daegu Gyeongbuk Institute of Science & Technology (DGIST), Daegu, South Korea

II. Honors and awards

- KOSEF - National Junior Research Fellowship (2009) - approx. €10,000
- New Investigator Award - Leukemia Research Foundation (2019) - $99,080

III. Grants and Fundings

- **Extramural fundings (>1.5M)**

1.	**2024–2029:** Horizon Europe (Co-PI), “SPatial Analysis of Cancer Evolution in the Tumour Immune MicroEnvironment (SPACETIME)”	€374,935 (of €12M)
2.	**2023–2027**: NWO, “Establishing a Reproducible and Accessible Bioinformatics Framework to determine Tumor microenvironment and heterogeneity”	€300,000
3.	**2023–2026:** Health Holland, “An affordable RNA profiling-based tumor microenvironment characterization for the optimal care of cervical cancer patients”	€410,873
4.	**2022–2026**: Dutch Cancer Society (KWF-13774), “A comprehensive multi-layer characterization of intra-tumoral heterogeneity in pancreatic ductal adenocarcinoma”	€605,463

- **Intramural fundings (>2M)**

1.	**2025–2029**: Stitching ADORE, “Cell2sample”	€688,129
2.	**2024–2029**: Stitching ADORE (Co-PI), “GEN-BioDORA”	€1,000,000
3.	**2020–2021**: Cancer Center Amsterdam (CCA2019-9-62), “A computational framework to address within-tumour heterogeneity of pancreatic ductal adenocarcinoma”	€149,687
4.	**2019–2020**: Amsterdam UMC (Co-PI, non-competitive), “Molecular markers for upfront identification of 1p/19p-codeleted oligodendroglioma patients with long, ‘treatment-naïve’ postoperative survival”	€100,000
5.	**2018–2023**: Amsterdam UMC (non-competitive), “Computational approaches for enhancing knowledge discovery using digital cancer genomic biobank”	€300,000

III. Other relevant experience, output and professional memberships

- Has been serving as a reviewer for peer-review journals, including but not limited to below:
    - *Nature Communications (x3)*
    - *Cell Systems*
    - *Genome Biology*

3. Output

I. Preprint / Peer-reviewed publications (selected)

- J. Janssen*, T. Radonic*, M.F.B. Steketee*, S. van Asten, P.P. Eijk, F. van Maldegem, D.P. Noske, I. Bahce, J.J. Garcia Vallejo, M.A. van de Wiel, B. Ylstra†, Y. Kim†, Hidden RNA profiles of cells in the tumor microenvironment accurately revealed by malignant cell fraction-informed deconvolution. Preprint at https://doi.org/10.21203/rs.3.rs-4252952/v1 (2024).
- 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).
- Y. Im, Y. Kim†, A Comprehensive Overview of RNA Deconvolution Methods and Their Application. *Mol Cells*. 46, 99–105 (2023).
- 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).
- Y. Kim, T. Bismeijer, 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).
- 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).
- 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).
- 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).
- Y. Kim, S. Han, S. Choi, D. Hwang, Inference of dynamic networks using time-course data. *Briefings in Bioinformatics*. 15, 212–228 (2014).
- 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).

II. Metrics (Google scholar)

- **H-index:** 21
- **i10-index:** 31

III. Education

- **Co-promoter for PhD students**
    - Barbara Andrade Barbosa
        - Thesis title: Solutions to navigate the oncogenomic maze through advanced computational methods
        - PhD thesis with reviewer committee
    - **Jurriaan Janssen** - started in 2021
    - **Mischa Steketee** - started in 2022
    - **Stef Eflings** - started in 2024
    - **Dominika Martinovicová** - to start in 2025
    - **Nicola Miolato** - to start in 2025
- **MSc internship supervision**
    - > 5 students mostly from Bioinformatics / Systems Biology Master program
- **Teaching**
    - BKO-UTQ (university teaching qualification) at 22nd May, 2025 from VU
    - Tumor Biology and Clinical Behavior (TBCB) - course coordinator since 2023

IIII. Patents

- One patent in preparation

4. Brief summary of research over the last five years

My research is centered on efficiently analyzing multi-omics methods to understand disease better. My work has led to the development of several multi-omics integration methods to identify distinct subtypes of male breast cancer and prostate cancer, as well as to predict patient responses to various drugs. In recent years, many of my projects have been devoted to profiling the tumor microenvironment, particularly deconvolution methods using routinely collected bulk RNA-seq data. We are actively expanding this methodology to incorporate additional data modalities, including DNA-seq, proteomics, and spatial transcriptome data, to enable a more comprehensive characterization of cellular states through multiple lenses.