

15th Annual Meeting of the Korean Society of Medical Oncology & 2022 International Conference

- **Name:** Peter Jungsoo Park
- **Current Position & Affiliation:** Professor of Biomedical Informatics
Department of Biomedical Informatics
Harvard Medical School
- **Country:** USA

 • **Educational Background:**

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|-----------|-------|---------------------|------------------------------------|
| 1990-1994 | BA/MS | Applied Mathematics | Harvard College |
| 1994-1999 | PhD | Applied Mathematics | California Institute of Technology |
| 1999-2000 | MS | Biostatistics | Harvard School of Public Health |

 • **Professional Experience:**

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|-----------|---------------------|--|-----------------------------------|
| 2001-2006 | Instructor | Pediatrics | Harvard Medical School |
| 2006-2010 | Assistant Professor | Pediatrics | Harvard Medical School |
| 2010-2015 | Associate Professor | Pediatrics | Harvard Medical School |
| 2015-2016 | Associate Professor | Biomedical Informatics | Harvard Medical School |
| 2016- | Professor | Biomedical Informatics | Harvard Medical School |
| 2014- | Director | PhD Program in Bioinformatics & Integrative Genomics | Harvard Medical School |
| 2015- | Co-leader | Cancer Data Science Program | Harvard/Dana-Farber Cancer Center |

 • **Main Scientific Publications:**

1. Cortés-Ciriano I, Gulhan DC, Lee JJ, Melloni GEM, **Park PJ**. (2021) Computational analysis of cancer genome sequencing data. *Nat Rev Genet.* Online Dec 8.
2. Bizzotto S*, Dou Y*, Ganz J*, Doan RN, Kwon M, Bohrsen CL, Kim SN, Bae T, Abyzov A, NIMH Brain Somatic Mosaicism Network; **Park PJ****, Walsh CA** (2021). Landmarks of human embryonic development inscribed in somatic mutations. *Science*, 371:1249-1253
3. Dou Y, Kwon M, Rodin RE, Cortes-Ciriano I, Doan R, Luquette LJ, Galor A, Bohrsen CL, Walsh CA, **Park PJ**. (2020) MosaicForecast: accurate detection of mosaic variants in sequencing data without matched controls. *Nature Biotech*, 38:314-319.
4. Cortés-Ciriano I, Lee JJK, Xi R, Jain D, Jung YL, Yang L, Gordenin D, Klimczak LJ, Zhang CZ, Pellman DS, **Park PJ**. (2020) Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. *Nat Genet*, 52:331-341.
5. Gulhan DC, Lee JJK, Melloni GEM, Cortés-Ciriano I, **Park PJ**. (2019) Detecting the mutational signature of homologous recombination deficiency in clinical samples. *Nat Genet*,

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51:912-919.

6. Bohrson CL, Barton AR, Lodato MA, Rodin RE, Luquette LJ, Viswanadham VV, Gulhan DC, Cortés-Ciriano I, Sherman MA, Kwon M, Coulter ME, Galor A, Walsh CA, **Park PJ**. (2019) Linked-read analysis identifies mutations in single-cell DNA-sequencing data. *Nat Genet*, 51:749-754.
7. Yang L, Luquette LJ, Gehlenborg N, Xi R, Haseley PS, Hsieh C, Zhang C, Ren X, Protopopov A, Chin L, Kucherlapati R, Lee C, **Park PJ**. (2013) Diverse mechanisms of somatic structural variations in human cancer genomes, *Cell*, 153:919-29.
8. Kim TM, Laird PW, **Park PJ**. (2013) The landscape of microsatellite instability in colorectal and endometrial cancer genomes, *Cell*, 155:858-68.
9. Lee E, Iskow R, Yang L, Gokcumen O, Haseley P, Luquette LJ, Lohr JG, Harris CC, Ding L, Wilson RK, Wheeler DA, Gibbs RA, Kucherlapati R, Lee C, Kharchenko PV, **Park PJ**, and The Cancer Genome Atlas Research Network (2012) Landscape of somatic retrotransposition in human cancers, *Science*, 337:967-71.