

Research Opportunities in Computational Biology and Bioinformatics Targeting Cancer

Overview: A new group at the University of Arizona Cancer Center is recruiting individuals with expertise in the analysis of large data sets and the application of mathematical and statistical methods to complex problems.

Projects include: Direct analysis of molecular data (DNA or RNA sequencing), statistical analysis of prognostic and predictive markers, development of algorithms for the integration of independent forms of data. Representative publications are provided below.

Requirements: The ideal applicant must have expertise in R, and have the capacity to interact well with others in a multidisciplinary setting. Self-motivation and high degree of organization will be required for success in the positions. The exact job title and numeration will be dependent on the level of experience and training.

Enquiries: Individuals interested in the positions should send a brief letter of interest, and CV or resume by email to Erik Knudsen (eknudsen@email.arizona.edu)

Representative Recent Publications:

Metabolic Reprogramming of Pancreatic Cancer Mediated by CDK4/6 Inhibition Elicits Unique Vulnerabilities. Franco J, Balaji U, Freinkman E, Witkiewicz AK, Knudsen ES.
Cell Reports. 2016

Immunologic and Metabolic Features of Pancreatic Ductal Adenocarcinoma Define Prognostic Subtypes of Disease. Hutcheson J, Balaji U, Porembka MR, Wachsmann MB, McCue PA, Knudsen ES, Witkiewicz AK.
Clinical Cancer Research. 2016

Whole-exome sequencing of pancreatic cancer defines genetic diversity and therapeutic targets.
Witkiewicz AK, McMillan EA, Balaji U, Baek G, Lin WC, Mansour J, Mollaei M, Wagner KU, Koduru P, Yopp A, Choti MA, Yeo CJ, McCue P, White MA, Knudsen ES.
Nat Communications. 2015.

Systematically defining single-gene determinants of response to neoadjuvant chemotherapy reveals specific biomarkers.
Witkiewicz AK, Balaji U, Knudsen ES.
Clinical Cancer Research. 2014