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The Golji bioinformatics lab is dedicated to advancing drug discovery by mining through omics datasets to uncover drug mechanism of action, discover predictive biomarkers of response, find optimal patient stratification strategies, understand mechanism of drug resistance, and discover effective drug combinations. Our lab maintains an innovative atmosphere, ready both to apply new emerging machine learning methods where they can have impact and to apply established statistical analysis frameworks where needed.

We are currently interested in therapies targeting the MAPK pathway, which have been developed to treat RAS- or RAF-mutant tumors with high constitutive MAPK signaling. While single-agent targeted therapeutics are effective in inducing temporary tumor regression, almost all tumors develop - resistance. To overcome these challenges, targeted therapies have been combined in the clinic, including the combination of dabrafenib (BRAFi) and trametinib (MEKi) in BRAF+ melanoma and, more recently, in BRAF+ lung cancer. Identifying further effective therapeutic combinations for MAPK agents will be critical to progress in cancer treatment. Yet, systematically finding the ideal combination regimen remains a difficult

task. A priori it is not clear what combinations are likely to be most effective or what indication would be most susceptible to a given combination; empirically testing all possible combinations is impractical.

We propose to build computational models, which take into account the state of the tumor cell (i.e. its gene expression profile) combined with measured state changes upon single agent treatment and known sensitivity patterns from pooled shRNA and CRISPR screening to accurately predict synergistic combination partners for MAPK inhibitors.

## Selected Publications

### Tumor-derived IFN triggers chronic pathway agonism and sensitivity to ADAR loss. [2]

Liu H, Golji J, Brodeur LK, Chung FS, Chen JT, deBeaumont RS, Bullock CP, Jones MD, Kerr G, Li L, Rakiec DP, Schlabach MR, Sovath S, Gowney JD, Pagliarini RA, Ruddy DA, MacIsaac KD, Korn JM, McDonald ER.  
*Nat Med.* 2019 Jan;25(1):95-102.

### Project DRIVE: A Compendium of Cancer Dependencies and Synthetic Lethal Relationships Uncovered by Large-Scale, Deep RNAi Screening. [3]

McDonald ER, de Weck A, Schlabach MR, Billy E, Mavrakis KJ, Hoffman GR, Belur D, Castelletti D, Frias E, Gampa K, Golji J, Kao I, Li L, Megel P, Perkins TA, Ramadan N, Ruddy DA, Silver SJ, Sovath S, Stump M, Weber O, Widmer R, Yu J, Yu K, Yue Y, Abramowski D, Ackley E, Barrett R, Berger J, Bernard JL, Billig R, Brachmann SM, Buxton F, Caothien R, Caushi JX, Chung FS, Cortés-Cros M, deBeaumont RS, Delaunay C, Desplat A, Duong W, Dvoske DA, Eldridge RS, Farsidjani A, Feng F, Feng J, Flemming D, Forrester W, Galli GG, Gao Z, Gauter F, Gibaja V, Haas K, Hattenberger M, Hood T, Hurov KE, Jagani Z, Jenal M, Johnson JA, Jones MD, Kapoor A, Korn J, Liu J, Liu Q, Liu S, Liu Y, Loo AT, Macchi KJ, Martin T, McAllister G, Meyer A, Mollé S, Pagliarini RA, Phadke T, Repko B, Schouwey T, Shanahan F, Shen Q, Stamm C, Stephan C, Stucke VM, Tiedt R, Varadarajan M, Venkatesan K, Vitari AC, Wallroth M, Weiler J, Zhang J, Mickanin C, Myer VE, Porter JA, Lai A, Bitter H, Lees E, Keen N, Kauffmann A, Stegmeier F, Hofmann F, Schmelzle T, Sellers WR.  
*Cell.* 2017 Jul 27;170(3):577-592.

### CRISPR Screens Provide a Comprehensive Assessment of Cancer Vulnerabilities but Generate False-Positive Hits for Highly Amplified Genomic Regions. [4]

Munoz DM, Cassiani PJ, Li L, Billy E, Korn JM, Jones MD, Golji J, Ruddy DA, Yu K, McAllister G, DeWeck A, Abramowski D, Wan J, Shirley MD, Neshat SY, Rakiec D, de Beaumont R, Weber O, Kauffmann A, McDonald ER 3rd, Keen N, Hofmann F, Sellers WR, Schmelzle T, Stegmeier F, Schlabach MR.  
*Cancer Discov.* 2016 Aug;6(8):900-13.

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[3] <https://www.ncbi.nlm.nih.gov/pubmed/28753431>

[4] <https://www.ncbi.nlm.nih.gov/pubmed/27260157>

[5] <https://www.ncbi.nlm.nih.gov/pubmed/?term=Golji+J%5BAuthor%5D>