Temple

Neuroscience Institute and Department of Neurosurgery, Baylor Scott & White Health, Temple, Texas 76502, USA.

Understanding the functional impact of cancer somatic mutations represents a critical knowledge gap for implementing precision oncology. It has been increasingly appreciated that the interaction profile mediated by a gene mutation provides a fundamental link between genotype and phenotype. However, specific effects on biological signaling networks for the majority of mutations are largely unknown by experimental approaches. To resolve this challenge, Li et al. developed e-MutPath (edgetic Mutation-mediated Pathway perturbations), a network-based computational method to identify candidate 'edgetic' mutations that perturb functional pathways. e-MutPath identifies informative paths that could be used to distinguish disease risk factors from neutral elements and to stratify disease subtypes with clinical relevance. The predicted targets are enriched in cancer vulnerability genes, known drug targets but depleted for proteins associated with side effects, demonstrating the power of network-based strategies to investigate the functional impact and perturbation profiles of genomic mutations. Together, e-MutPath represents a robust computational tool to systematically assign functions to genetic mutations, especially in the context of their specific pathway perturbation effect [1)].

1)
Li Y, Burgman B, Khatri IS, Pentaparthi SR, Su Z, McGrail DJ, Li Y, Wu E, Eckhardt SG, Sahni N, Yi SS. e-MutPath: computational modeling reveals the functional landscape of genetic mutations rewiring interactome networks. Nucleic Acids Res. 2020 Nov 19:gkaa1015. doi: 10.1093/nar/gkaa1015. Epub ahead of print. PMID: 33211847.