This is a question which, after generic clinical trials, is still very much answered by observing patient outcomes. Methods from bioinformatics and systems biology are making some inroads into answering this question more systematically through integration of a variety of data sources and important algorithmic developments. I will dig in to some of our work in this area, but if you can’t wait refer to Xie et al. (2012) Annual Review of Pharmacology and Toxicology 52: 361-379. I’ll also describe the importance of open science to this collective effort.