

**PAIRWISE PRINCIPLE FOR PREDICTING
THE EFFECTS OF MULTI-DRUG
COMBINATIONS ON BACTERIA
AND HUMAN CANCER CELLS**

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4:00 P.M. NSH 184

Drugs are commonly used in combinations larger than two for treating multi-component diseases, severe bacterial infections, and many types of cancer. However, the actions of individual drugs are often coupled through their effects on complex intracellular networks. As a result, it is generally impossible to infer directly from the effects of individual drugs the net effect of a multi-drug combination. Here, we combine automated measurements of population growth with classical tools from statistical physics to develop a mechanism-independent framework for calculating the bacterial growth response to a variety of drug combinations, including protein synthesis inhibitors, fluoroquinolones, folic acid synthesis inhibitors, and analgesics. Specifically, we experimentally show that the responses of gram negative, *Escherichia coli*, and gram positive, *Staphylococcus aureus*, bacteria to drug pairs are sufficient to infer the effects of larger drug combinations. We also extend this approach to include multiple types of human cancer cells as well as drug-resistant bacteria, providing perhaps a step towards a unified view of multi-drug response that does not rely on specific drug chemistry. Remarkably, the accurate predictions of this framework suggest that the growth responses of both bacterial and cancer cells obey statistical rather than chemical laws for combinations larger than two.

Condensed
Matter
Seminar

All interested
persons are
cordially
invited to
attend.