

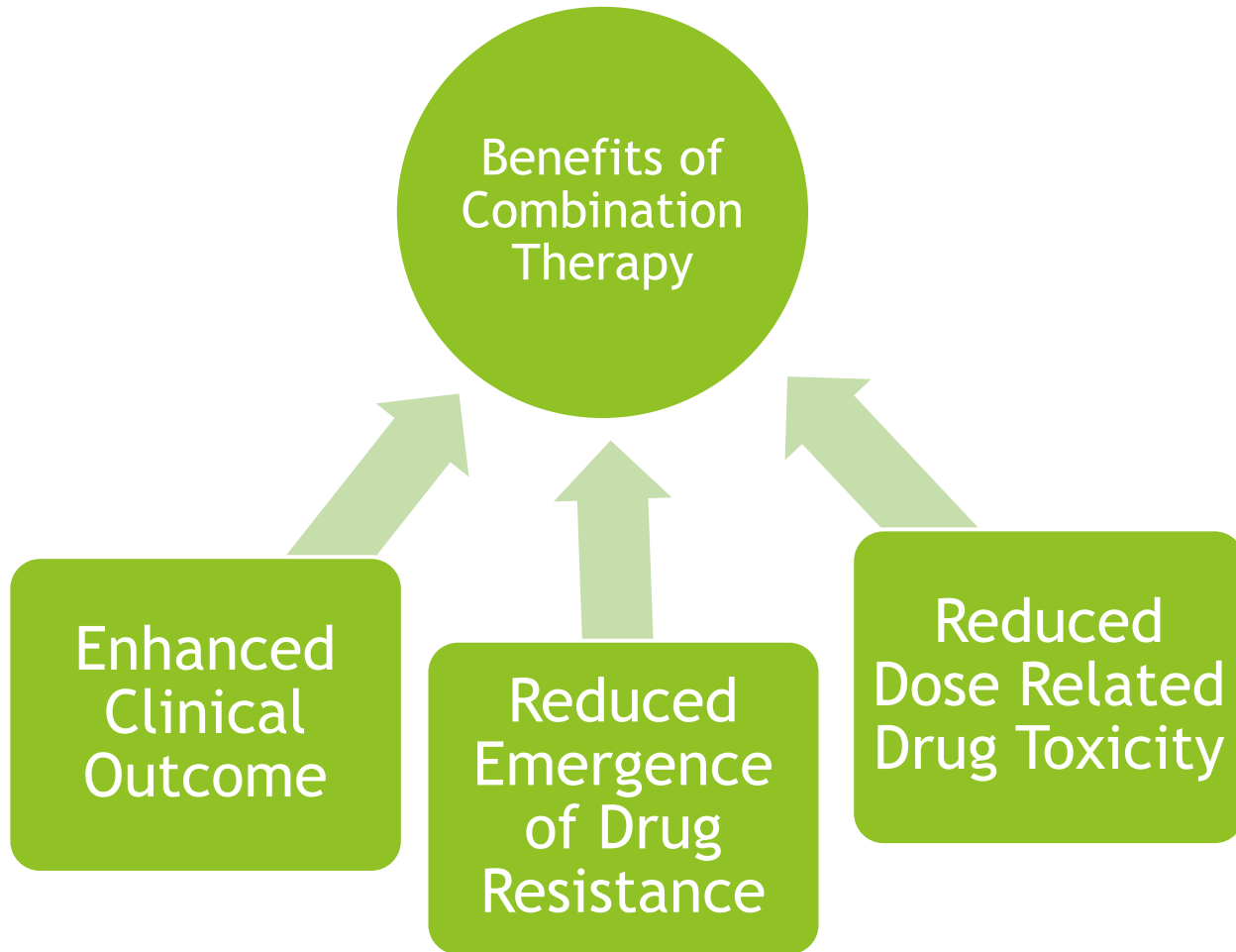
# Advancing Research through Computing 2021

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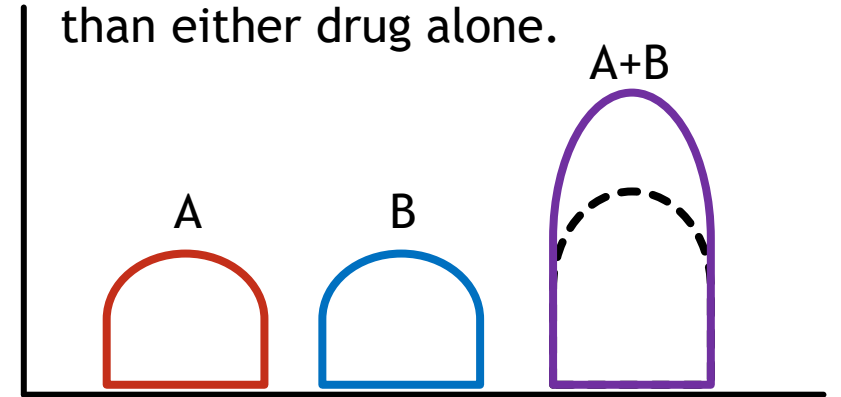
Ron Nafshi

Predicting the Effects of Drug Combinations Using  
Probabilistic Matrix Factorization

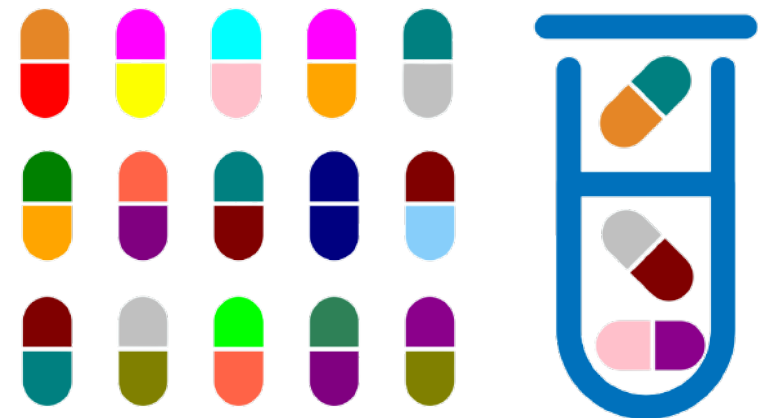
Combination therapies are increasingly used to treat disease, but discovering them requires a lot of resources



The combination of drugs A and B has a greater therapeutic effect than either drug alone.



Testing all possible 2-drug combinations is costly and inefficient. Computation can help.



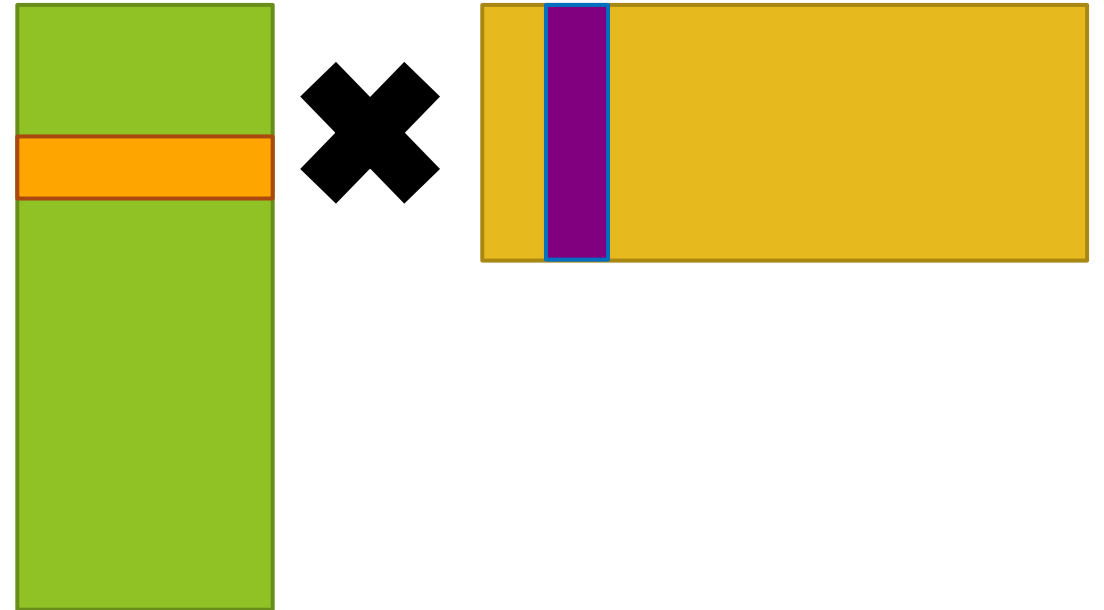
Probabilistic Matrix Factorization (PMF) can impute missing efficacies for drug combinations

$$\mathbf{M}_{ij} = \mathbf{A}_i \mathbf{B}_j^T$$

Drug Effect

	Red Pill	Purple Pill	Orange Pill	Green Pill	Blue Pill
Red Pill		★	★★★		★★★
Purple Pill	★				★
Orange Pill	★★★			★	
Green Pill			★		★★★
Blue Pill		★		★★★	

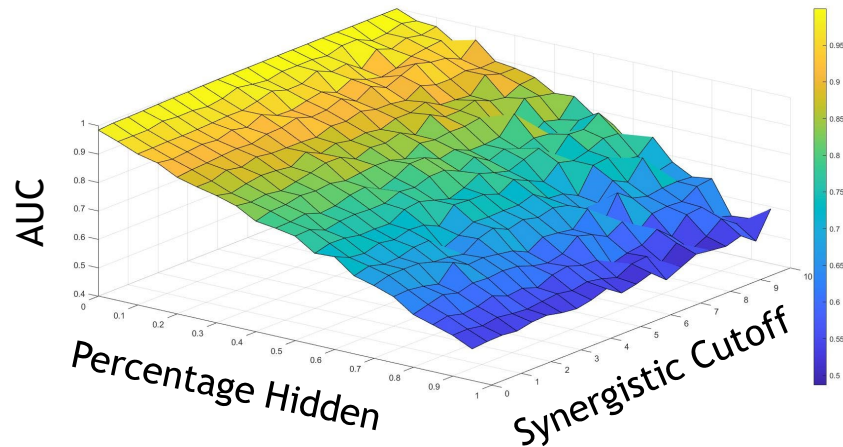
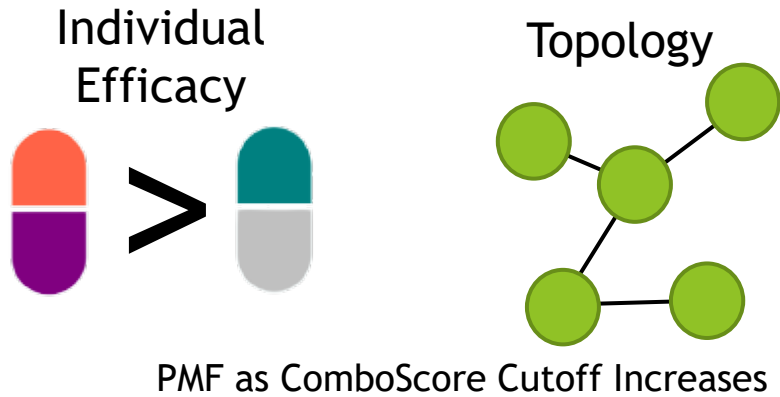
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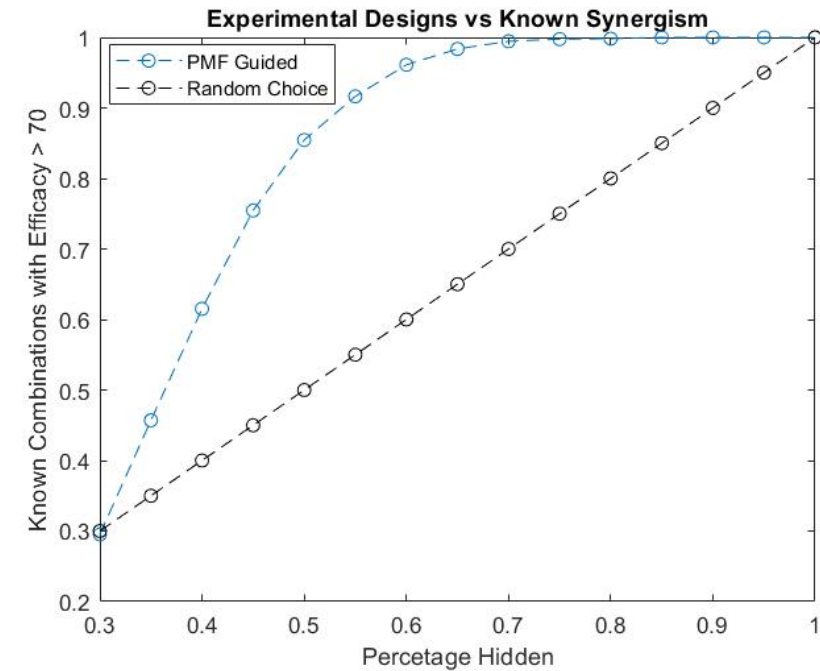
- We can express the matrix as the product of two low-rank matrices of latent factors, and then estimate them using gradient descent.
- For very large datasets, using low-rank approximations greatly decreases computational time

# PMF reduces experimental burden by 58%

- We investigate the effects of the starting set of accuracy



- PMF is robust to changes in node identity and topology and predicts all elements with equal accuracy.



## Conclusions

- A guided assay can identify 95% of all efficacious combinations while testing 60% of all available combinations.
  - Much greater than random chance.
- Since the accuracy of PMF does not change depending on node identity or topology, PMF guided assays could expediate current drug synergism assays.