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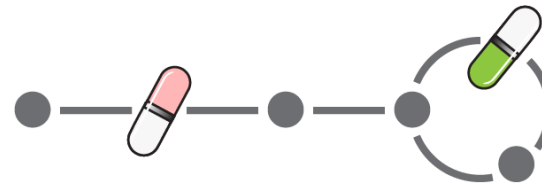
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Step 2

Identify existing drugs that mimic the effect of gene variants through pathway analysis



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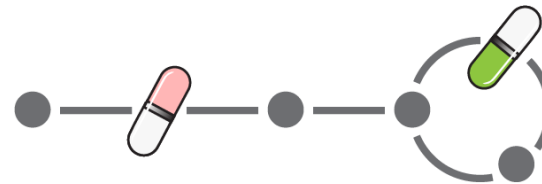
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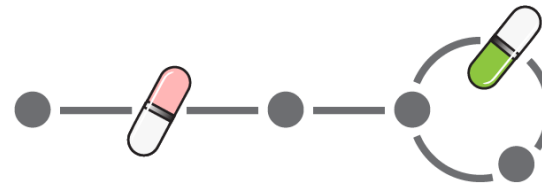
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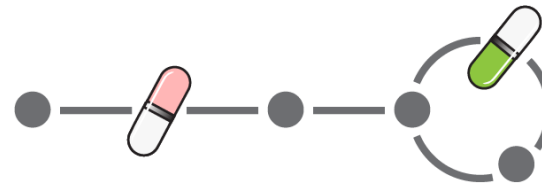
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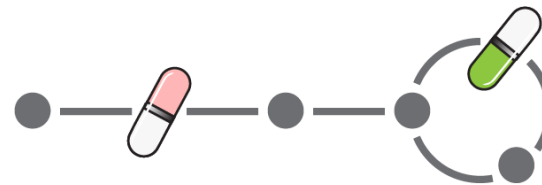
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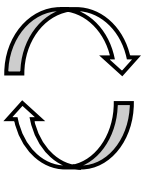
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Fuel hypotheses back to step 4 and iterate!



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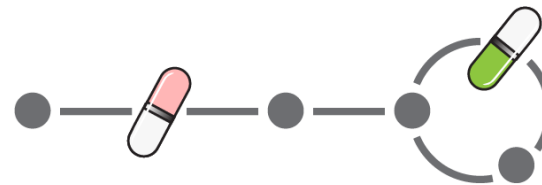
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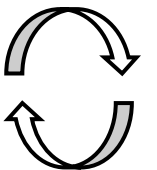
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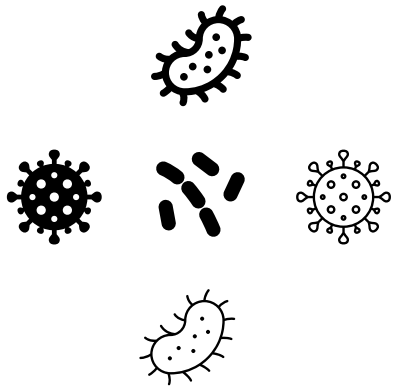
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Ongoing clinical example

Leveraging heterogeneity in antibiotic prescribing preferences across hospitals and physicians to emulate target trials using electronic health records

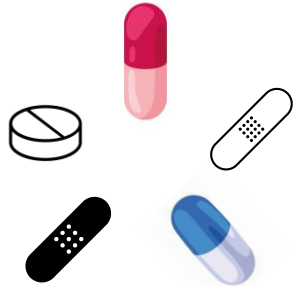
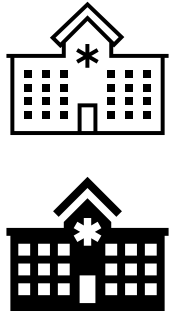


~100–200 known
bacterial species
causing sepsis

Comparative effectiveness



Across hospitals:
≠ guidelines
≠ practices

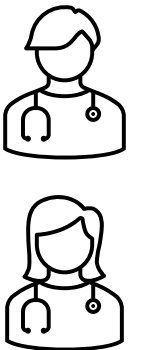


80+ antibiotics
in hospital drug
libraries



Drug safety

Among physicians:
≠ training
≠ preferences



Next steps

1. Extend the trial emulation pipeline to other drug classes.
2. Identify subgroups of patients likely to benefit the most/least from treatment.
3. Understand the mediating role of biomarker control.
4. Contrast matching/weighting approaches with other inferential strategies (e.g., using prescribing preferences as IVs).
5. Develop a framework to federate target trial emulations across databases, healthcare systems, and countries.

Current engineering needs

1. Build cohort datasets at scale, across 5+ databases, by extending existing algorithms
 - a) AP-HP (2 ICUs, at Pitié-Salpêtrière and Henri Mondor hospitals)
 - b) MIMIC
 - c) eICU
 - d) NIH All of Us
 - e) UK Biobank and UK CPRD
2. Replicate a target trial investigating the renal and cognitive side effects of an antibiotic combination therapy of interest (piperacillin-tazobactam + vancomycin)

Thanks for your attention!

Any questions?

Feel free to reach out!
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Sorbonne Public Health Institute, PEPITES team

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