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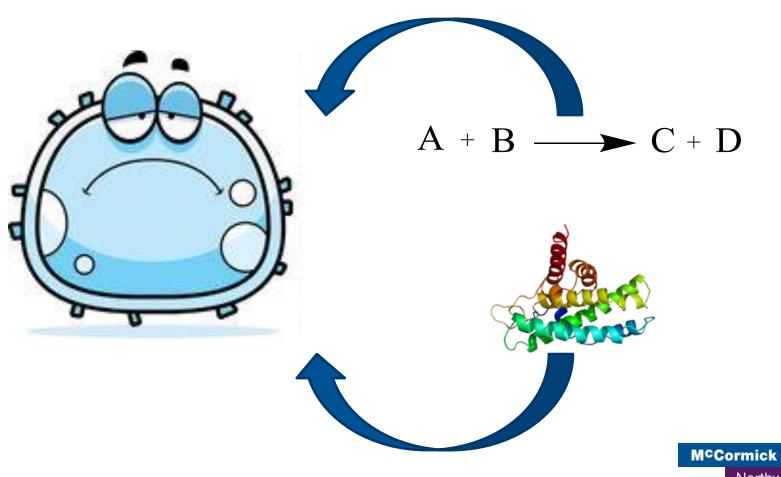
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The Known Unknown: Computational Identification of Promising Enzymatic Reactions and Associated Genes

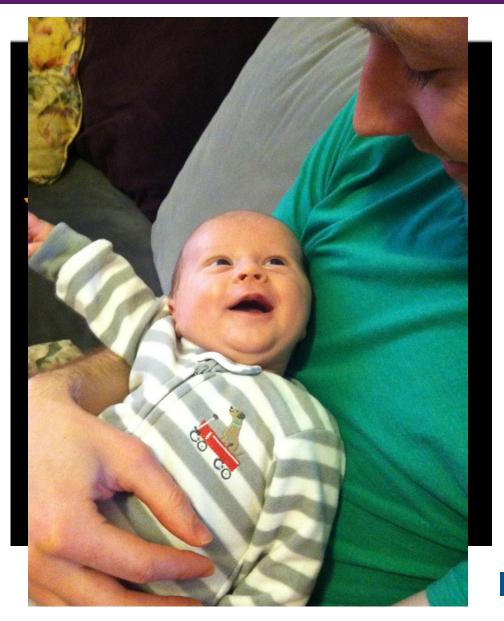
Andrew Stine

MCCormick Northwestern Engineering

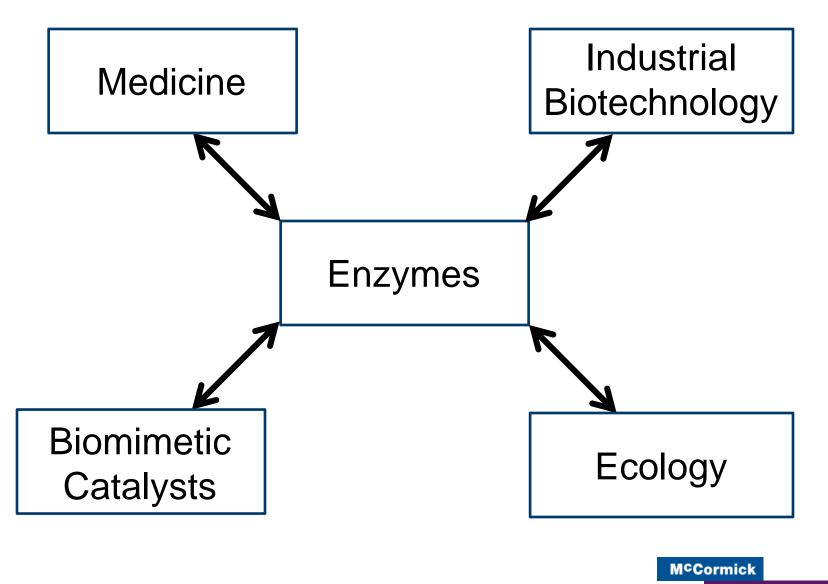
What is an Enzyme?



Importance of Enzymes

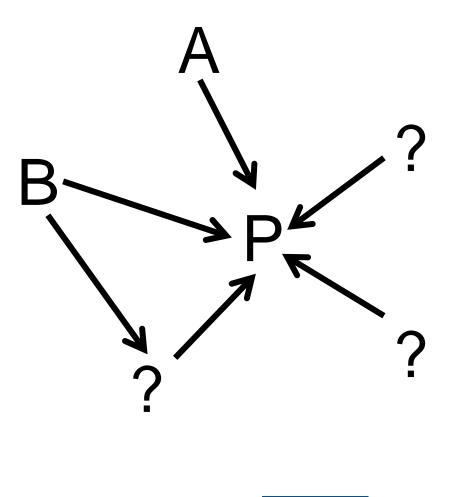


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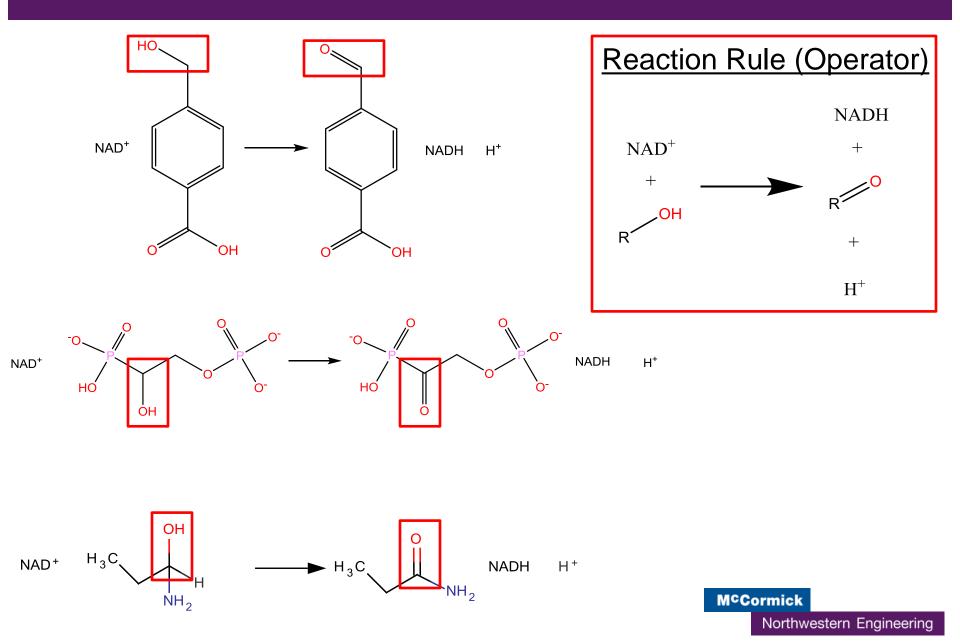
Enzyme Research: An Unknown Unknown

- What makes enzymatic research difficult?
- An unknown unknown
- Still only know a small fraction of enzymatic chemistry
- Difficult to know what reactions are possible but just have not been observed
- Need some way to make predictions about enzymatic chemistry we have yet to observe



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A Known Unknown



Translating Rules for a Computer

+

+





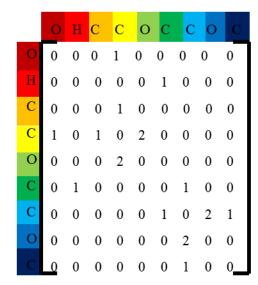
Site **BEM**

| | 0 | Н | С | С | 0 | С | С | 0 | С |
|---|---|---|---|---|---|---|---|---|---|
| 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Η | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| С | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| С | 0 | 0 | 1 | 0 | 2 | 1 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| С | 0 | 0 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| С | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 2 | 1 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 |
| С | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |

Operator Matrix

| | 0 | Н | С | С | 0 | С | С | 0 | С |
|---|----|----|---|----|---|----|---|---|---|
| 0 | 0 | -1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| Η | -1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| С | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| С | 1 | 0 | 0 | 0 | 0 | -1 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| С | 0 | 1 | 0 | -1 | 0 | 0 | 0 | 0 | 0 |
| С | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| С | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

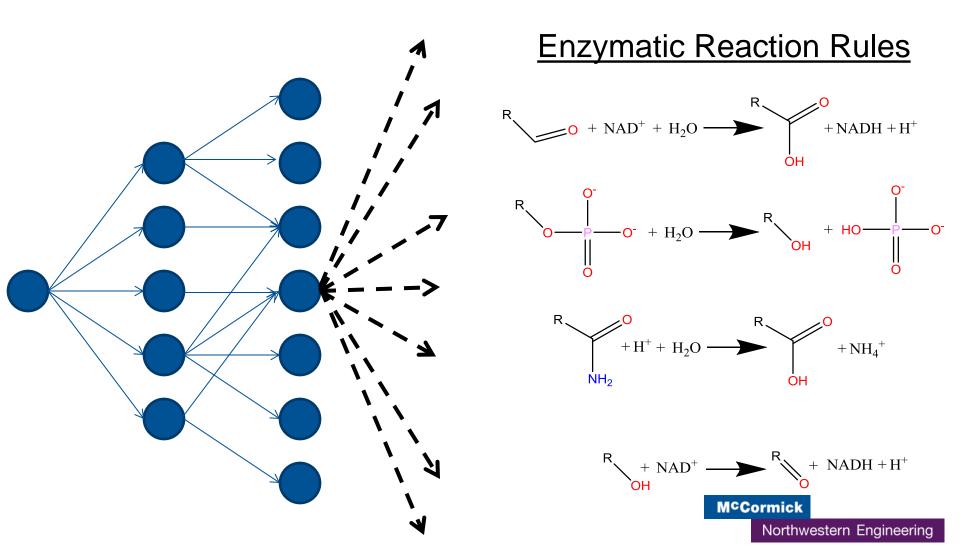
Product Matrix

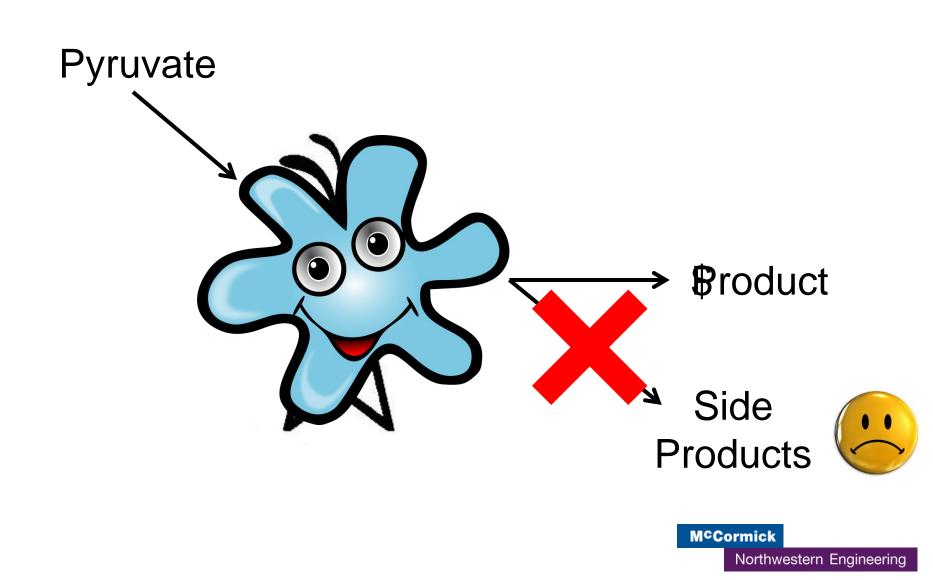


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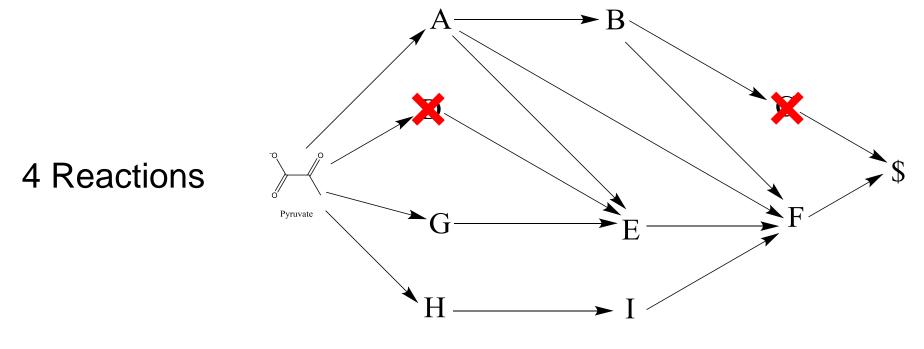
BNICE Reaction Network Generation

Biological Network Integrated Computational Explorer¹





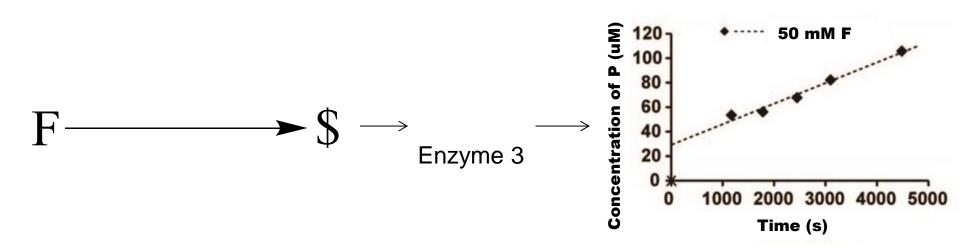
Analysis of Longer Pyruvate Pathways



| Reactants of the final step | # of pathways |
|-----------------------------|---------------|
| F | 1259 |
| Y | 36 |
| Z | 32 |
| С | 24 |
| Total Pathways | 1410 |

5 Reactions

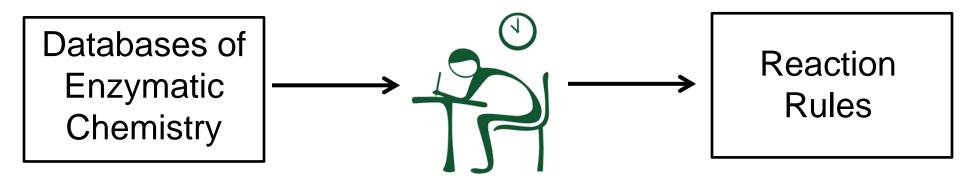
Experimental Confirmation



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Unpublished work by Miaomin Zhang, Soo Ro, and Keith Tyo

Creating Biochemical Reaction Rules

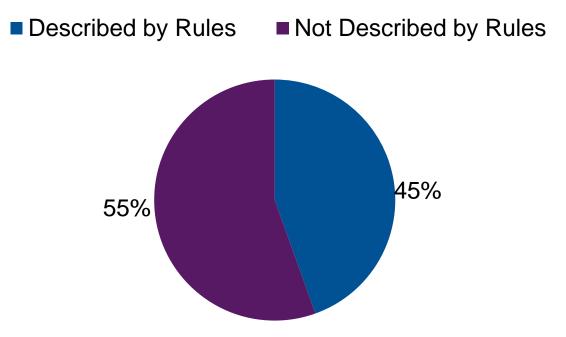


- Problems with this method:
 - 1. Potential for human error
 - 2. Rules may be designed for a different application
 - 3. Slow



Results for Manual Reaction Rules

• Applying reaction rules to KEGG¹:



Can we do this computationally?

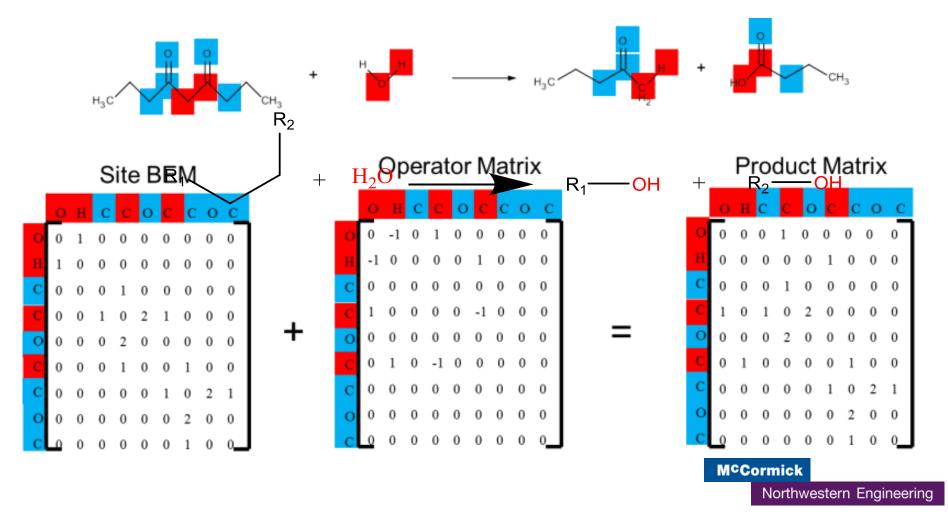
Yes!

1. Kanehisa, M., & Goto, S. (2000). KEGG: Kyoto Encyclopedia of Genes and Genomes. *Nucleic Acids Research, 28*(1), 27-30.

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Automatic Reaction Rule Generation

- Simplest rule consists of bonds broken across reaction
- Can obtain from our matrix representations



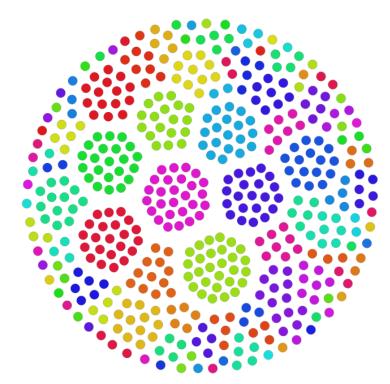
Automatic Operator Results

• Applying automatic reaction rules to MetaCyc¹:





Distribution of Reaction Rules

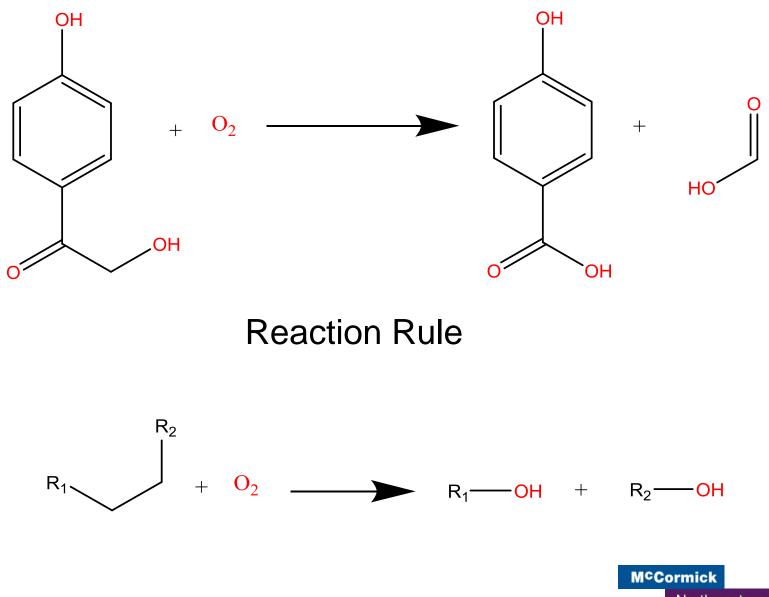


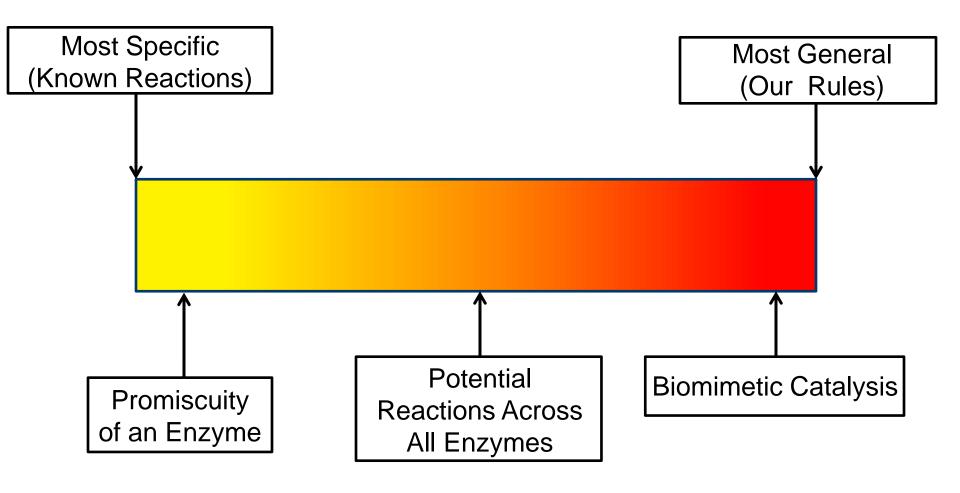
Visualization of MetaCyc. Each dot represents ten reactions, each color represent a rule

| Number of | |
|-----------|---------------|
| Reaction | Reactions |
| Rules | Described (%) |
| 5 | 14.4% |
| 9 | 22.6% |
| 13 | 28.5% |
| 28 | 40.0% |
| 49 | 49.4% |
| 110 | 59.6% |
| 215 | 67.5% |
| 375 | 73.7% |
| 661 | 80.4% |
| 2329 | 100.0% |

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Problem with This Approach



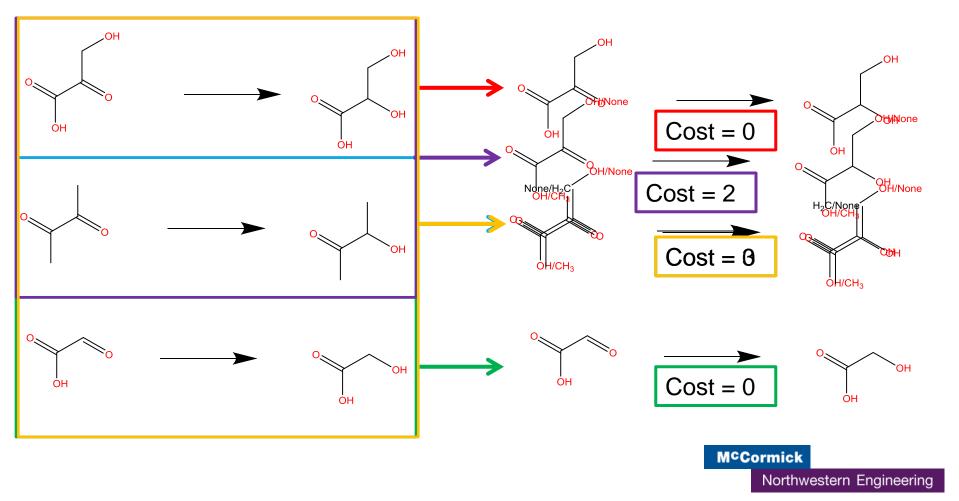


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Grouping Reactions

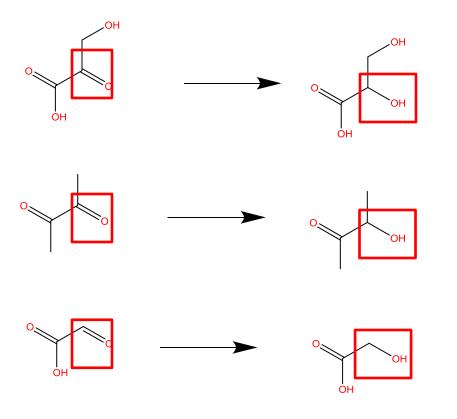
Find the Lowest Cost Rule that Describes all the Reactions in the Group

Cost = Number of Atoms that must be generalized



Grouping Reactions

Find the Lowest Cost Rule that Describes all the Reactions in the Group



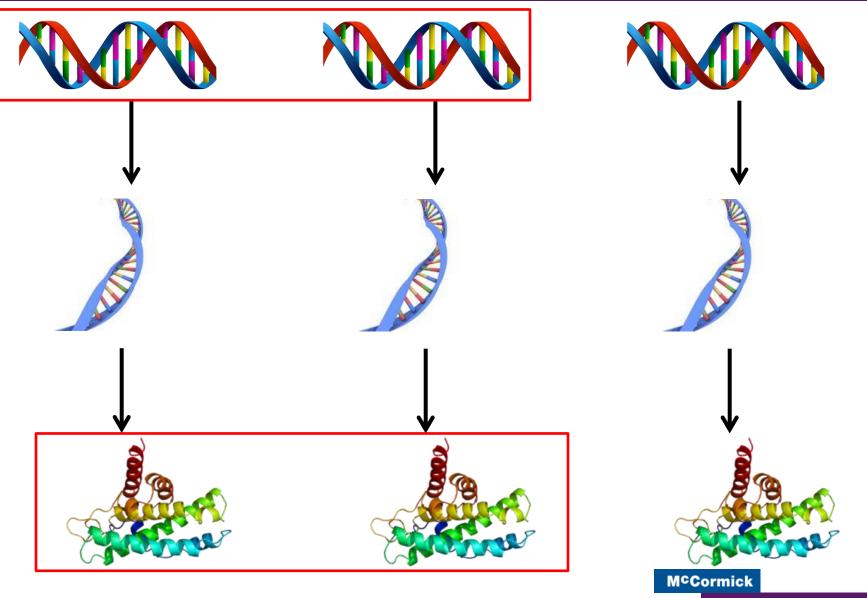
Cost = Number of Atoms that must be generalized

Simplifying Assumptions:

- Atoms whose bonds change are the same across all reactions
- 2. Atoms are only allowed to be generalized with atoms that are the same distance from the atoms whose bonds change

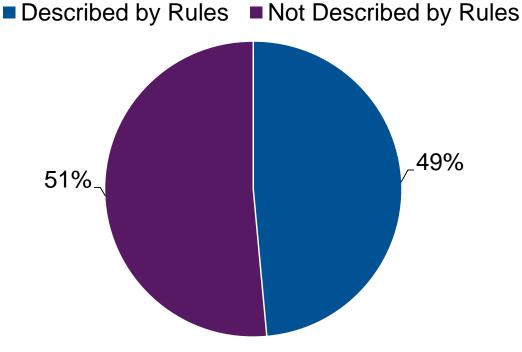
Simplifications allowed us to develop a dynamic programing algorithm to quickly solve this problem

Genetic Groupings



Genetic Grouping Results

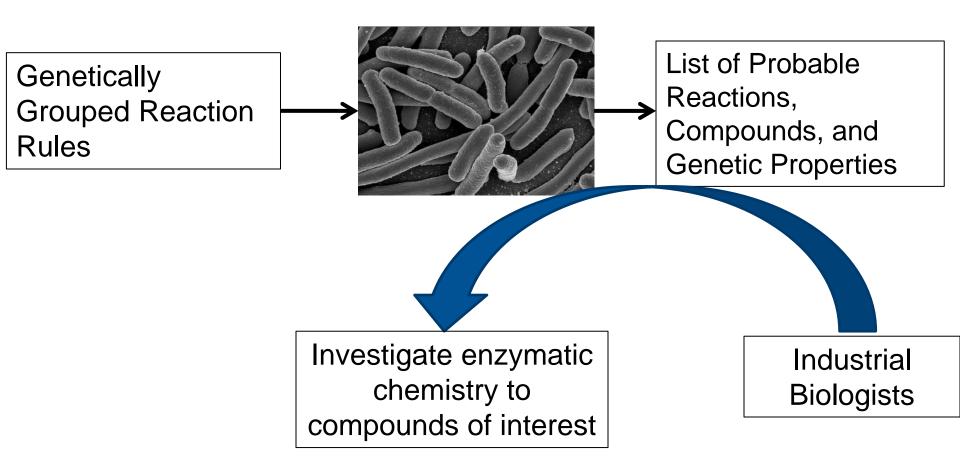
Used Conserved Domain Database¹
Superfamilies to group reactions by genetic similarity



1. Marchler-Bauer A, Derbyshire MK, Gonzales NR, et. al. CDD: NCBI's conserved domain database. Nucleic Acids Res. 2015 Jan 28;43(Database issue):D222-2. doi: 10.1093/nar/gku1221. Epub 2014 Nov 20. [PubMed PMID: 25414356]

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Future Work



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1. Rocky Mountain Laboratories, NIAID, NIH

- Enzymatic chemistry is an important but difficult topic
- Utilizing generalized reaction rules we can generate intelligent hypothesis about probable enzymatic chemistry
- We have developed an algorithm for the automatic generation of rules based upon user defined reaction groupings
- Using a genetic based grouping method has the potential to not only predict reactions but also properties of genes associated with those reactions

Acknowledgements

- Linda Broadbelt (Northwestern)
- Keith Tyo (Northwestern)
- Chris Henry (Argonne)
- Broadbelt Research Group





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