#### The Properties of Known Drugs

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- The Properties of Known Drugs: 1.
   Molecular Frameworks, 1996, JMC
- Properties of Known Drugs: 2. Side Chains, 1999, JMC

by Guy W. Bemis and Mark A. Murcko

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#### Problem

- The data is a database of known drugs the MDL® Comprehensive Medicinal Chemistry (CMC) database with more than 6700 compounds (over 8,400 pharmaceutical compounds now).
- The problem is to try to classify the shapes of drug molecules and provide a "highlevel overview of the gross structural features of these molecules.

#### **Purpose**

 The purpose of doing this is that there is a wealth of information implicitly encoded in the two-dimensional and threedimensional structures of drug molecules and they might be applied to design of new drugs.

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#### Methods

- The analysis of the structures has been carried out on two levels, using graph properties and atomic properties.
- Two classification:

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G--->Atomic Properties

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#### Methods

- Graph representation of a molecule is gotten by considering each atom to be a vertex and each bond to be an edge on a graph.
- Graph properties of molecules are the connectivity properties of atoms representing a molecule.
- Atomic properties include such information as element type, atomic hybridization, and atomic charge.

# Methods graph representation of a molecule (pyridine) b Figure 1. Graph representation of molecules.

#### Methods

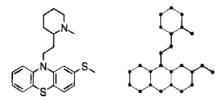
structural elements of a molecule graph

- Ring Systems: cycles within graph representation of molecules and cycles sharing an edge, benzene.
- Linker Atoms: atoms that are on the direct path connecting two ring systems.
- Side Chain Atoms:
- Framework: union of ring systems & linkers in a molecule.

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#### Methods

structural elements of a molecule graph



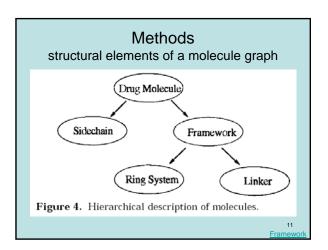
Thioridazine

Graph Representation

Figure 2. Graph representation of a typical drug molecule.

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## Methods structural elements of a molecule graph 2 Side Chains 1 Framework Figure 3. Distinguishing between ring systems, linkers, and side chains.



### Methods (Framework part) algorithm for identification of linker & framework

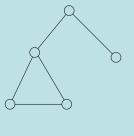
- Identifying side chain atoms first: each atoms bonded to only one other atom is identified as a side chain atom and removed from the molecule; repeat. The remaining atoms are framework atoms.
- · Ring systems are identified using depthfirst search.
- · Linker atoms.

#### Depth-first Search of a Graph

Edges are explored out of the most recently discovered vertex v that still has unexplored edges leaving it. When all of v's edges have been explored, the search "backtracks" to explore edges leaving the vertex from which v was discovered.

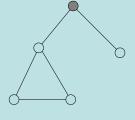
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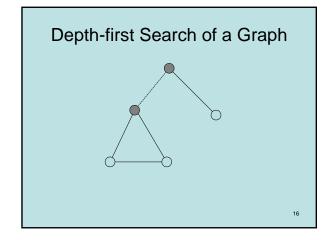
#### Depth-first Search of a Graph

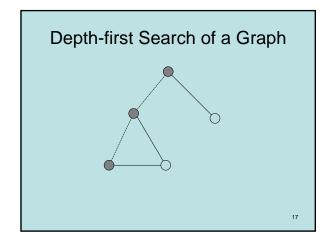


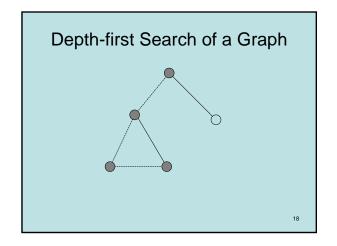
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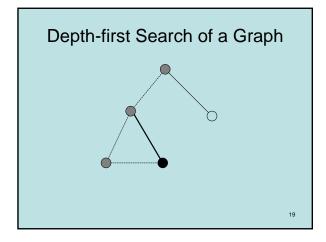
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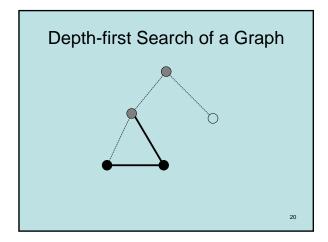


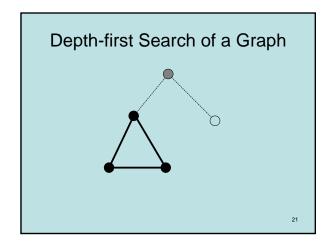












# Depth-first Search of a Graph

## Depth-first Search of a Graph

#### Data (Framework part)

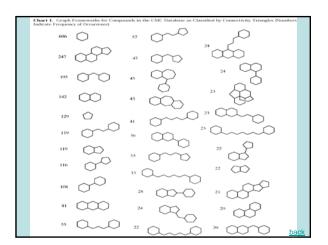
- All compounds for which no therapeutic activity class was given, as well as such compounds: radiopaque agents, contrast agents, solvents, anesthetics, disinfectants, topicals, ....
- After the above process, the CMC database had 5120 remaining entries.

#### Results (Framework part)

the graph theory analysis

- There are 1179 different frameworks among the 5120 compounds analyzed.
- Of these framework, 783 (66%) are unique.
- There are 32 frameworks which exist in at least 20 drugs. This set of frameworks accounts for 50% of the total.
- Acyclic molecules account for 306 (6%) of the total.

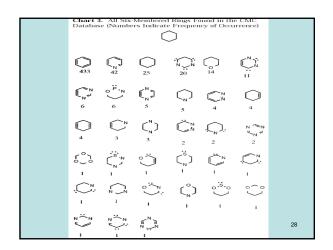
atomic 25



#### Results (Framework part)

relation between graph & atomic property

 the graph theory frameworks can be viewed as providing a generic classification scheme, and the atom property-based framework further subdivide classes of framework based on their chemical properties.

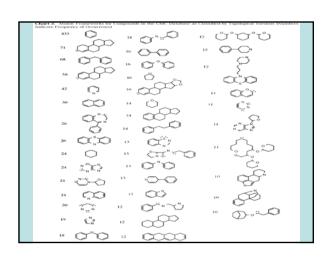


#### Results (Framework part)

the atomic property analysis

- Atom properties ( atom type, hybridization, and bond order ) are considered.
- There are 2506 different frameworks
- A large majority of these frameworks (1908, or 76%) are unique.
- The 41 frameworks that occur at least 10 times accounts for 1235 (24%) of the total.





#### Discussion (Framework part)

- The preferences for certain shapes do not necessarily reveal some fundamental truth about drugs, receptors, metabolism, or toxicity.
- Instead, it may reflect the constraints due to synthetic or patent considerations, cost, or the tendency to make new compounds which are structurally similar to known compounds.

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#### Discussion (Framework part)

- Half of the known drugs fall into only 32 shape categories (graph theory). The drugs are quite different in their chemical properties.
- The analysis result might be used to direct a de novo design effort.

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#### Side Chains

 Properties of Known Drugs: 2. Side Chains, 1999, JMC

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# Methods (Side Chains) Directors removed and Statement Interest. Pleas Layer Second Layer Secon

#### Methods (Side Chains)

- But it is important to recognize both chain patterns and the way these patterns are connected to molecule frameworks
- Augmented side chains..

(a) original necleoules	$\gamma\gamma$ (	$\mathcal{Y}$
(h) aldorheins	$\checkmark$	$\checkmark$
(c) sugmented siductions	$\sim$	$\sim$

Figure 2. Example of side chain overlap problem. Side chains (b) determined from molecules (a) are identical. Augmented side chains (c) are necessary to distinguish these.

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#### Methods (Side Chains)

- But it is important to recognize both chain patterns and the way these patterns are connected to molecule frameworks
- Augmented side chains..

(g) religiand as thereisa	5	Š
(t) dilectries	~ <i>_</i>	~
(c) regressed sidechoins		7

Figure 3. Example of an additional side chain overla problem. Side chains (b) determined from molecules (a) ar identical. Augmented side chains (c) are again necessary to distinguish those.

#### Methods (Side Chains)

- But it is important to recognize both chain patterns and the way these patterns are connected to molecule frameworks
- Augmented side chains..
- Labeled side chains.

(t) retained sectoralise	
O) albebrium	$\checkmark$
(6) Segmannoi siduelloissa 💮 🚉	~
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(v) (1) unmasse in Chorn 3	4

Figure 4. Example of augmented side chain overlap problen Augmented side chains (c) derived from molecules (a) an identical. Only by inclusion of a dummy atom (Du) can the side chains be properly distinguished. Part e shows how result

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#### Data (side chains)

- Part of the undesirable compounds are removed from CMC database.
- 5090 entries remains.

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#### Results (side chains)

- A total of 4689 contains labeled side chains.
- There are a total of 18664 labeled side chains (including C=O) attached to these scaffolds. The "average" drug scaffold contains 4 labeled side chains.

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Most scaffolds have between one to five labeled side chains.

Figure 5. Histogram showing number of labeled side chains per drug framework.

Of these labeled side chains the vast majority contain one heavy atom in their actual side chain component.

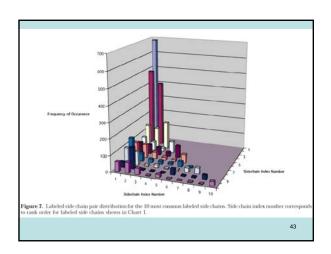


Table 2. Most (top) and Least (bo Labeled Side Chain Pairs from Fig		
side chain pair	frequency	-
Most Common	ly Found	_
C=O/C=O	686	
$C=O/C-CH_3$	488	
C-CH <sub>3</sub> /C-CH <sub>3</sub>	412	
C-OH/C-OH	172	
C=O/C-OH	139	
$C=O/C-NH_2$	138	
C-CH <sub>3</sub> /C-F	131	
C-CH <sub>3</sub> /C-OH	127	
C=O/C-CO <sub>2</sub> H	98	
$C=O/N-CH_3$	89	
Least Common	nly Found	
$C-NH_2/S=O$	1	
C-Cl/C-F	3	
$N-CH_3/S=O$	3	
C-F/S=O	3	
C-OCH <sub>3</sub> /C-F	4	
C-OCH <sub>3</sub> /S=O	4	
$C-NH_2/C-F$	4	
C-CO <sub>2</sub> H/S=O	4	

thanks