

# Revising the Topliss decision tree

## ...based on 30 years of medicinal chemistry literature

**Noel O'Boyle and Roger Sayle** 

**NextMove Software** 

Jonas Boström

**AstraZeneca** 





# American Chemical Society Division of Medicinal Chemistry Hall of Fame



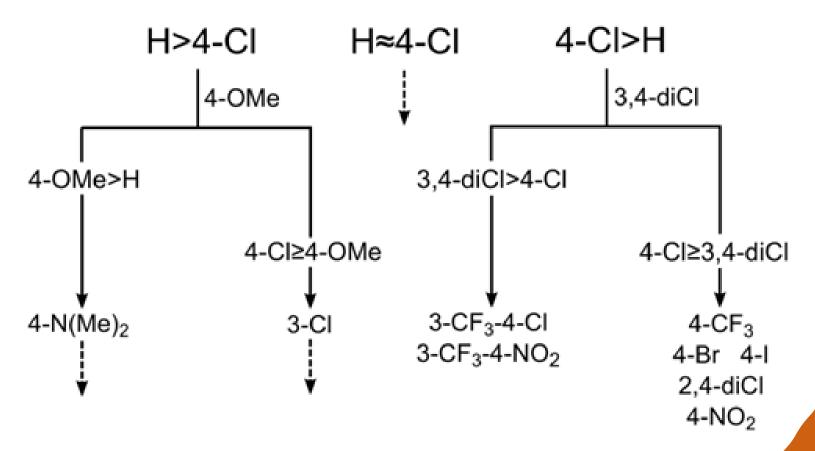
John G. Topliss, Ph.D.

Dr. John G. Topliss was born near Mansfield, England in 1930. He received a BSc degree with honors in chemistry, first class, in 1951 from The University of Nottingham and a Ph.D. degree in organic chemistry with Professor F. E. King on the total synthesis of tricyclic diterpenoids from the same institution in 1954. He then did postdoctoral research with Professor Holger Erdtman at The Royal Technical College in Stockholm, Sweden, on the isolation and structure determination of heartwood constituents, and with Professor Gilbert Stork at Columbia University on natural product total synthesis.

Dr. Topliss joined the Schering Corporation (now Schering-Plough) as a synthetic medicinal chemist in 1957, and in the following years worked primarily in the diuretic, antihypertensive, CNS, and antiandrogen areas. In a roughly 10 year period he and his research group synthesized and patented 5 drugs (trichlormethiazide, diazoxide, halazepam, quazepam, and flutamide) which were subsequently marketed.

Seeking a more rational, theoretically based approach to analog synthesis than was generally employed at that time, Dr. Topliss was one of the early medicinal chemists in the pharmaceutical industry to use quantitative structure-activity relationships (QSAR) methodology. This led him to formulate Operational Schemes for Analog Synthesis in Drug Design (later known as the Topliss Tree) published in 1972, and also a related Manual Hansch Approach published in 1977, which are simplified non-mathematical approaches for rapidly optimizing benzene ring

## TOPLISS TREE FOR SUBSTITUTED PHENYL



Topliss, J. G. Utilization of Operational Schemes for Analog Synthesis in Drug Design. *J. Med. Chem.* **1972**, *15*, 1006–1011.

#### FEATURES OF THE TOPLISS TREE

- Maximize the chances of synthesizing the most potent compound in the series as soon as possible
- Based on inferring Hansch structure-activity relationship from relative potencies of R groups
  - Electronic ( $\sigma$ ), hydrophobic ( $\pi$ ), steric ( $E_s$ )
- General scheme
  - for any target
  - for any scaffold

#### CHEMBL BIOACTIVITY DATABASE

 July 2008 - ChEMBL established with Wellcome Trust grant



- John Overington, EMBL-EBI
- Open access source of bioactivity data abstracted from the literature
  - Chemical structures, activity values, activity type, assay description, journal article name, target
  - www.ebi.ac.uk/chembl/



#### CHEMBL BIOACTIVITY DATABASE

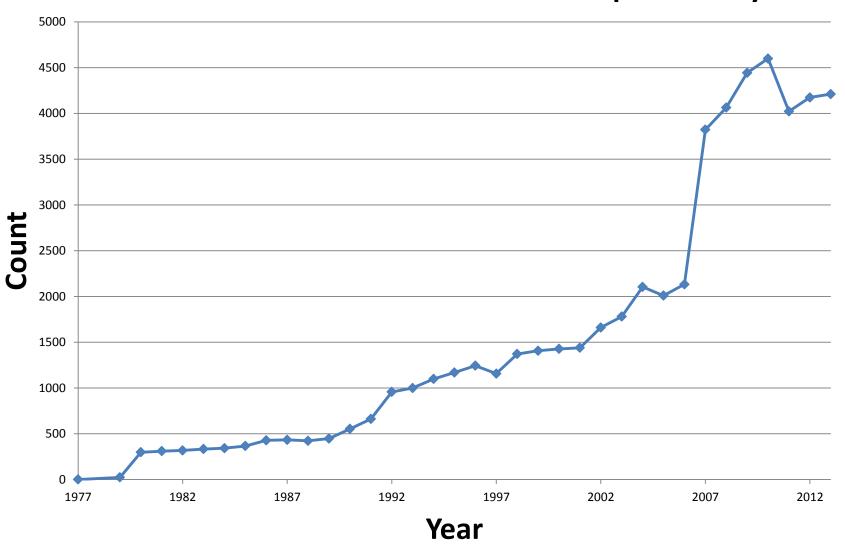
ChEMBL 19 – July 2014



- 57k papers
  - 94% from Bioorg. Med. Chem. Lett., J. Med. Chem., J. Nat. Prod., Bioorg. Med. Chem., Eur. J. Med. Chem., Antimicrob. Agents Chemother., Med. Chem. Res.
- 1.4 million compounds with 12 million activities
- 1.1 million assays against 10k targets



#### Number of articles extracted from a particular year



#### MATCHED (MOLECULAR) SERIES

- Recent concept in cheminformatics (\*)
  - ... not so recent in medicinal chemistry
- Series of structural analogs
  - same scaffold
  - different R groups at a single position

\* "Matching molecular series" introduced by Wawer and Bajorath J. Med. Chem. **2011**, 54, 2944

## MATCHED SERIES OF LENGTH 3

[CI, F, NH<sub>2</sub>]



### MATCHED SERIES OF LENGTH 3

[4-Cl-Ph, 4-F-Ph, 4-NH<sub>2</sub>-Ph]

#### ORDERED MATCHED SERIES

 $pIC_{50}$ 

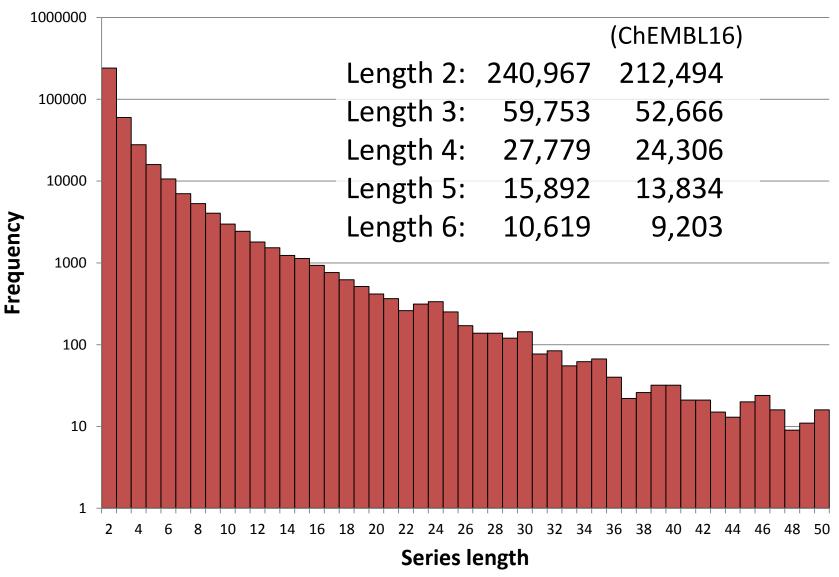
3.5

 $[4-Cl-Ph > 4-F-Ph > 4-NH_2-Ph]$ 

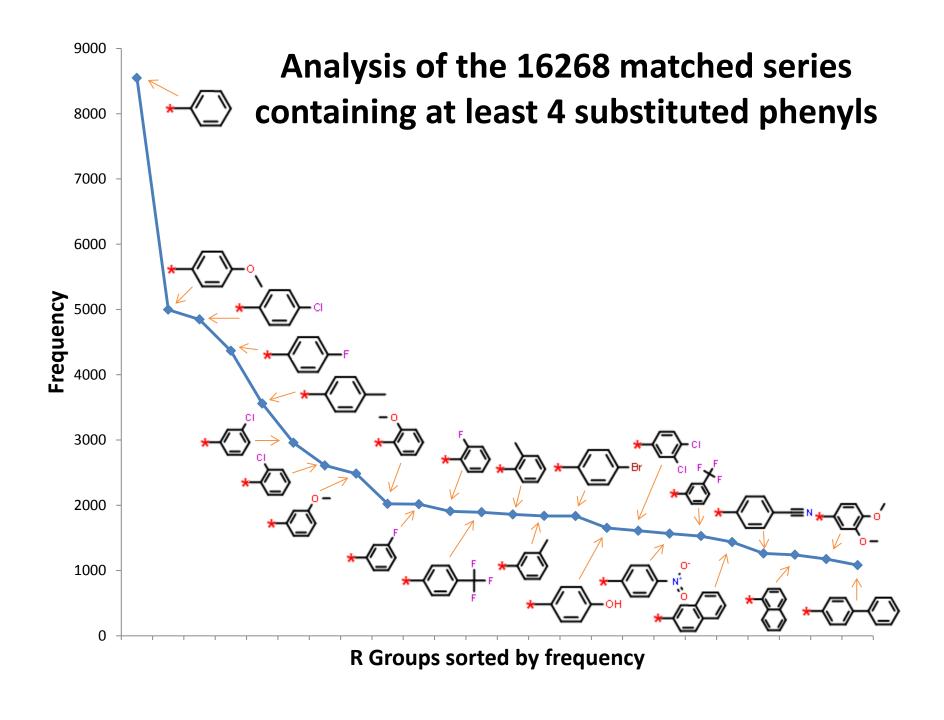
2.1

1.6

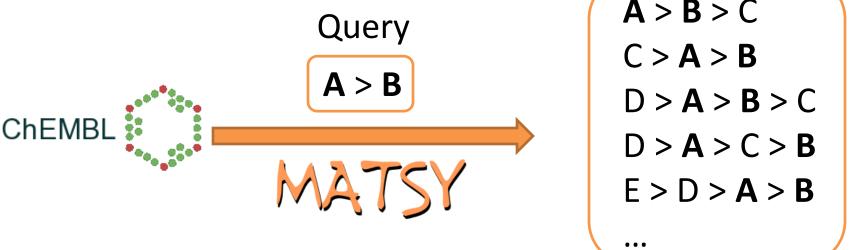
#### Matched series in ChEMBL19 IC50 binding assays



Method described in O'Boyle, Boström, Sayle, Gill. Using Matched Molecular Series as a Predictive Tool To Optimize Biological Activity. *J. Med. Chem.* **2014**, *57*, 2704.



#### FIND R GROUPS THAT INCREASE ACTIVITY

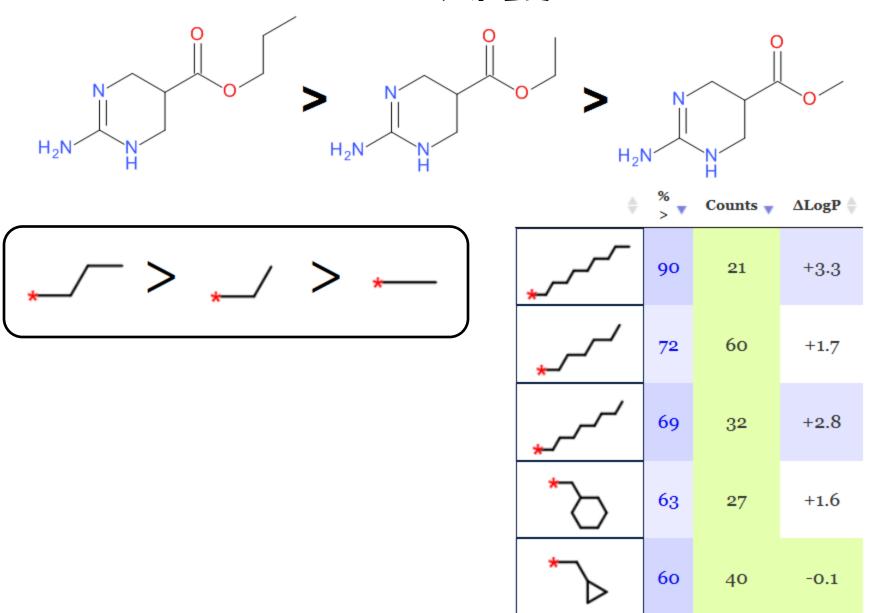


| <b>A</b> > <b>B</b> > C |  |
|-------------------------|--|
| C > A > B               |  |
| D > A > B > C           |  |
| D > A > C > B           |  |
| E > D > A > B           |  |
| •••                     |  |

| R Group | Observations | Obs that increase activity | % that increase activity |
|---------|--------------|----------------------------|--------------------------|
| D       | 3            | 3                          | 100                      |
| Е       | 1            | 1                          | 100                      |
| С       | 4            | 1                          | 25                       |
| •••     | •••          |                            | •••                      |

O'Boyle, Boström, Sayle, Gill. Using Matched Molecular Series as a Predictive Tool To Optimize Biological Activity. J. Med. Chem. 2014, 57, 2704.

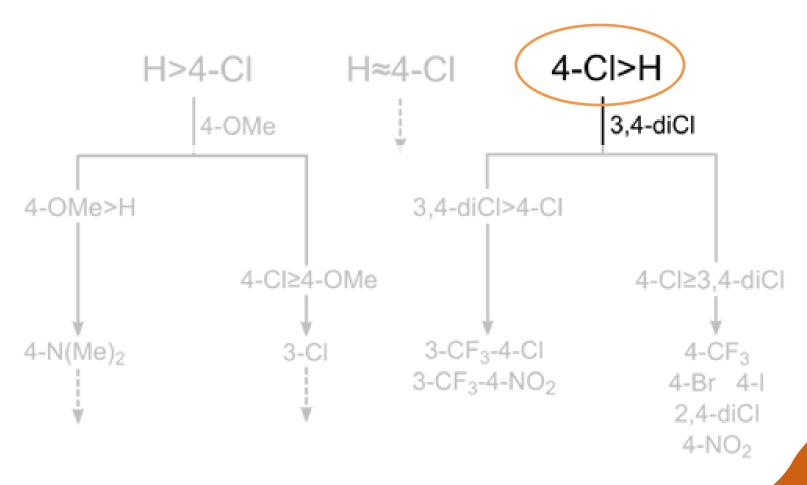
#### EXAMPLE



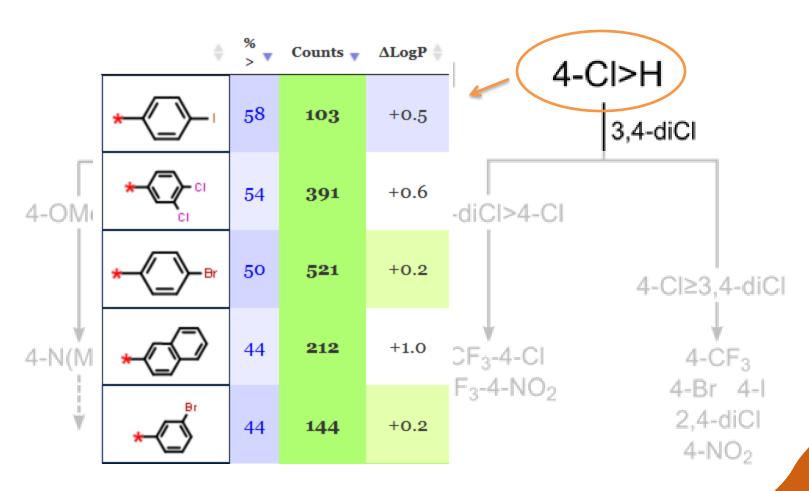
#### EXAMPLE II



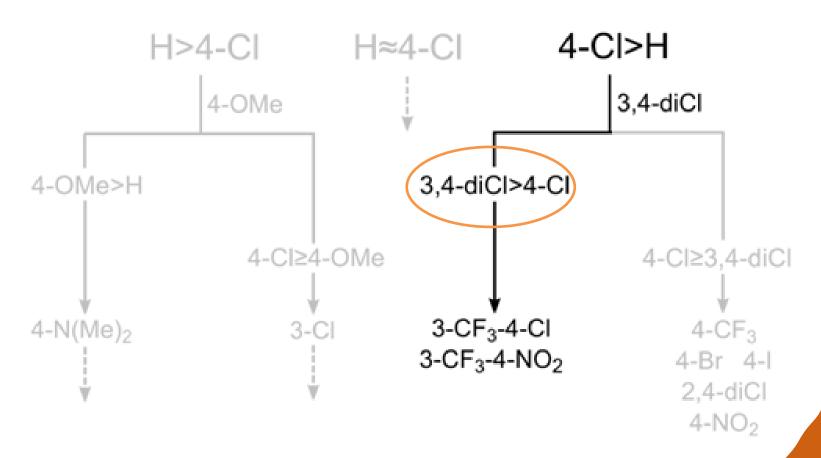
| * Br | 38 | 21  | -0.8 |
|------|----|-----|------|
| *    | 37 | 27  | +0.9 |
| *-   | 33 | 111 | +0.3 |
| *    | 33 | 27  | +1.0 |
| *ОН  | 33 | 21  | -1.6 |



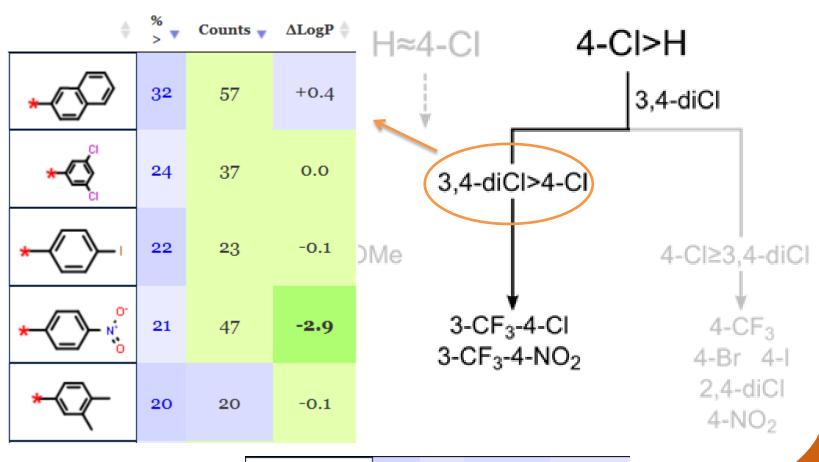




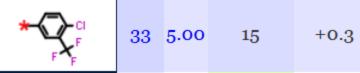




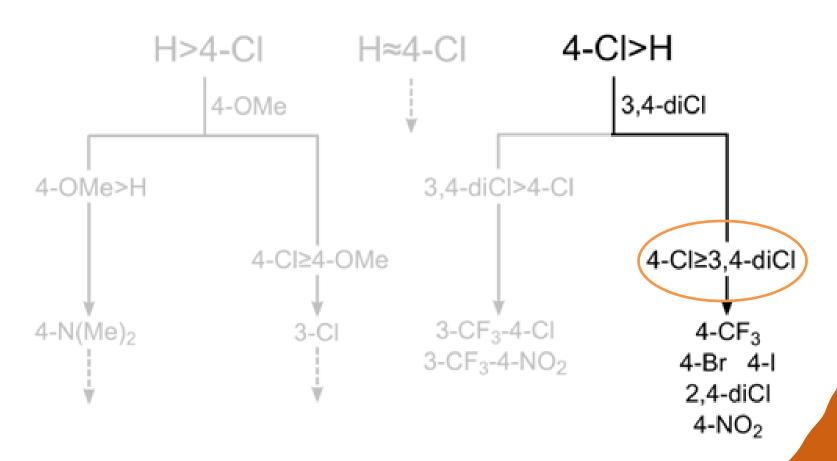




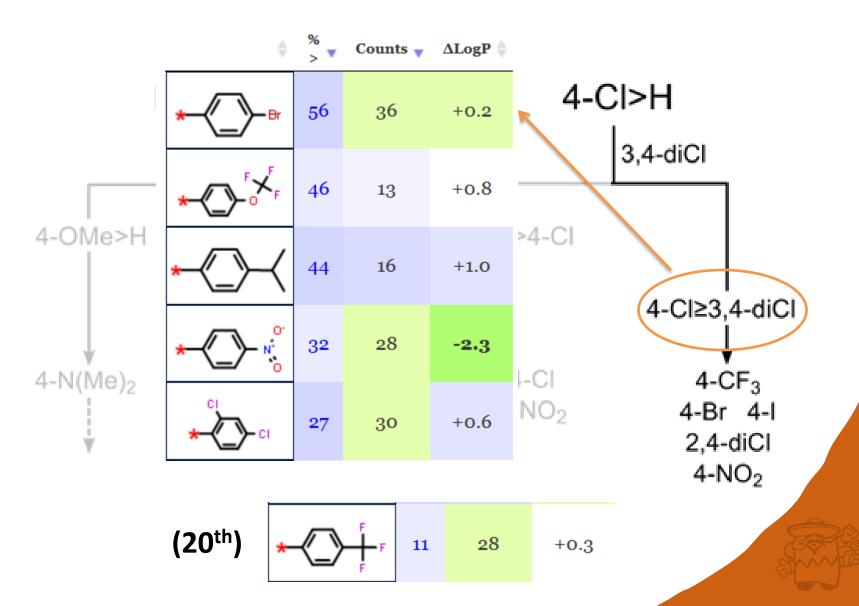
(1st if lower cutoff)

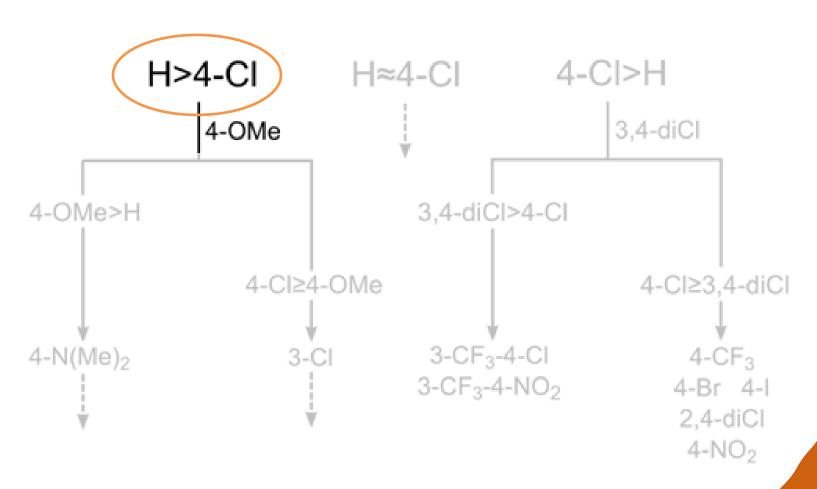




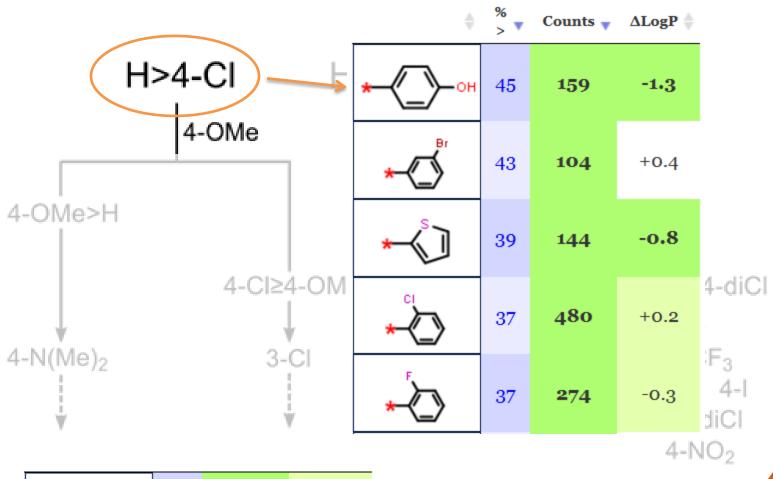




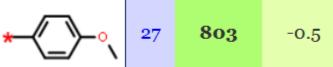




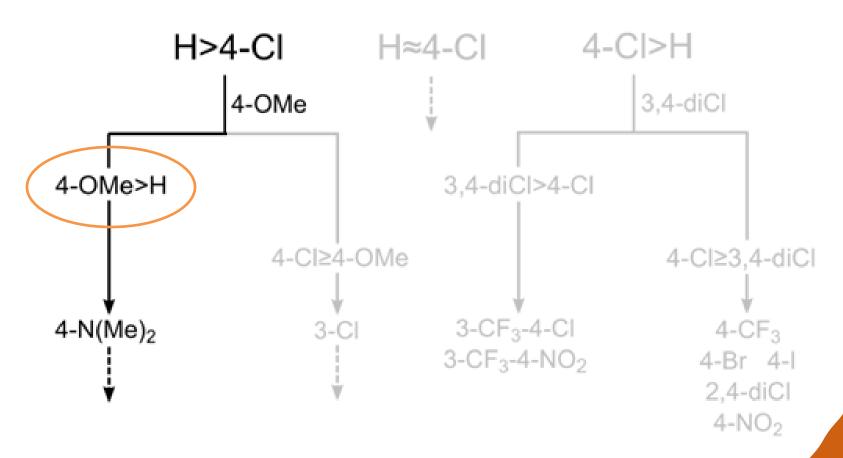




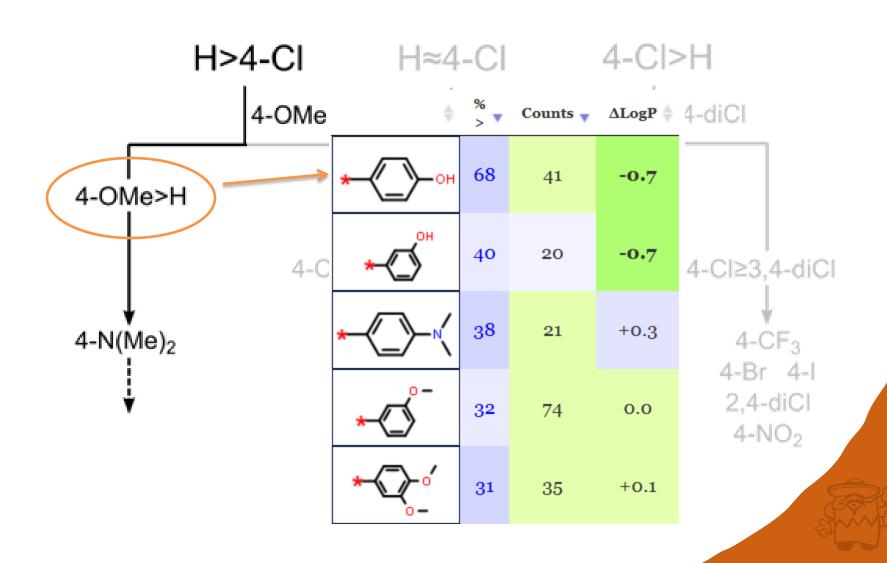
(21<sup>st</sup>)

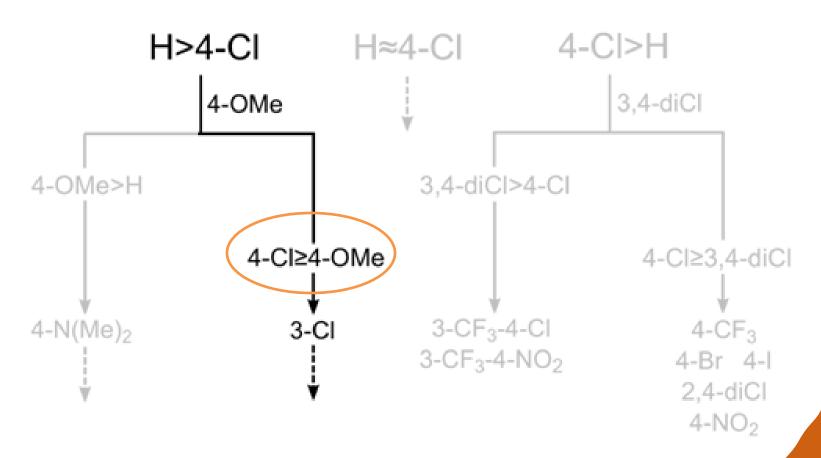


"Assuming that the –σ effect is the most probable explanation..."

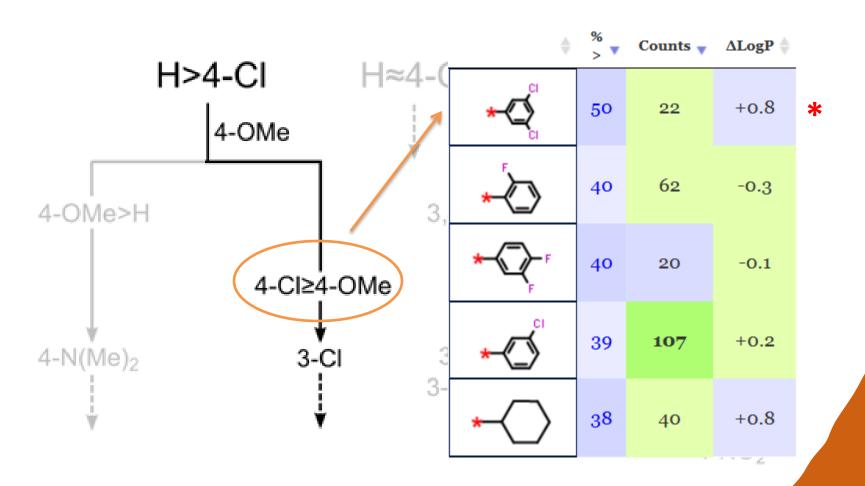






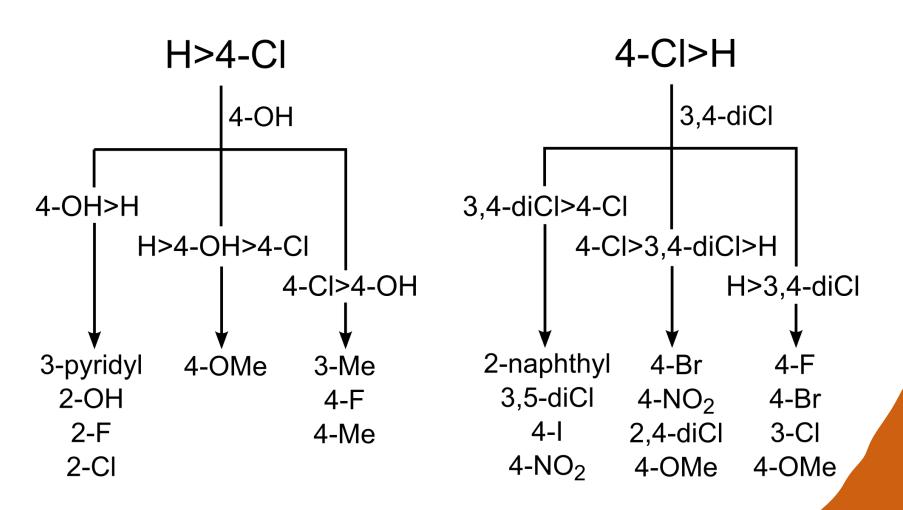




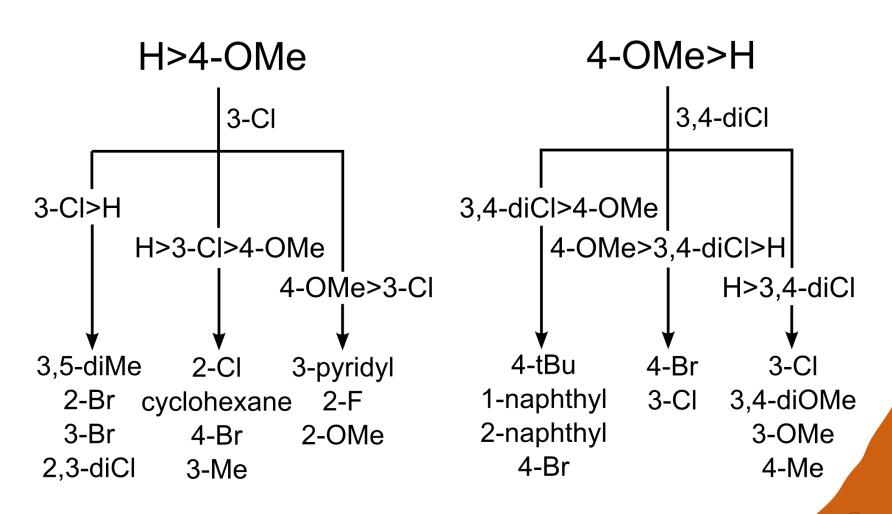




#### MATSY DECISION TREE

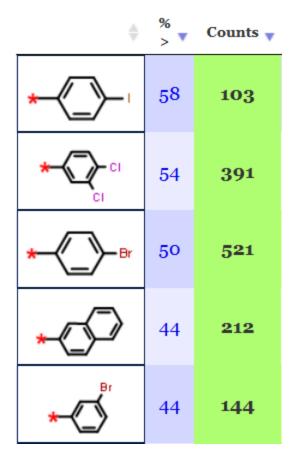


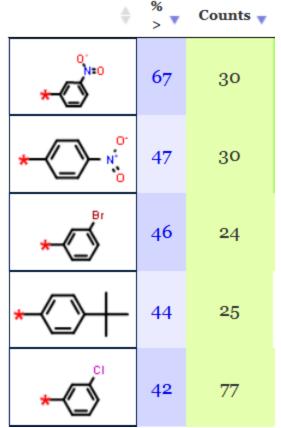
#### MATSY DECISION TREE (TAKE 11)

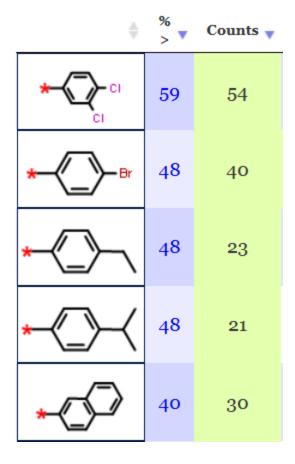


## TARGET SPECIFIC SUBSETS

#### 4-Cl > H







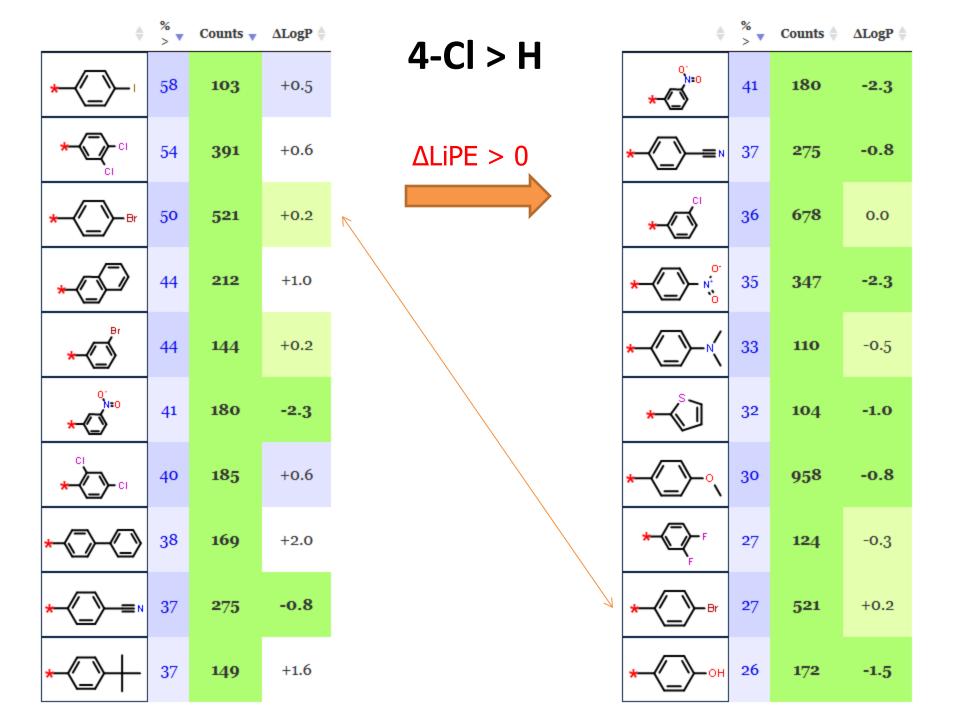
**Everything** 

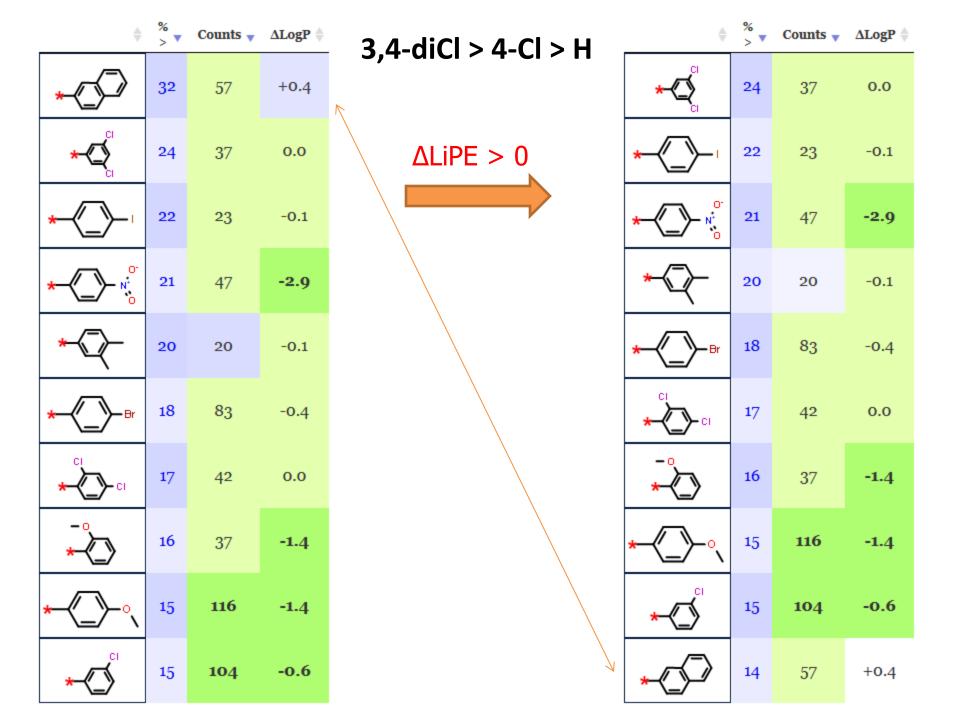
Kinases

**Class A GPCRs** 

#### ACCOUNT FOR LIPOPHILIC EFFICIENCY

- $\Delta \text{LiPE} = \Delta \text{pIC}_{50} \Delta \text{LogP}$
- The "%>" value is based on the number of times a particular R group has greater pIC<sub>50</sub>
  - $i.e. \Delta pIC_{50} > 0$
- Redefine it to only include cases where the increase in pIC<sub>50</sub> was larger than any increase in LogP
  - i.e.  $\Delta pIC_{50} > 0$  and  $\Delta LiPE > 0$





#### DATA-DRIVEN APPROACH

Not limited to the two trees in the Topliss paper

- All predictions backed by experimental data
  - Can drill-down into the data, look at targets, scaffolds
  - Can restrict experimental data used to particular targets, use in-house data rather than ChEMBL

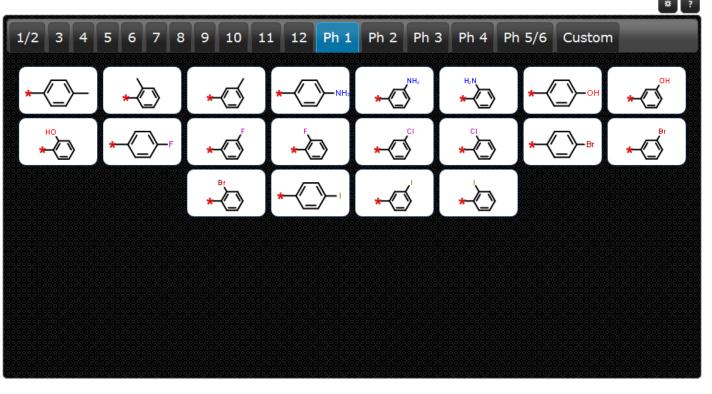
Does not explain why, only that it happens

#### CONCLUSIONS

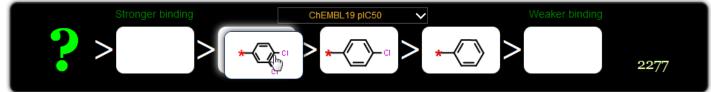
- In the main, the Topliss Tree is supported by published data
  - Largest difference is recommendation of 4-OMe rather than 4-OH
  - Suggestion of 4-CF<sub>3</sub> is also problematic

 We have generated the corresponding 'Matsy Tree' derived from experimental data

#### DRAG-AND-DROP INTERFACE TO MATSY



| *-(                    | 58 | 103 | +0.5 |
|------------------------|----|-----|------|
| *C:                    | 54 | 391 | +0.6 |
| *— Br                  | 50 | 521 | +0.2 |
| *                      | 44 | 212 | +1.0 |
| *—                     | 44 | 144 | +0.2 |
| *—€∑N=0                | 41 | 180 | -2.3 |
| <b>★</b>               | 40 | 185 | +0.6 |
| *-(>-(>)               | 38 | 169 | +2.0 |
| <b>*</b> ─ <b></b> ■ N | 37 | 275 | -0.8 |
| *                      | 37 | 149 | +1.6 |



Showing 1 to 10 of 40 entries



Previous Next

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noel@nextmovesoftware.com

Want to hear more?

Poster COMP 394
Tuesday 6:00-8:00pm Marriott Marquis

Interested in an evaluation copy of Matsy?

Come by our booth



Using Matched Molecular Series as a Predictive Tool To Optimize Biological Activity

J. Med. Chem. **2014**, *57*, 2704.