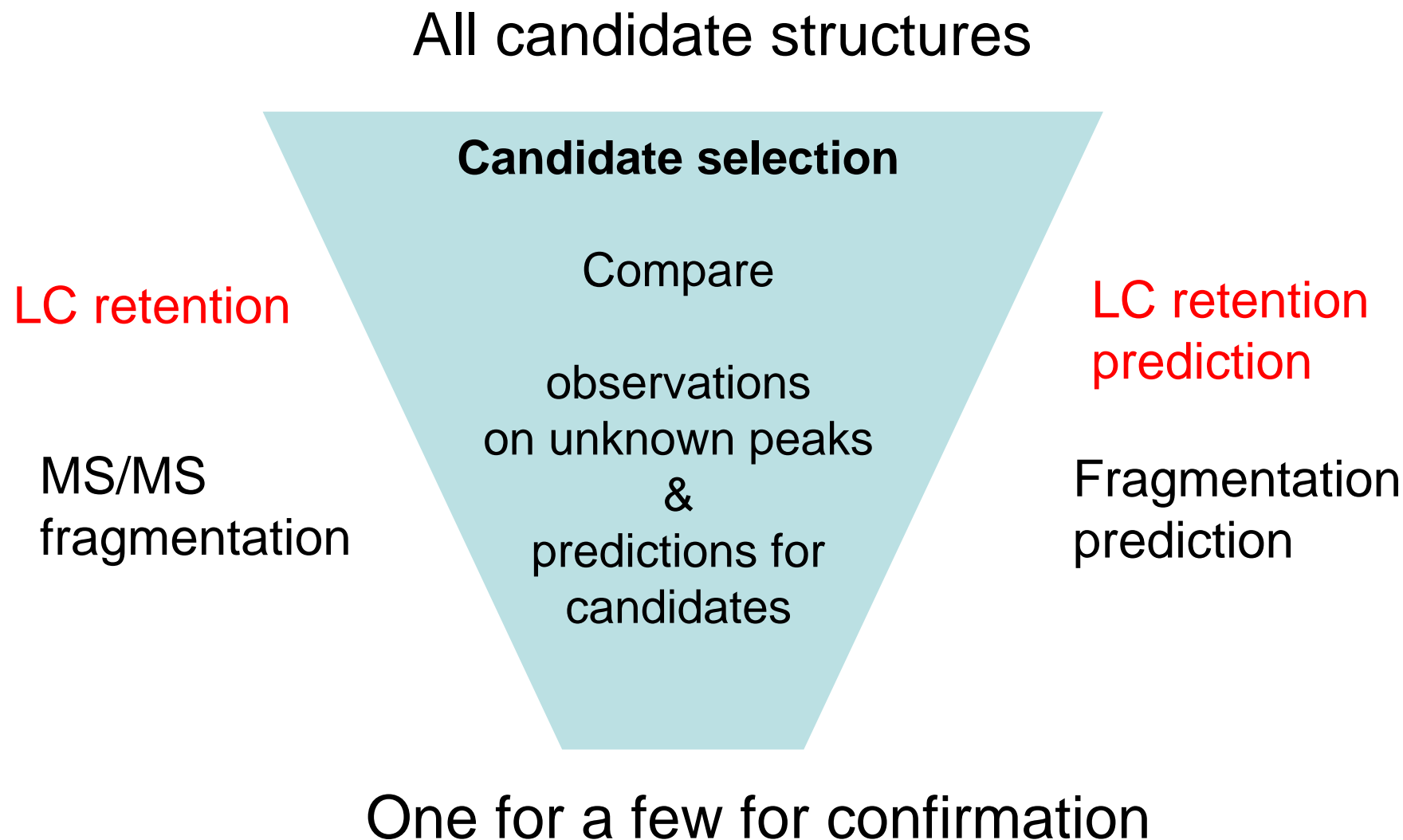


Comparison of approaches for retention prediction Useful in LC-HRMS Nontarget-Screening

Martin Krauss, Janek Dann, Meng Hu, Werner Brack

Department Effect-Directed Analysis,
Helmholtz-Centre for Environmental Research – UFZ, Leipzig



Retention time = f (eluent properties (composition, gradient, pH, I),
molecular structure, stationary phase chemistry,
temperature)

If we use always the same system, eluent, column:

Retention time = f (molecular structure)

Build a QSRR model!

Many different approaches in the literature

Héberger, 2007, J. Chromatogr. A 1158, 273. (Review)

High accuracy

“Small domain” models

Alkylic acids

RT = f (chain length)

Alkylic acids

RT = f (chain length,
branching, topology...)

Single parameter

100s of pharmaceuticals

RT = f (log K_{OW})

Poly-parameter

100s of pharmaceuticals

RT = f (phys.-chem.,
topological descriptors, ...)

Lower accuracy

“Large domain” models

Better accuracy?

“Is my unknown at 12.3 min your unknown at 18.6 min?”

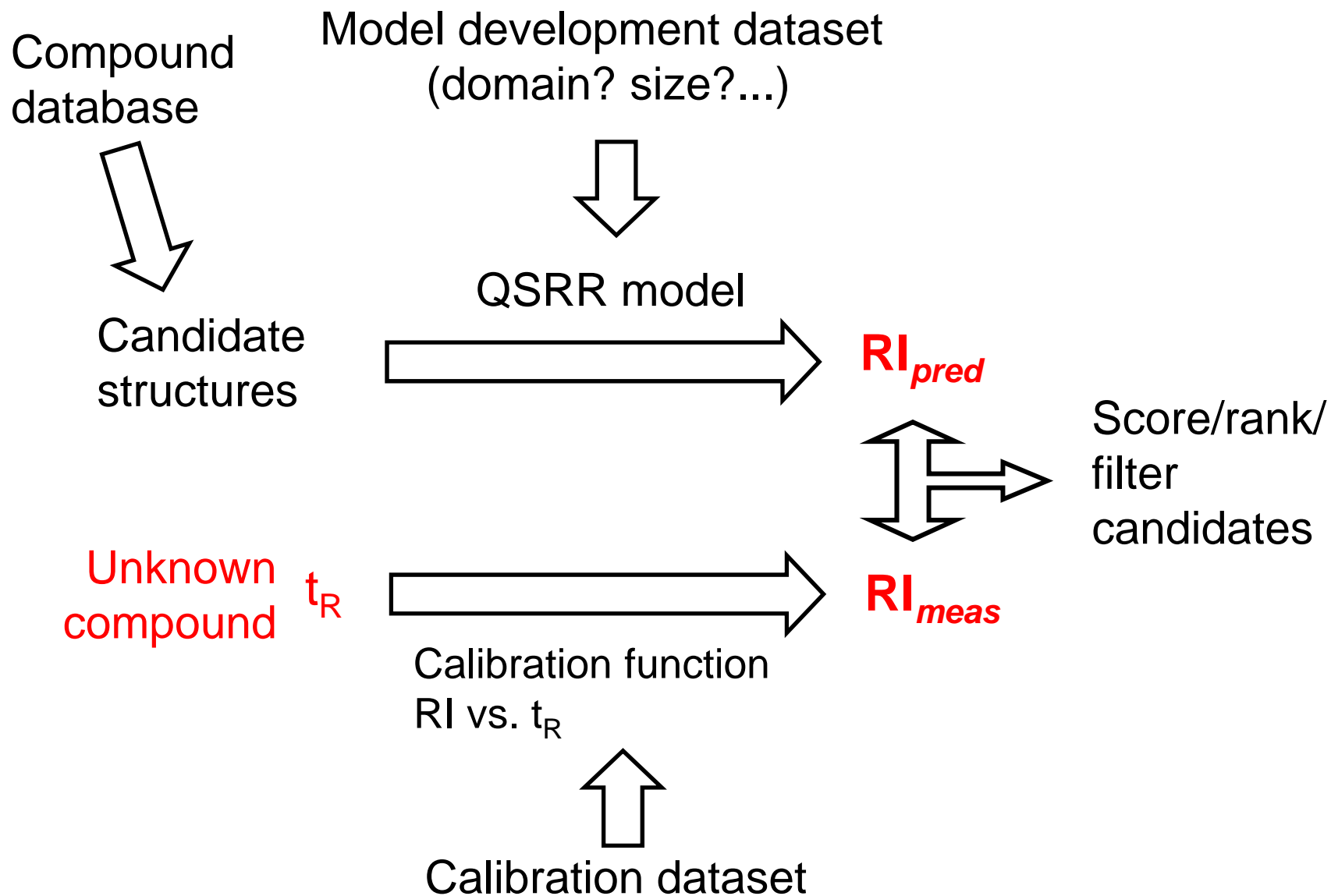
- Comparison among different LC methods, working groups
- Storage in shared databases
- Consistency/validation of LC methods over years

⇒ Normalizing or indexing retention times RI

GC(-MS) (Kovats‘) Retention Index: simple & quite accurate!

LC(-MS): ???

Using retention prediction in practice



Chromatographic Hydrophobicity Index (CHI)

Linear Solvation Energy Relationship (“Abraham equation”)

Dept. Effect-Directed Analysis, UFZ

Ulrich et al. (2011) J. Chromatogr. A 1218, 8192.

based on Valko et al. (1997) Anal. Chem. 69, 2022

Retention time index (RTI)

Based on similarity of C18 retention and octanol-water partitioning

Thomas Letzel & coworkers, TU München

Nitroalkane retention index (NARI)

RI on homologue series of n-nitroalkanes

Grant Lab, Univ. of Connecticut

Hall et al., (2013) J. Chem. Inf. Model 52, 1222

Implemented in MolFind software,

Menikarachchi et al., (2013) Anal. Chem. 84, 9388.

CHI: Retention prediction by LSER

$$CHI = aA + bB + sS + eE + vV + C$$

Substance descriptors

Regression coefficients (system descriptors)

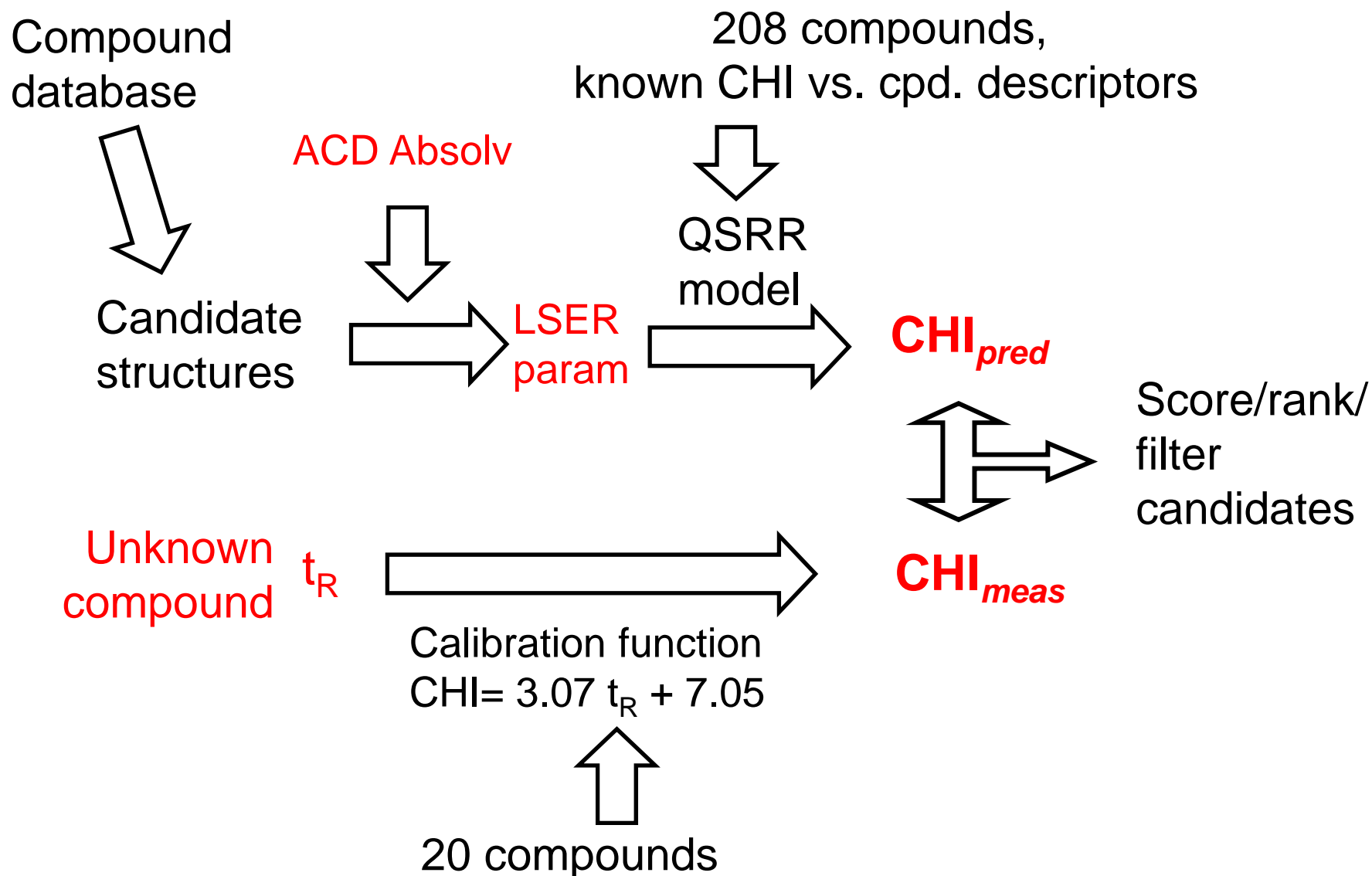
CHI \approx Percentage of organic modifier required to elute the analyte in a linear gradient (Valko et al., 1997, Anal. Chem. 69, 2022).

CHI is (nearly) independent from gradient setup and column dimensions, but different for ACN and MeOH

CHI is very similar for different (endcapped) C18 columns

Model does not account for ionic interactions and intramolecular H bonding

CHI: Retention prediction by LSER



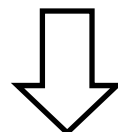
RTI: The beauty of simplicity

Compound
database

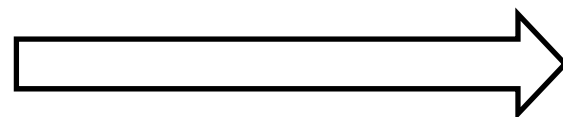


Candidate
structures

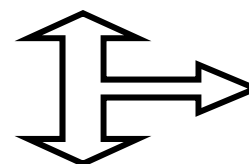
10000s of compounds



different or consensus
log P prediction models

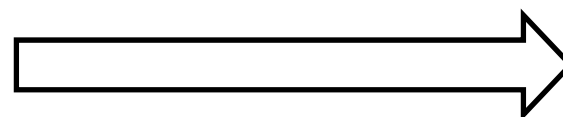


log P_{pred}



Score/rank/
filter
candidates

Unknown
compound t_R



log P_{meas}

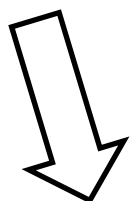
Calibration function
 $\text{Log P} = x t_R + y$



10 compounds

RTI: The beauty of simplicity

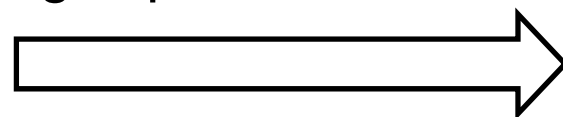
Compound
database



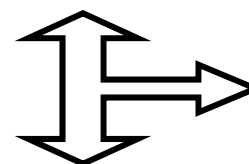
Candidate
structures

**Easy extension to log D
for ionic compounds!**

log D prediction models

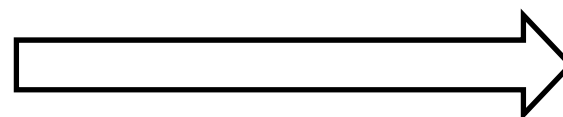


log D_{pred}



Score/rank/
filter
candidates

**Unknown
compound** t_R

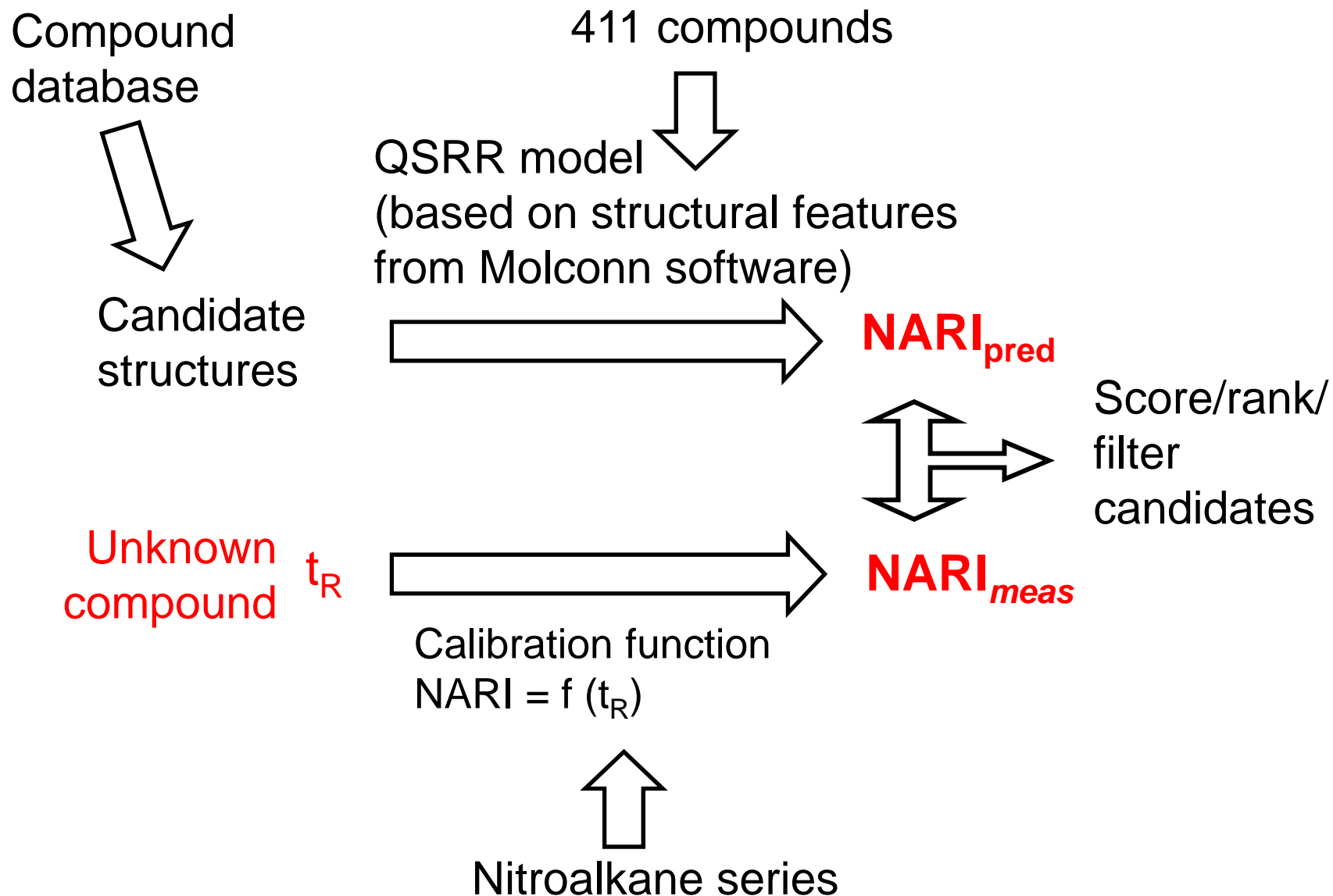


log D_{meas}

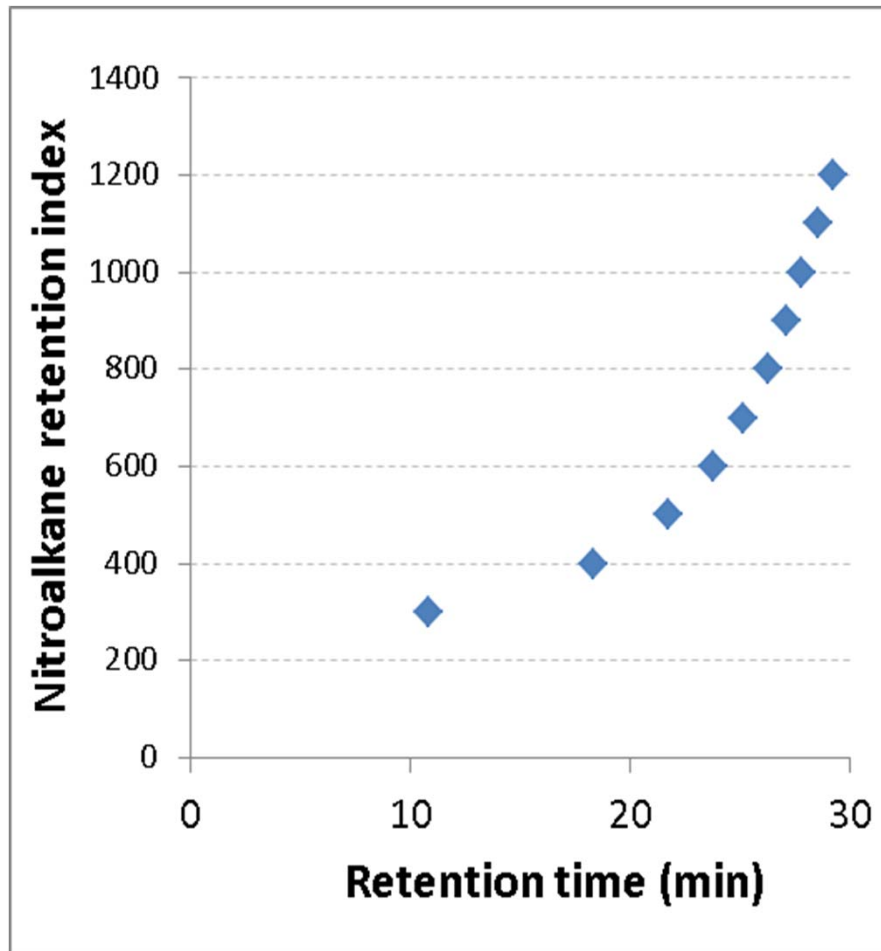
Calibration function

$$\text{Log D} = x t_R + y$$

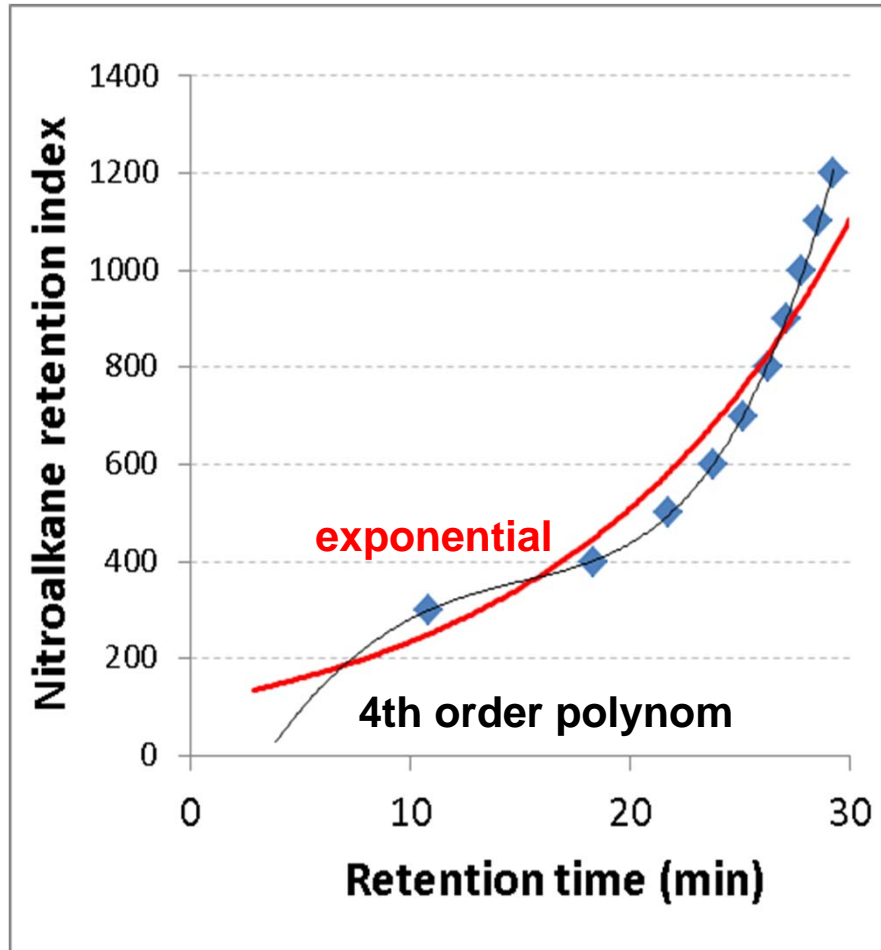
NARI: Kovats' for LC?



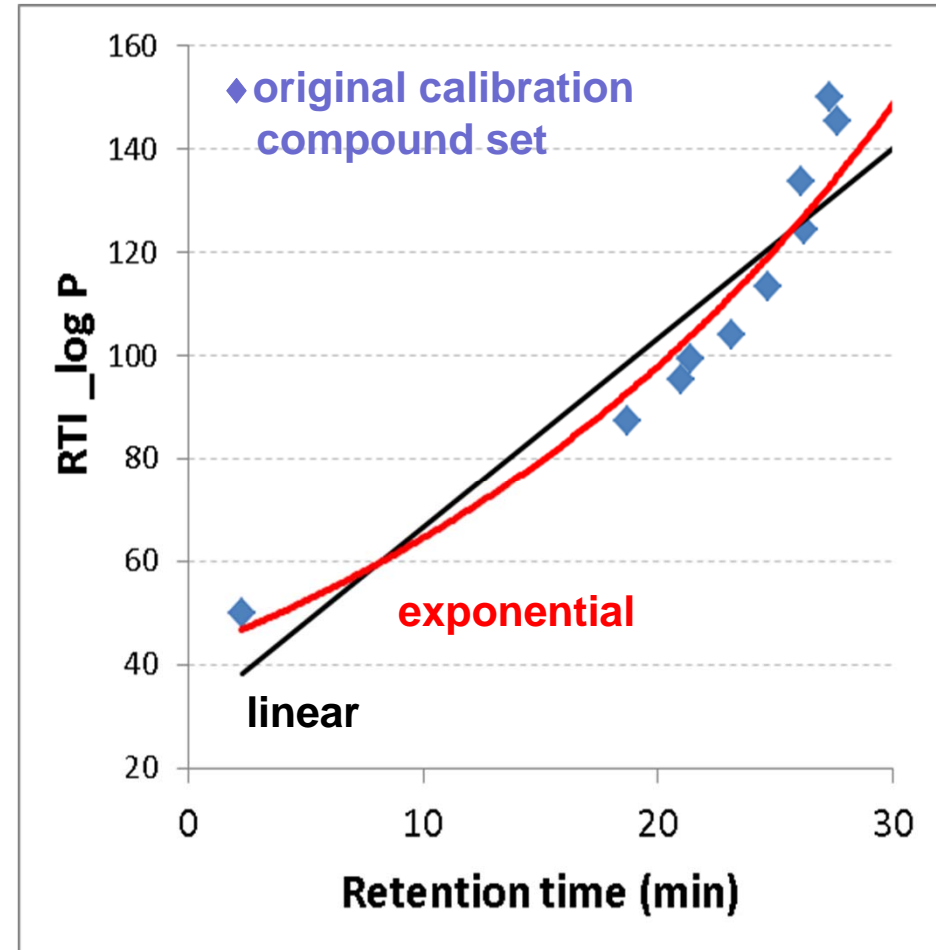
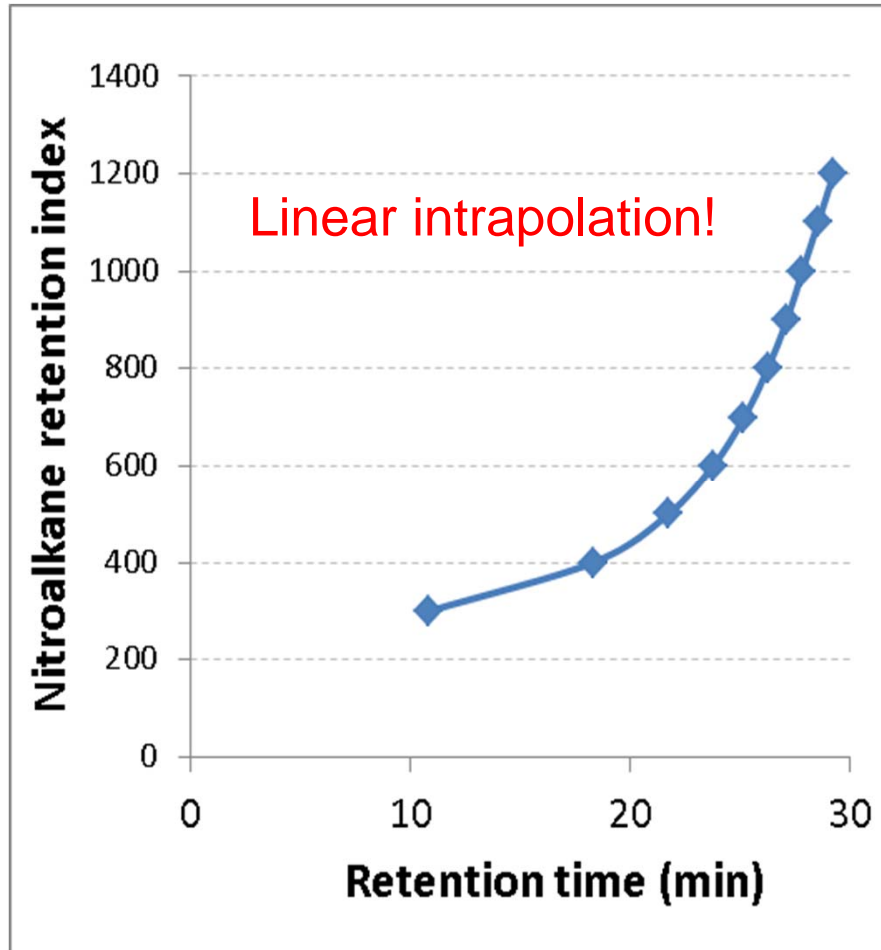
LC method calibration issues



LC method calibration issues

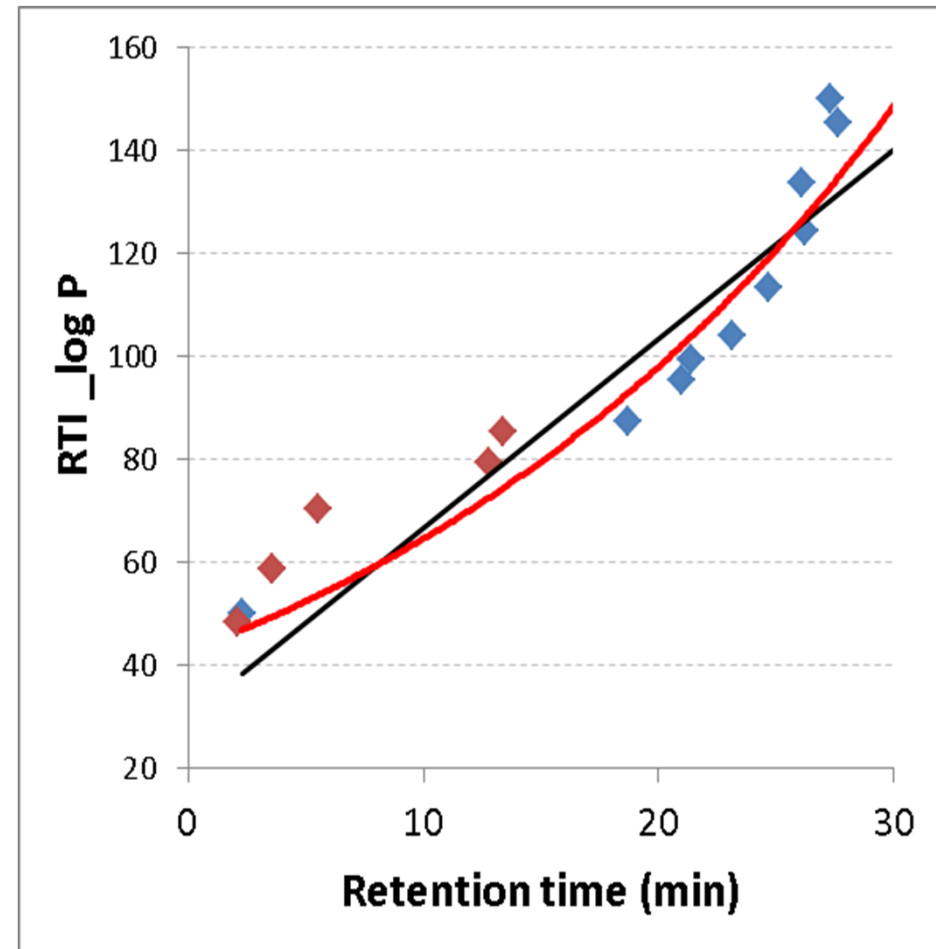


LC method calibration issues

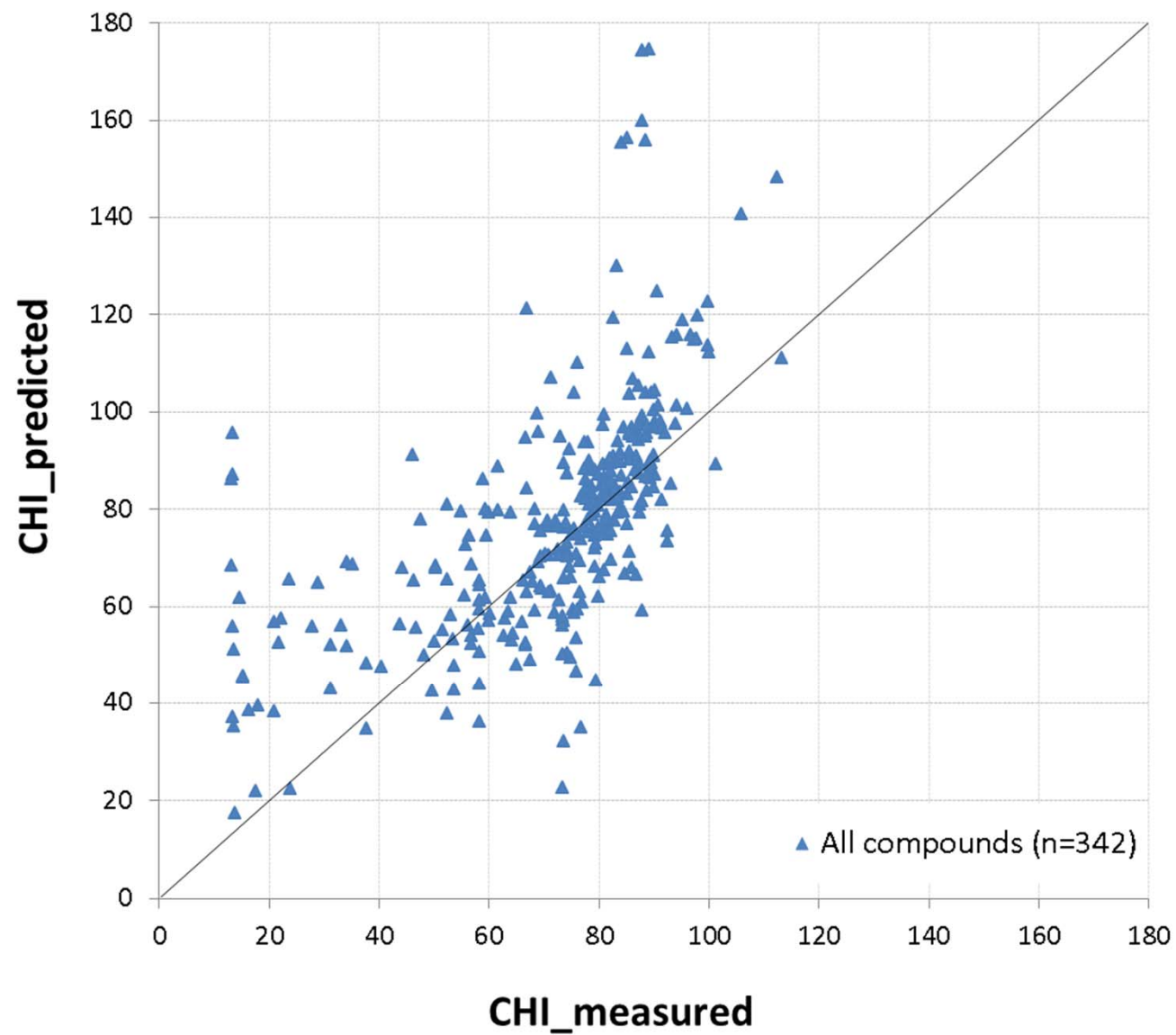


LC method calibration issues

Finding additional calibration
compounds might be
difficult...



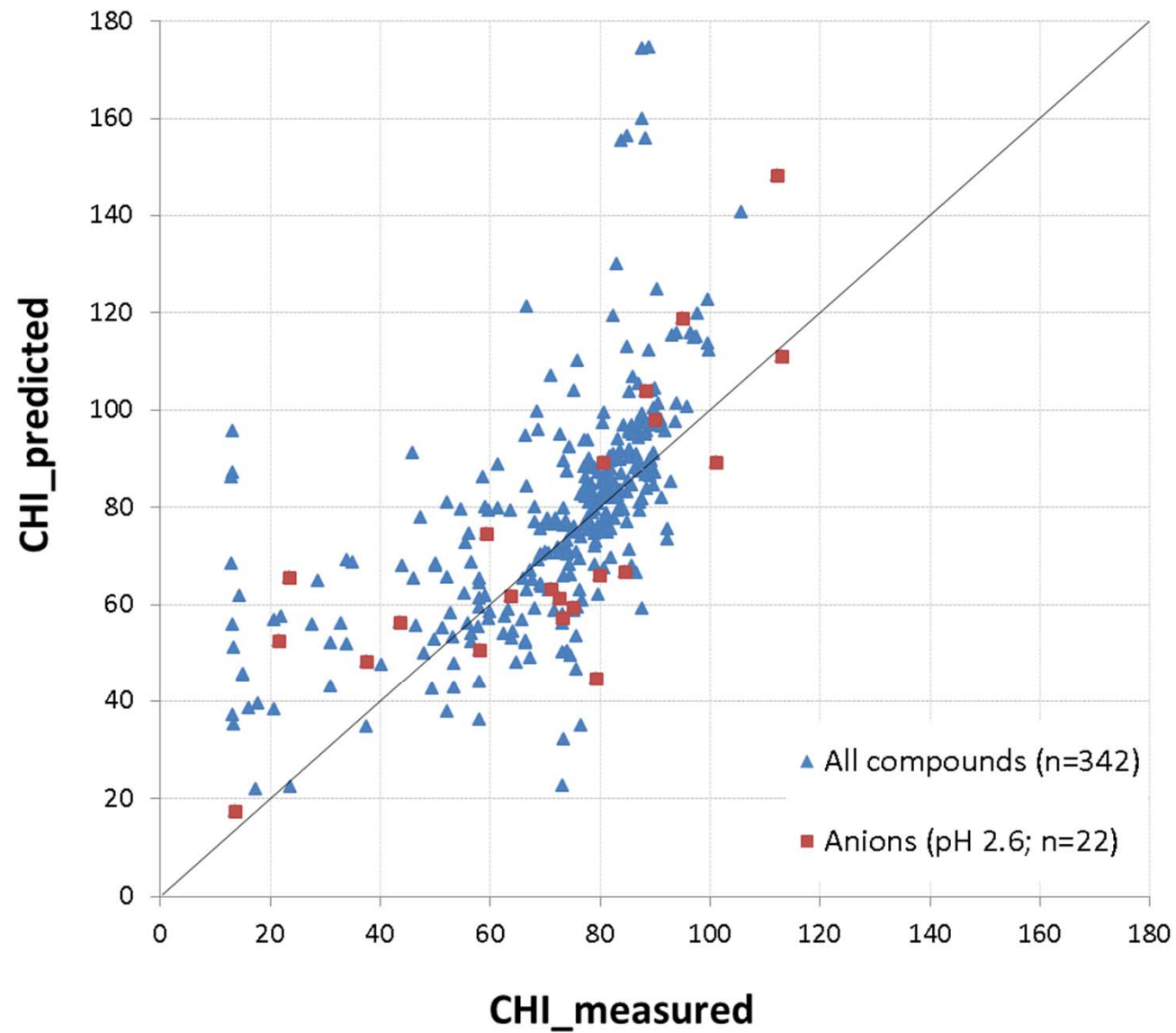
CHI model



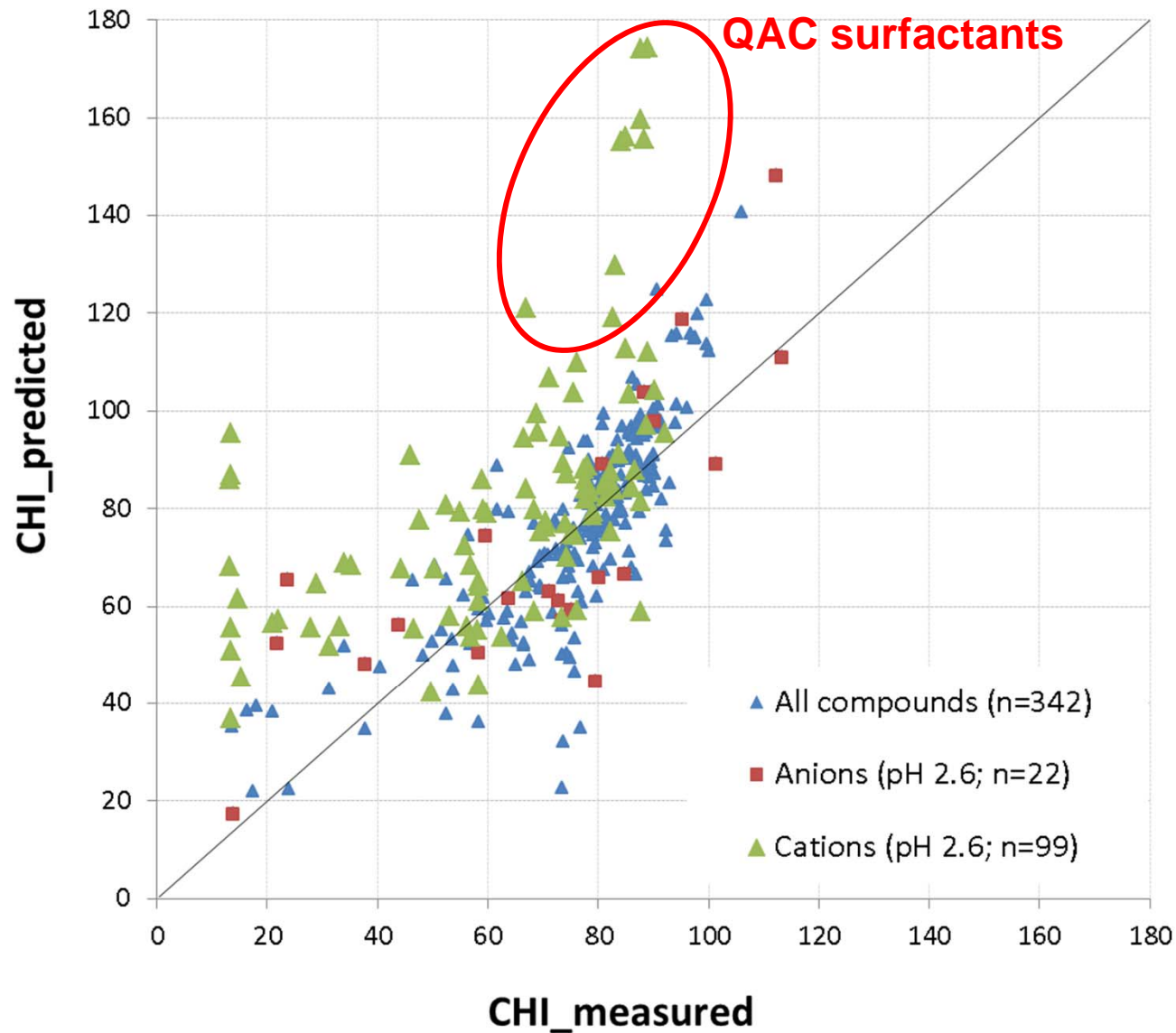
MAE 15.9

R^2 0.43

CHI model



CHI model

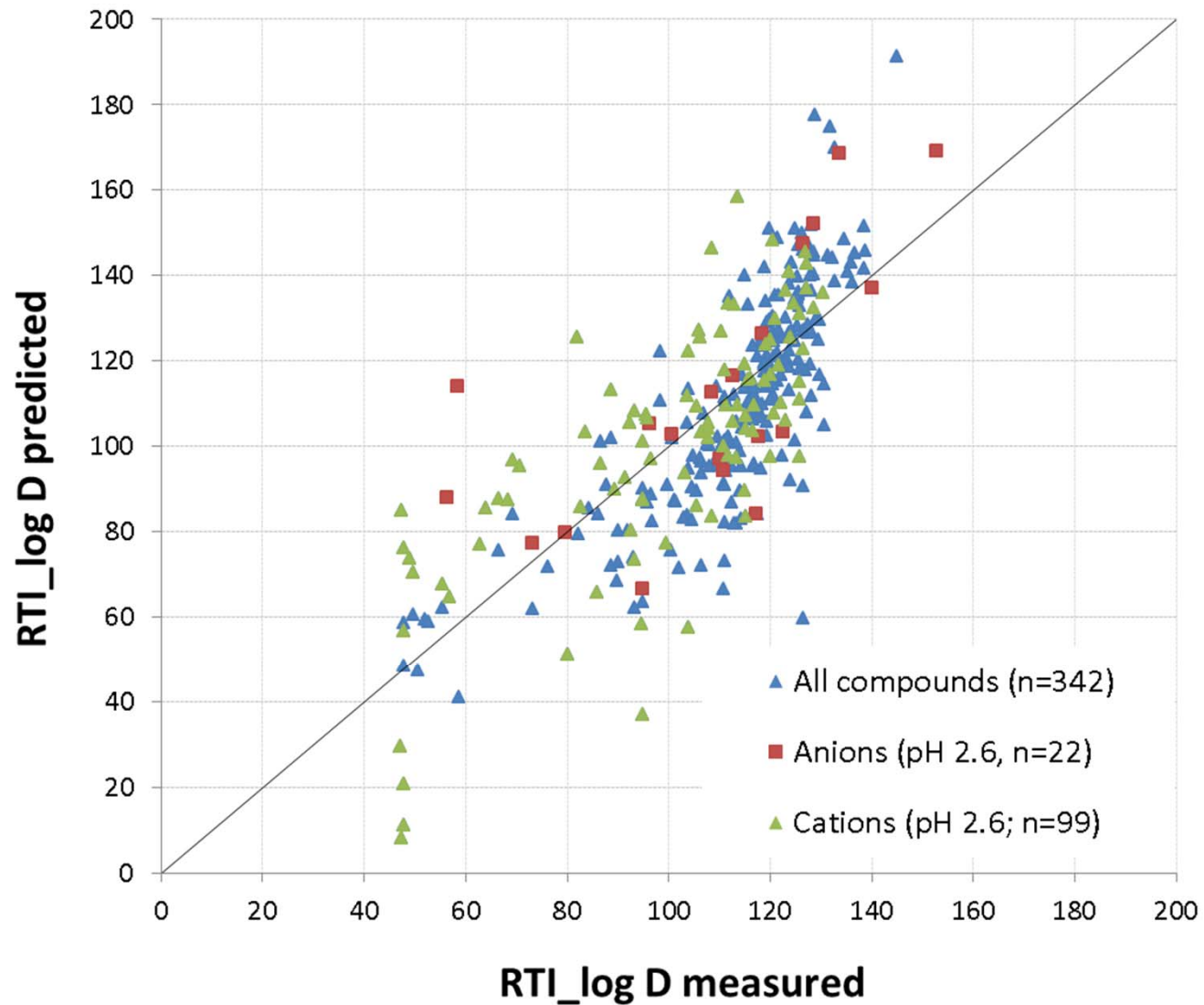


Neutrals
MAE 11.9
(≈ 3.9 min)
 R^2 0.63

Anions
MAE 15.8
(≈ 5.1 min)

Cations
MAE 24.9
(≈ 8.1 min)

RTI model

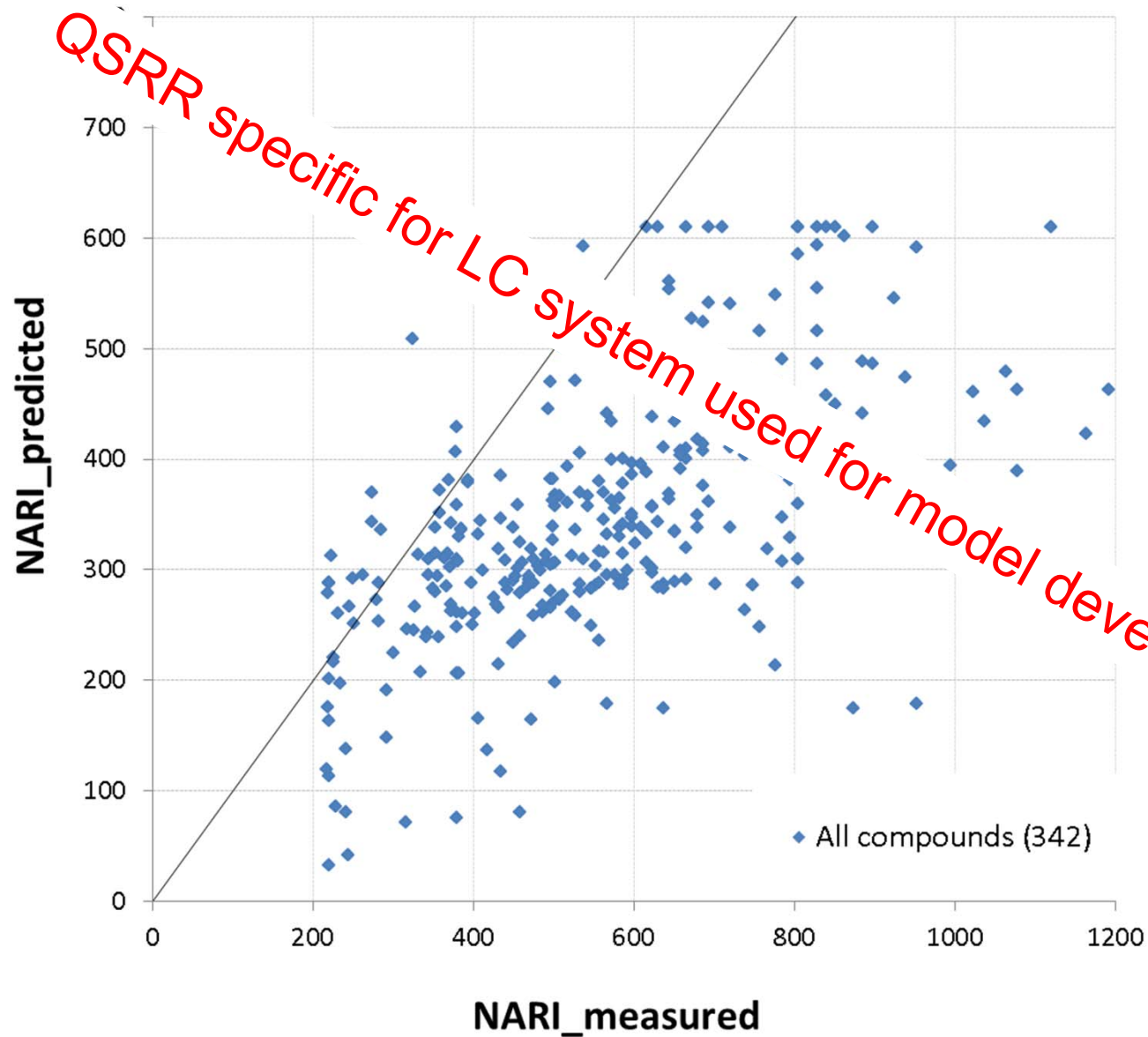


Neutrals
MAE 12.3
(≈ 3.9 min)
 R^2 0.63

Anions
MAE 20.8
(≈ 6.6 min)

Cations
MAE 16.4
(≈ 5.2 min)

NARI model

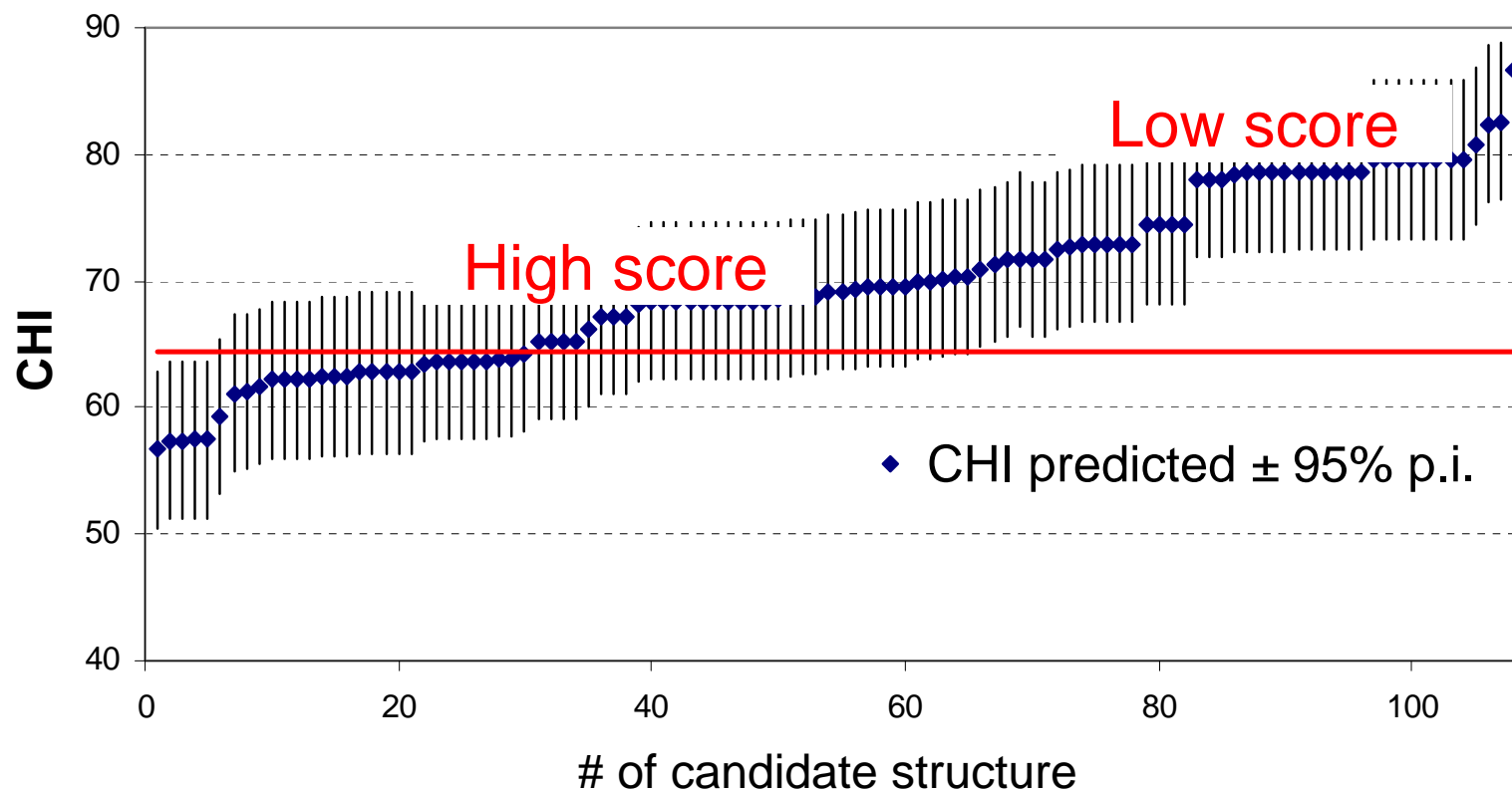


MAE 251

R^2 0.36

Candidate selection: not all about accuracy

Unknown t_R 19.5 min \Rightarrow CHI 64.4



Retention prediction models

- Are often far from accurate (hydrophilic, ionic & tricky compounds)
- Nevertheless provide useful information for confirmation of suspects or candidate exclusion
- A conceptually correct model might not be better than an analogy model

⇒ Be aware of compound domains the model is applicable

⇒ Be aware of prediction uncertainty

We have to develop some guidance on that!