

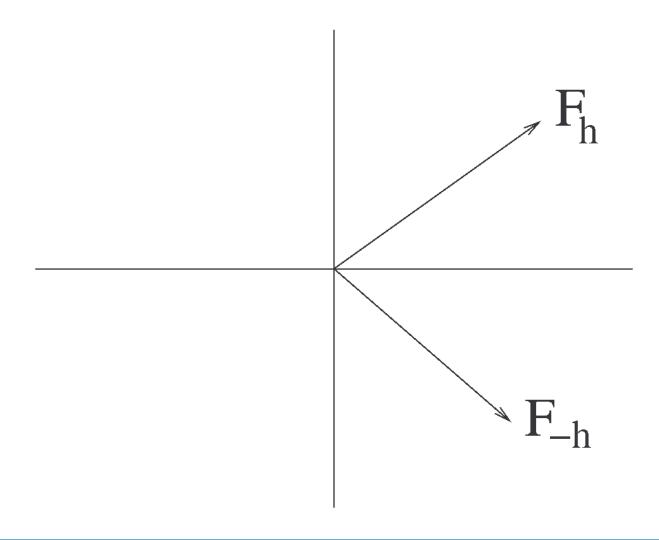
The absolute configuration of pharmaceutically interesting molecules

Optimal use of measured data

Rob W.W. Hooft, Bruker AXS, Delft Leo H. Straver, Bruker AXS, Delft Anthony L. Spek, Utrecht University

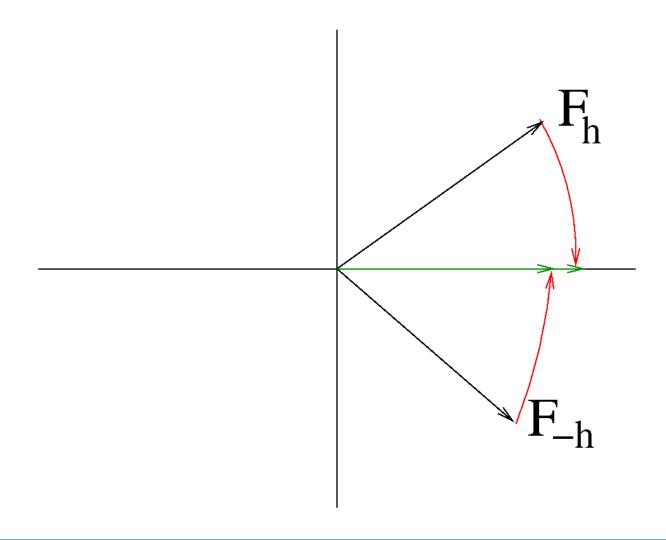


A Bijvoet pair in the complex plane





The Bijvoet difference



Bruker AXS

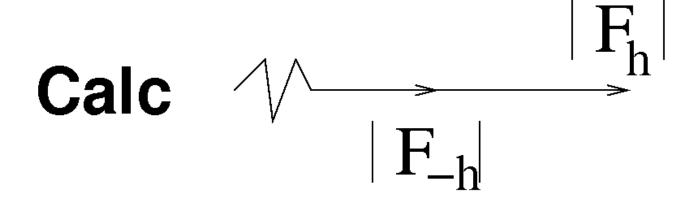


The resonant scattering signal: f"

	f"(CuKα)	f"(MoKα)	
Se	1.14	2.23	
Cl	0.70	0.16	
S	0.56	0.12	
О	0.032	0.006	



Model and observation

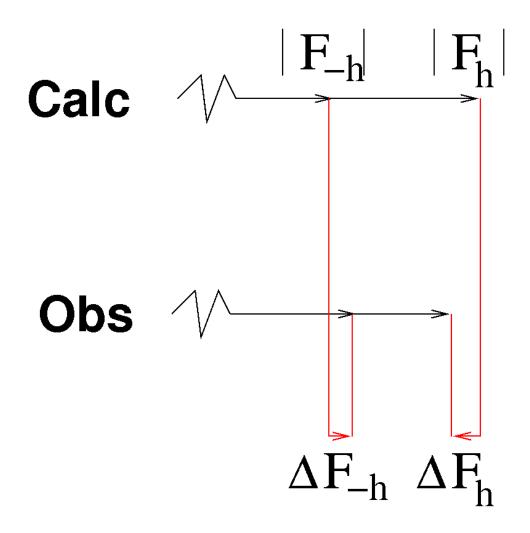


Obs
$$//$$
 $|F_h|$

Bruker AXS

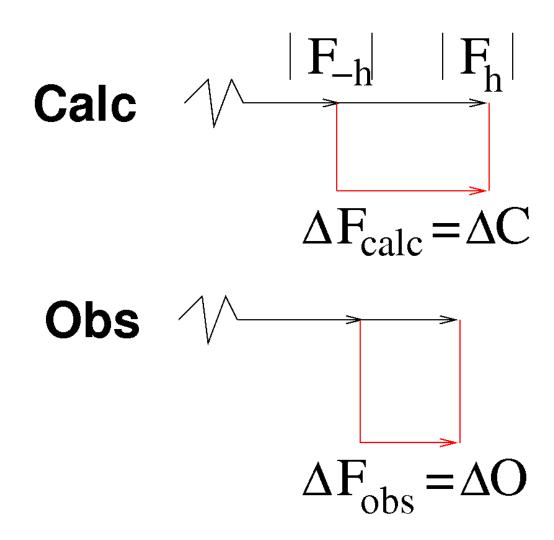


Difference between observations and model



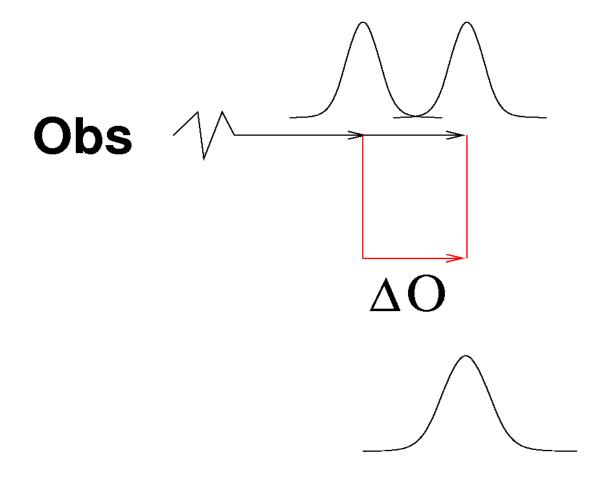


Observed and calculated differences



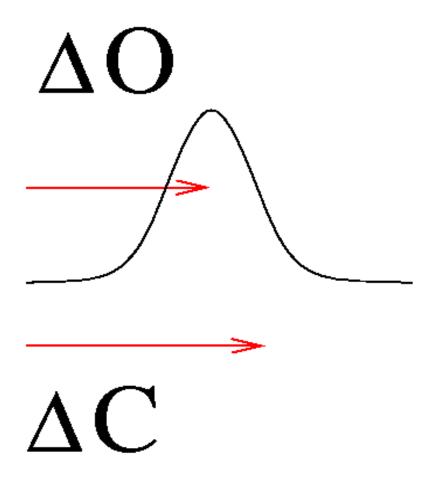


Standard deviations





Likelihood of correspondence





Absolute structure sensitivity

	Strong signal		Weak signal S		rong signal
$\Delta C/\sigma $ »1				-	++ or
ΔC/σ≈1		-	-	+	
ΔC/σ≈0		-	+	-	
ΔC/σ≈-1		+	-	-	
ΔC/σ«-1	++ or	-			
	ΔΟ/σ«-1	ΔΟ/σ≈-1	ΔΟ/σ≈0	ΔO/σ≈1	ΔΟ/σ»1



Normal distribution for a single model

$$z = \frac{\Delta C - \Delta O}{\sigma_{\Delta O}}$$

$$p(z) = \frac{1}{\sqrt{2\pi}} e^{-z^2/2}$$



Generalized model

Mix between the opposite structures at arbitrary ratios:

$$(1-y)\Delta C + y(-\Delta C) = (1-2y)\Delta C \equiv \gamma \Delta C$$

This gives:

$$x(\gamma) = \frac{\gamma \Delta C - \Delta O}{\sigma_{\Delta O}} \qquad p(x(\gamma)) = \frac{1}{\sqrt{2\pi}} e^{-x(\gamma)^2/2}$$



What is p?

$$x(\gamma) = \frac{\gamma \Delta C - \Delta O}{\sigma_{\Delta O}} \qquad p(x(\gamma)) = \frac{1}{\sqrt{2\pi}} e^{-x(\gamma)^2/2}$$

p is the chance of observing the given intensities, given the structural model and given the value of γ



Bayesian statistics

$$p(\gamma/\text{observations}) = \frac{p(\text{observations}/\gamma)p(\gamma)}{p(\text{observations})}$$



Delayed normalization

We delay normalization until we have determined the complete probability distribution:

$$p(\gamma/\text{observations}) = \frac{p(\text{observations}/\gamma)p(\gamma)}{\sum p_u(\gamma/\text{observations})}$$



Prior selection: enantiopure compound

In the case of enantiopure pharmaceuticals there are only two models: the proposed model and its opposite.

- P for the proposed model we call P2(OK)
- P for the opposite model we call P2(wrong)
- The prior $p(\gamma)$ is $\frac{1}{2}$ if $\gamma=1$ or $\gamma=-1$, and 0 otherwise.



Prior selection: racemic twinning

In the case of a potential racemic twin, γ becomes a continuous function

- Physics restrains values to $\gamma \ge -1$ and $\gamma \le 1$
- Prior: $p(\gamma)=1$ if $\gamma \ge -1$ and $\gamma \le 1$, $p(\gamma)=0$ elsewhere

This makes sense from a statistical point of view, but it does not give any warning if there would be a serious aberration

Alternative:

- Prior definition $p(\gamma)=1$ everywhere
- i.e. no prior knowledge is used



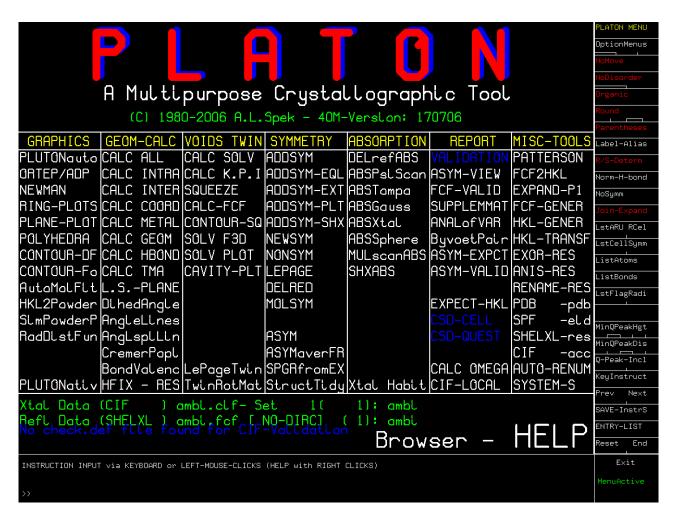
Prior selection: racemic twinning (2)

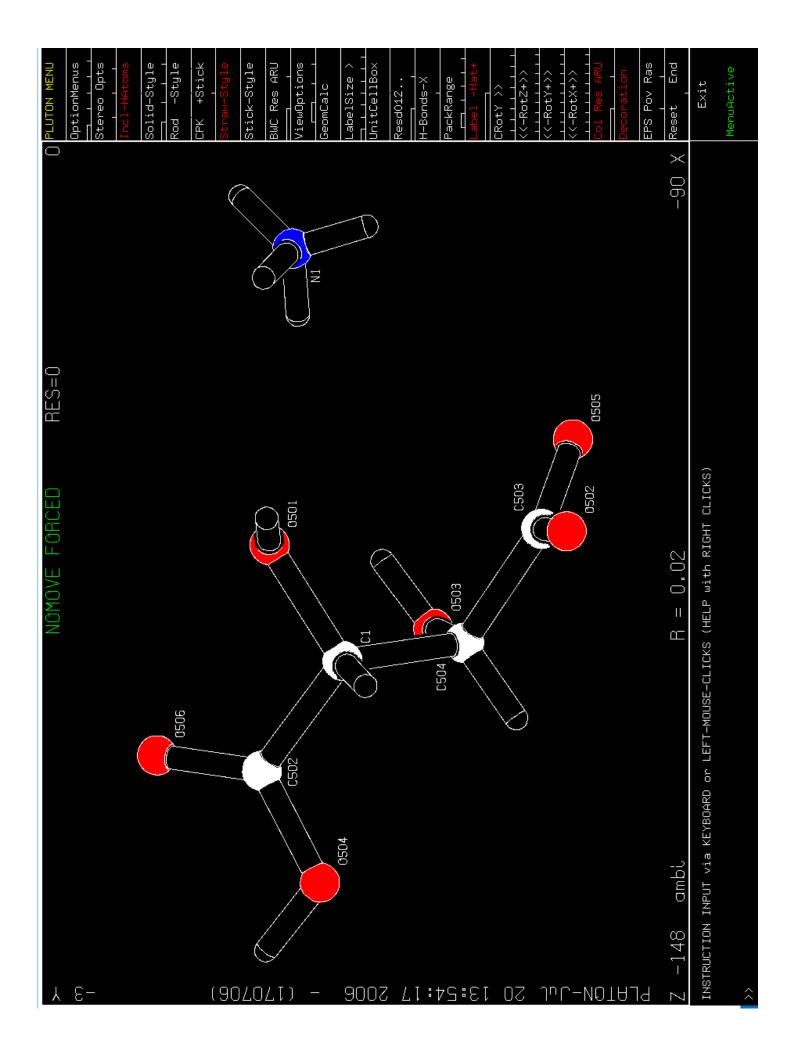
Prior definition $p(\gamma)=1$ everywhere, i.e. no prior knowledge $p_u(\gamma|\text{observations})$ looks like a Gaussian. We can calculate a mean, G, and associated standard deviation:

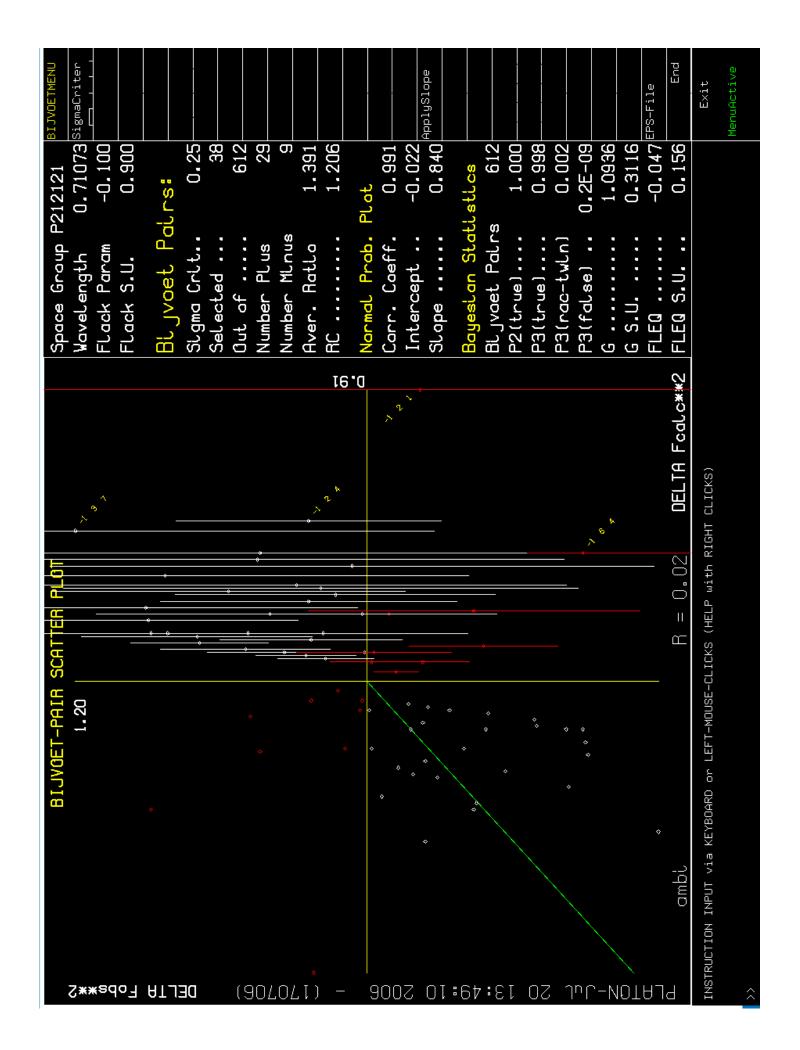
$$G = \frac{\int \gamma p_u(\gamma) d\gamma}{\int p_u(\gamma) d\gamma} \qquad \sigma^2(G) = \frac{\int (\gamma - G)^2 p_u(\gamma) d\gamma}{\int p_u(\gamma) d\gamma}$$



Example









Experiences

 σ_{v} is about half of σ_{x} sometimes even less

y clusters very well around 0.0

absolute structure of $C_xH_yO_z$ can be determined reliably using $CuK\alpha$ radiation

When Bijvoet pairs are measured explicitly, the least-squares refinement of the Flack x parameter is not correlated with atomic coordinates



Conclusions

A new method to determine absolute structure

Pharmaceutical compounds, known to be enantiopure.

Explicit calculation of the likelihood of an inversion (P2) without assumption about the Gaussian shape of the probability curve

The method can be used for very weak anomalous scatterers

But:

Bijvoet pairs must be measured explicitly

This absolute structure determination can not take place inside the full matrix refinement.