## **@derived:** post-processing

```
1 @derived begin
2     dv ~ @. Normal(conc,sqrt(conc^2 *Σ.diag[1] + Σ.diag[end])+eps())
3 end
```

The derived block specifies variables that can be used for post-processing of results. It can be an continuous distribution shown above or a discrete one like

```
1 @derived begin
2      dv ~ @. Poisson(baseline*(1-dose/(dose + d50)))
3 end
```

Let's suppose that there was clinical trial for a new exciting drug JuliaCon, it relieves you of headaches due to using other languages.

We observed the concentrations but we did not see the response we wanted. We think that the dosage we were giving, say 100mg was not sufficient, we need to ramp it up.

The question arises, what if I increase the dose to say, 200mg, does that fix the problem? What about 150mg would that work?

To answer this question we would have to run the entire clinical trial again with these different doses.

## That is slow and costs a lot!

So how do we answer this question?