# BIOKMOD APPLICATION FOR THE EVALUATION OF DIFFERENT TYPES OF BIOASSAYS

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The Biokmod software for bioassay evaluation, allows to perform different types of calculations (dose calculation, retention fractions, etc..). This latest module, using data from different bioassay, gives the estimated intake using best fit approach.
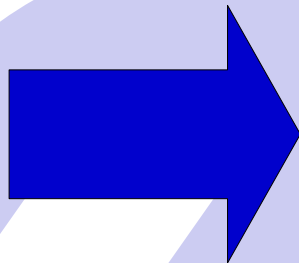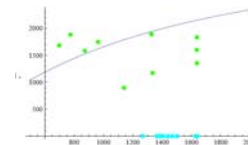
Using the data, the best fit is applied

$$\{Mean \rightarrow 81.285,\ s \rightarrow 1.17044\}$$

Insert the data from the bioassay (date, activity, deviation) and intake way (inhalation, injection or ingestion)

The final result is the intake and standard deviation

The unknown intakes can be estimated as function of the bioassay data. The program uses non linear regression models to find the best fit. Not only the intake can be assumed unknown but also other parameters such as the AMAD, sp, spt and st can be unknown. The are two Biokmod version: a) A web version called BiokmodWeb that run using a navigator, it has some limitation about the parameters and characteristic of the intake and b) The BIOKMOD full version (it is Mathematica tool box, an therefore Mathematica is required) many parameters can be modified by users, including additional fitting option, even the user can build new models. Optimal design experiment can be used to chose the best moment where taken the bioassay analysis

For the fit of the bioassay in Biokmodweb the following equations are used

$$I = \frac{\sum_{i=1}^{N} r_{c,j}(t_i)\,\frac{m_i}{u_i^2}}{\sum_{i=1}^{N} \frac{r_{c,j}^2(t_i)}{u_i^2}}$$

$$u_i = \frac{1}{\sum_{i=1}^{N} \frac{r_{c,j}^2(t_i)}{u_i^2}}$$

I=intake

$r_{c,j}$=retention function associated with measure i (for chronic or acute intakes)

u_i=uncertainty associated with measure i

m_i=measure of bioassay

CONCLUSION

With this new module for Biokmod it is possible to study the best estimation for intake and AMAD, using as input the data from different bioassays. The software is available for free in the following webpage.

BIOKMOD WEBPAGE

http://www3.enusa.es/webMathematica/Public/biokmod.html