CABAS – a Freely Available PC Program for Fitting Calibration Curves in Chromosome Aberration Dosimetry

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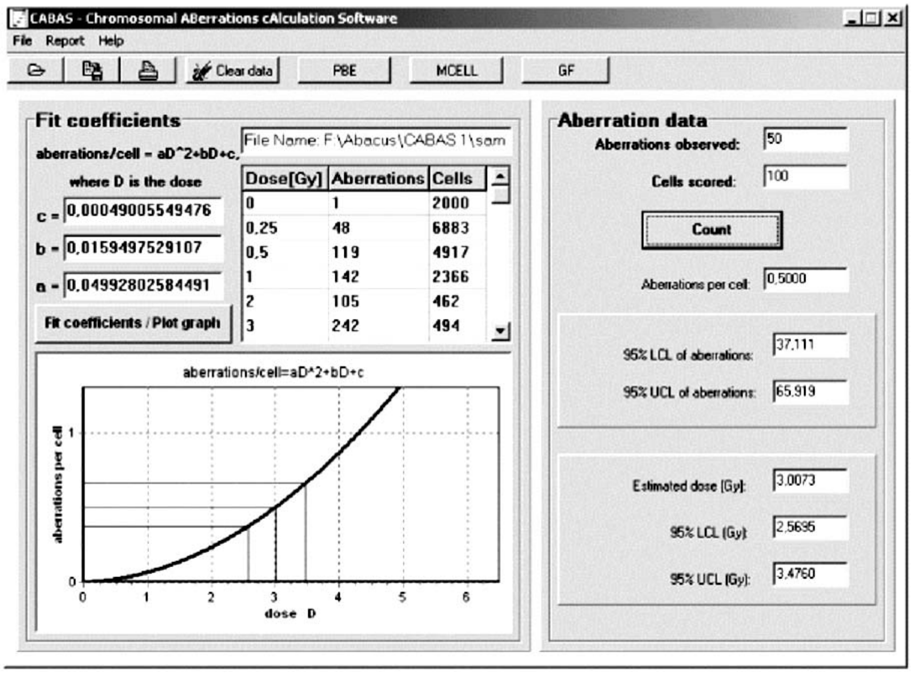
The aim of biological dosimetry is the calculation of the dose and the range of uncertainty to which an accident victim was exposed. This process requires the use of the maximum likelihood method for the proper fitting of an in vitro calibration curve, a procedure which is not implemented in popular, commercially available statistical computer programs.

The most specific and sensitive technique of biological dosimetry relies on estimating the frequency of unstable chromosomal damage in peripheral blood lymphocytes of the exposed person [1,2]. The dicentric chromosome aberration assay is the most frequently used, sometimes combined with centric rings, and the cytokinesis blocked micronucleus (CBMN) assay has also been developed. Numerous studies, performed both on animals and humans, have demonstrated a close correspondence between aberrations or micronuclei induced in peripheral blood lymphocytes under in vitro and in vivo conditions. This allows one to estimate a radiation dose absorbed during an accident by reference to an in vitro calibration curve.

This curve is generated by irradiating blood samples, collected from control donors, with several doses of radiation. Following culturing of lymphocytes, microscopic slides are prepared and the frequencies of dicentrics and rings are estimated in first division metaphases or micronuclei in binucleate cells. The points of the dose-response relationship are fitted to an equation which is linear-quadratic for low LET (linear energy transfer) radiation and linear for high LET radiation.

The correct fitting procedure is not trivial because it requires an appropriate weighting of data points. Several laboratories have produced their own curve fitting programs for internal use but these are frequently not user-friendly and not available to outside users. Therefore, a PC-based freely available program called CABAS, for fitting dose-response curves to chromosomal aberration or micronucleus data and for calculating the dose and confidence limit (CL) has been developed and tested. The program consists of (i) the main curve-fitting and dose estimating module, (ii) a module for calculating the dose in cases of partial body exposure, (iii) a module for estimating the minimum number of cells necessary to detect a given dose of radiation, and (iv) a module for calculating the dose in the case of a fractionated or protracted exposure (see Fig.1).



aberrations/cell = aD^2+bD+c,
where D is the dose

c = 0,00049005549476
b = 0,0159497529107
a = 0,04992802584491

File Name: F:\Abacus\CABAS 1\sam

Dose[Gy]	Aberrations	Cells
0	1	2000
0,25	48	6883
0,5	119	4917
1	142	2366
2	105	462
3	242	494

Aberrations observed: 50
Cells scored: 100
Aberrations per cell: 0,5000
95% LCL of aberrations: 37,111
95% UCL of aberrations: 65,919
Estimated dose [Gy]: 3,0073
95% LCL (Gy): 2,5695
95% UCL (Gy): 3,4760

Fig. 1: A screenshot of the menu of the program

The program can be downloaded as freeware from http://www.pu.kielce.pl/ibiol/cabas or obtained from any of the present authors. The use of the program is straightforward and it can be expected that its use will improve the precision of dose estimates by biological dosimetry in cases of radiation accidents. Furthermore, it should facilitate setting up inter-laboratory dose effect curves.

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