

DOSE ESTIMATION SOFTWARE FOR RADIATION CYTOGENETICS

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There exists a core group of methods which are used to produce an estimate of radiation dose by chromosome analysis of blood samples. At the Health Protection Agency's Centre for Radiation, Chemical and Environmental Hazards, blood from a suspected irradiated person is cultured in the laboratory and dicentric, metaphase and/or translocation assays are carried out to investigate the extent of the DNA damage within the cultured blood.

Mathematical and statistical analysis is extremely important for accurate assessment of the data and results, and there are a number of statistical methods which are commonly used. For instance, a calibration curve for the specific type and energy of radiation can be used to link the amount of damage to an estimated dose, and associate standard errors and confidence limits with the estimate. However, the large number of different statistical techniques which are routinely employed and the complexity of some of the methods can lead to errors in data analysis and thus misinterpretation of results.

Cytogenetics dose estimation software has been developed to simplify mathematical and statistical analysis of cytogenetic data. 'Dose Estimate' is a collection of mathematical and statistical methods based on the cytogenetics methods detailed in IAEA (2001) and programs written by Alan Edwards¹, David Papworth² and others. The mathematics and the graphic user interface have been implemented using Borland Delphi 6.

On running the software, the user is presented with the main screen, entitled 'Aberration Dose Estimation.' The user can then choose the analysis methods from a drop down list located on the menu at the top of the screen. The seven main options that are currently available are: Aberration Dose Estimate; Simple Isotropic Dose; Criticality; Partial Body Exposure; Yield Curve Fitting; Translocation Analysis (FISH), and Other Statistics (currently the χ^2 and t-tests). For each tool, the raw data may be loaded from a text file or entered into tables or text boxes. Selection boxes are used to specify techniques, and increase the sophistication of the analysis. The results are then displayed graphically or in text format, in tables or results boxes located on each screen, as well as a case report which records all the analysis carried out in a single session.

A demonstration of the software will be given. Details the biology and mathematics behind the techniques and proposals for increasing the sophistication of the software, for instance through implementation of Bayesian probability analysis, will also be presented.

Reference.

IAEA. Cytogenetic Analysis for Radiation Dose Assessment, A Manual. Technical reports series No. 405. International Atomic Energy Agency, Vienna, 2001.

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