# Size Distributions of Misrejoining DNA Fragments in Irradiated Cells

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## Abstract

When ionizing radiation strikes a cell it induces DNA double strand breaks (DSBs). Subsequently, some of the DSBs misrejoin and thus cause alterations in the size distribution of the DNA fragments. We derive a system of non-linear integro-differential equations describing the misrejoining interactions of five classes of DNA fragments, including rings and various types of linear fragments. The fragment classes are represented by density functions; the shape of a density function determines the probability that a fragment has a particular size and the amplitude (integral) equals the expected number of such fragments per cell. The equations are solved: analytically for exponentially distributed initial fragment sizes (corresponding to high doses) and numerically for arbitrary initial conditions.

Computed final fragment size distributions are applied to situations representative of flow karyotypes and pulsed-field gel assays. For human flow karyotypes, the model can be used to obtain misrejoining estimates at doses too high for conventional methods of data analysis. For pulsed-field gel assays in which human chromosomes are digested with restriction endonucleases to form "cut-somes" (restriction fragments), the model provides a means of misrejoining estimation when the cut-some sizes are non-random. The model suggests that if the cut-some size distribution for unirradiated cells is completely random, misrejoining of radiation-induced DSBs will not be detectable in the final size distribution.