

Integrating Large Scale Data Sets to Develop Predictive Hypotheses of Low-Dose Radiation-Induced Health Effects

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Over one hundred years of radiation biology research has revealed much about the DNA damages induced by the deposition of energy from exposure to ionizing radiation and the subsequent cellular responses. However, there are still significant gaps in our understanding of how these might lead to detrimental health effects, particularly at low doses (<100 mGy). Recent advances in high throughput 'omics technologies enable interrogation of induced radiation effects at the genomic, proteomic and metabolomic levels. These include changes in gene expression, protein modifications, e.g., phosphorylation, acetylation, and methylation, and metabolic changes. We will discuss the integration of data obtained from multiple 'omics platforms to understand radiation dose, and dose rate effects in a complex human tissue model as a function of time. We will use as an example our results on the low dose responses in a 3D human skin model.