

Monte Carlo peripheral dosimetry for primary breast cancer radiotherapy to estimate risks of secondary radiation-induced cancers

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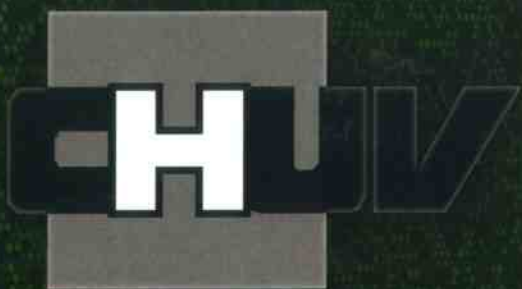
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Introduction : The aim of this study is to develop a Monte-Carlo based tool to estimate peripheral doses for breast cancer patients who underwent radiation therapy. Peripheral dosimetry has to be taken into account to estimate the risk of a secondary radiation-induced cancer, since most secondary cancers arise outside the fields in regions receiving lower doses than the target volume. The Monte-Carlo based tool will estimate doses at different organs as a function of the morphological parameters of the patient and the technical radiation parameters.

Material and methods : morphological and technical parameters were extracted from 109 breast cancer patient files. All patients developed a secondary cancer. The variability of each parameter was analyzed in order to identify the parameters that could be eliminated or fixed at a certain value and those that are kept as variables affecting peripheral doses.

Results : The analyses of the parameters show that height, weight, dimensions of the breast, gantry angle of the tangential fields and dimensions of the fields vary considerably. By modeling five types of fields (two tangential fields, one sternal field, one AP field and one PA field), we can reconstruct the doses for 85% of the cases. All the photon treatments were either delivered by a cobalt-60 unit or a LINAC 6 MV. Electrons will be neglected since they do not contribute to the peripheral dose. A 6MV linac head has been modeled in the Monte Carlo program BEAMnrc. Dose calculation outside the fields with Monte Carlo show good agreement with measurements.

Discussion: The Monte-Carlo based tool will enable to compute dose distributions to organs outside the beams as a function of the morphology of the patient and the irradiation parameters. It will be possible to take into account inhomogeneous dose distributions across organs for risk estimations.



Research Day

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Couverture : Yannick Krempp, Département de Biologie Cellulaire et de Morphologie – UNIL

Photo : DNA microarray image of an RNA expression profiling experiment provided by
Manuela Weier and Henrik Kaessmann of the Centre Intégratif de Génomique - CIG
and Jérôme Thomas of the Lausanne DNA Array Facility, Centre Intégratif de Génomique - CIG



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