

DIPARTIMENTO/CENTRO Dipartimento di Medicina interna e Specialità mediche (DIMI)
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Finanziamento

Responsabile scientifico: Prof. Gabriele Zoppoli
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Title

Assessment of ploidy, purity, and subclonal populations through genomics analyses of large array-CGH, targeted NGS and low-pass whole genome sequencing in invasive breast carcinoma

Job description

The successful applicant will perform computational and bioinformatical analyses, including the development and optimization of dedicated pipelines and scripts in the Unix/Linux environment, on data from prospective translational trials and publicly available datasets. In particular, the effect of ploidy, purity, subclonal population presence will be evaluated in relation with the aggressiveness of hormone-receptor positive breast cancer. Skills required are in the field of bioinformatics/bioengineering and computational biology, with knowledge of tumor biology, programming capabilities in the Unix/Linux environment and knowledge of the perl, python, make, Java, and R languages.

Required degrees

Engineering, bioengineering, bioinformatics, statistics, mathematics or biology M.Sc. or equivalent recognized within the European Community

Call topics: Copy number assessment pipelines from array-CGH, targeted NGS, whole-genome sequencing. Evaluation and comparison of methods for assessment of cancer population clonality. Relative/absolute copy number estimation and optimization methods to estimate such measures through genomic analyses. Biological consequences of copy number, purity and ploidy in cancer, especially in breast cancer and its metastatic relapse.