



Computational Analysis of Next Generation Sequence data

Three Bioinformatics positions

Project outline

Genomic alterations are major determinant of responses to (targeted) therapies in cancer. In fact, the best positive and negative predictors of responses to targeted therapies are alterations in kinases or their direct downstream effectors. To gain insight into resistance mechanisms to therapy and thus better tailor treatment, we are approaching this problem from two different angles. First we have transplanted tumors from mouse models of breast cancer and treated these tumors with a range of (targeted) therapies. Matched pre- and post treatment pairs of resistant and sensitive tumors have been full exon sequenced and are available for analysis. The goal is to detect genomic alterations associated with response to therapy. Second, we have acquired large panels of human tumors, on which we are currently performing kinase exon sequencing. More specifically, we are performing sequencing on 1) 400 samples from the NEO-ALTTO study to find alterations associated with resistance to HER2 targeted therapies; 2) at least 200 colorectal samples and 300 breast cancers (triple negatives and invasive lobular carcinomas) to detect alterations frequently occurring in these patient populations. A very strong feature of all these datasets is that matched controls are available to ensure high accuracy in variant calling. The successful candidates will work closely with the biological groups to develop computational approaches for the detection of mutations and copy number alterations associated with specific cancer subtypes as well as therapy response in human and mouse model-derived tumors.

Candidate Requirements –Education and Experience

We are seeking highly motivated Postdoc and PhD candidates with a degree in bioinformatics or a mathematical discipline with a strong cancer biological interest. Applicants should either have strong modeling/applied statistics skills or strong documented experience in analyzing high-throughput sequencing data. In addition, we strongly value experience in one or more of the following: sequence analysis, machine learning, applied statistics and R, computer science and expression analysis. The candidate also needs to be proficient in a programming languages such as Java, Perl or Python, and be comfortable with Linux systems. Fluency in spoken and written English is a strong requirement.

Location

The project will employ the complementary expertise and tools of three groups participating in the Cancer Systems Biology Center (csbc.nki.nl) at the Netherlands Cancer Institute, Amsterdam: Rene Bernards (Molecular Carcinogenesis), Jos Jonkers (Mouse Models for Breast Cancer) and Lodewyk Wessels (Computational Biology). The position are primarily embedded within the Bioinformatics and Statistics Group (Wessels) (bioinformatics.nki.nl) at the Netherlands Cancer Institute, Amsterdam.

Contact details

Please contact Dr. Lodewyk Wessels, tel. +31 20 512 7987 or e-mail: l.wessels@nki.nl. When applying please ensure you include a CV, list of publications and the names and addresses of at least two persons that can be approached to obtain further information. Also see bioinformatics.nki.nl and csbc.nki.nl for further information.

Closing date: 31 January 2012