CARD WORKSHOP   *The Cancer Genome Atlas*
November 22nd and 23rd 2016
Place: Biografen, meeting room, 2nd floor

Program:

Day 1 – Tuesday, November 22nd 2016

10.00 Welcome and introduction

10.15-11.00 "**The Cancer Genome Atlas (TCGA) Initiative: an introduction**" – Dr. Elena Papaleo

11.00-12.00 "High-throughput technology in system biology: genomics epigenomics transcriptomics data: an introduction" – Dr. Antonio Colaprico

12.00-13.00 Lunch Break

13.00 Introduction to the practical session

13.15-14.15 "Web servers for the analyses of TCGA data" – Dr. Elena Papaleo – Presentation and exercises

14.15-14.30 Coffee break

14.30-16.30 "**Mining and analysis of transcriptomics data (TCGA) to identify candidate biologically relevant associated with cancer**" – Dr. Antonio Colaprico – Exercises with TCGAbiolinks

Day 2 – Wednesday, November 23rd 2016

10.00-11.00 "**Case studies from TCGA using R: using genomic data**" – Dr. Antonio Colaprico – Advanced exercise with TCGAbiolinks

11.00 - 11.15 Coffee break

11.15 – 12.15 "**Case studies from TCGA using R: Integrative (Epigenomic & Transcriptomic)**" – Dr. Antonio Colaprico – Advanced exercise with TCGAbiolinks

12.15 Closing remarks

Requirements

Participants will need to **bring their own laptops.**

It is possible to sign up for **only part I** of the workshop (day-1 until 2.15 pm) or to **both part I and II.** There will be room for 20 participants to attend part I and approximately 15 to attend part II. In case of a large number of applications we will select on the base of a short CV and motivation letter. CV and letter will be required only in case we reach the maximum number of participants.

R, Rstudio and TCGABiolinks installed prior to the workshop for part II - if you encounter any problem, please contact us well in advance (at least a week before the workshop). The participants can also ask (at least two weeks before the workshop) for a temporary account to the CBL local server where the software is already installed. This will require skills with the Linux shell and ssh/scp connection.

Prior Knowledge for part II
- **Basic R, Rstudio, Linux/Mac terminal** knowledge required
- Other programming and scripting abilities would be nice but are not necessary
- Basics statistical analyses applied to life science

The participation to the R-course organized by SBR in October-November 2016 would be an asset in the evaluation of the applications.

Please send your request to elenap@cancer.dk no later than November 7th 2016 indicating if you would like to participate to part I only or part I+II