ExomeAI: Detection Of Recurrent Allelic Imbalance In Tumors Using Whole Exome Sequencing Data

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Registering for an ExomeAI account:
1- Open a browser and go to http://genomequebec.mcgill.ca/exomeai
2- Under the “User” tab at the top of the page, select the “Register”.
   • Give your email address and choose a password.
   • Choose a public name (you can make your public name the same as your account name).
   • Verification email will be sent to your email address. Click on the activation link, in the email, and login.

Running ExomeAI
To demonstrate the usage of ExomeAI, we generated a small simulated dataset with 2 tumor samples having AI aberrations on 2 out of the 3 simulated chromosomes (hg19; chromosomes 1 to 3) with a shared AI segment on chromosome 2. To run the sample:

1- Go to http://genomequebec.mcgill.ca/exomeai/history/list_published
2- Click on “Test_Dataset_AI_1” -> “Import history”
3- Click on “ExomeAI” -> “Detection of AI on multiple tumor samples” and set the following parameters:
   • FileType -> “2”
   • Input File1 -> “Sample1.BAF”
   • Input File2 -> “Sample2.BAF”
   • Click on Execute
4- ExomeAI will generate four output files:
   • Segments.txt: Segmentation results along with corresponding level of significance for each segment and all samples.
   • Recurrent.txt and Recurrent.pdf: Recurrent AI segments and visualization.
   • PerSamplePlots.tar.gz: BAF profiles for each sample.

For more details see:

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