EWAS GALAXY: A TOOLS SUITE FOR POPULATION EPIGENETICS INTEGRATED INTO GALAXY

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Background

Epigenome-wide association studies (EWAS) analyse genome-wide activity of epigenetic marks in cohorts of different individuals to find associations between epigenetic variation and phenotype. With its high accuracy and low input DNA requirements, the Illumina 450k Methylation Assay has become one of the most comprehensive EWAS study solutions. Unfortunately, analysis of the existing 450k data requires considerable programming knowledge and experience as well as high-performance computational hardware.

Implementation

A collection of tools has been developed for the Galaxy platform aimed at comprehensive, Galaxy is a web-based solution that provides a user-friendly tools and workflows interface for scientists without programming experience. The tool suite includes methods for preprocessing, normalization, quality assessment and differentially methylated regions detection. All configuration files are publicly published on our GitHub repository, with scripts and dependencies settings available to download and install via Galaxy test toolshed (testtoolshed.g2.bx.psu.edu). Our suite was created and tested using a Planemo workspace, with a default configuration and shed tool setup available via Docker.

Conclusion

Discovery of epigenetic aberrations that involve DNA modifications allow researchers to identify novel non-genetic factors responsible for complex human phenotypes such as height, weight, and disease. To identify such methylation changes, researchers must perform complicated and time-consuming computational analysis.

Here, we propose a solution via utilization of the EWAS suite. This can provide in one complex set of tools (developed and published under the Galaxy platform) for data pre-processing and quality evaluation for the detection of differentially methylated Cpg sites in diseases including Melanoma.

REFERENCES