VizFaDa: Interactive visualizations of FAANG data

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The FAANG (*Functional Annotation of Animal Genomes*) international consortium aims to produce high-quality functional annotation of the genomes of domesticated animals [1]. Members of the community can submit their epigenomics, transcriptomics or genomics data to the FAANG Data Portal (https://data.faang.org) coordinated by a Data Coordination Centre at the EMBL-EBI [2]. The Data Portal allows users to find, select and download datasets relevant to their research using extensive sample and experimental metadata standards. VizFaDa aims to produce interactive data visualization through web applications intended to be integrated to the FAANG Data Portal, focusing on RNA-seq, ChIP-seq, ATAC-seq, and DNA methylation data. The raw data from the portal has to be processed. Quality control reports are created, providing valuable and previously unavailable insight into the quality of the data. Interactive clustered correlation heatmap are generated, allowing the user to compare experiments from each assay type within a species. Experiments with similar results are clustered together. The user can use FAANG metadata to annotate the heatmap or to filter experiments from the database. Stacked epigenetic profiles are created from gene expression and epigenetic data obtained either from the same sample or from two comparable samples, notatbly at transcription start sites. This allow the investigation of relationship between epigenetic marks and transcription levels. The web application will be open to all later this year. In future versions, additional functions will be added. Data submitted to the portal will be automatically processed and added to VizFaDa, ensuring the long-term relevance and accuracy of the project.

Acknowledgements

References

[1] The FAANG Consortium; Andersson, L.; Archibald, A. L.; Bottema, C. D.; Brauning, R.; Burgess, S. C.; Burt, D. W.; Casas, E.; Cheng, H. H.; Clarke, L.; et al. Coordinated International Action to Accelerate Genome-to-Phenome with FAANG, the Functional Annotation of Animal Genomes Project. *Genome Biology,* (16):57, 2015

[2] Harrison, P. W.; Fan, J.; Richardson, D.; Clarke, L.; Zerbino, D.; Cochrane, G.; Archibald, A. L.; Schmidt, C. J.; Flicek, P. FAANG, Establishing Metadata Standards, Validation and Best Practices for the Farmed and Companion Animal Community. *Animal Genetics,* (49):520–526, 2018