Animals, Samples and Assays Working Committee (ASA) Committee

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Plant and Animal Genome XXVII Conference – FAANG workshop – January 11th 2019 – San Diego (USA)

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ASA Committee

Main aim: to achieve and share standardized protocols for adequate sample collection, storage, processing, and respective assays as required for FAANG core assays.

By 10 Jan 2019: **157 Members**

Online meetings in 2018:

Date	Led by	# Participants	Topic
8 March	EG-INRA	25	Assays guidelines to achieve standards for DCC submissions/ ATAC-seq
6 June	HZ - UC Davis	33	Assays guidelines to achieve standards for DCC submissions/ ChIP-seq
27 November	EG - INRA	16	Assays guidelines to achieve standards for DCC submissions/ Hi-C

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ASA – Activities planned for 2019

The next online meetings (each 3-4 months; or on demand) will keep a main focus on data quality requirements of each specific assay. Additional items raised by the community will be included in agenda.

In pipeline:

Towards adoption and standardization of "3D" (Spatial Conformation of Chromatin) assays to capture targeted genomic regions of interest

Aim: to produce Hi-C interaction maps at high resolutions for many tissues and experimental conditions (by Capture Hi-C, PLAC-seq and possibly other approaches)

Hi-C: Foissac et al. 2018 bioRxiv. https://doi.org/10.1101/316091 *(submitted)*

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(i) Data deposition. Deposit data in public repositories, providing rich and detailed metadata
For imaging: primary images with appropriate metadata be stored and maintained until public repositories become available to the community.

(ii) Standards. Use standardized, benchmarked experimental protocols for sample preparation and analysis. If the approach involves establishing new strategies, accompany new data with a standard data set to allow comparison with previous work.

(iii) Homogenize. Reduce cellular heterogeneity by maximizing cell-type purity, reducing cell numbers studies and comparing cells in the same cell cycle stages. For single-cell studies, provide one replicate of bulk cells and sufficient numbers of single cells to allow merging of libraries to compare single-cell results with bulk population experiments.

(iv) Validate data orthogonally. For instance, Hi-C data may be validated by using DNA FISH or by other genomic approaches (…) Different super-resolution microscopy technologies should be compared to cross-validate a portion of the results of any given series of new experiments other methods (such as DamID, or by testing interactions of chromatin associated proteins with techniques such as FRET or BiFC. These validations can be used to set up or improve modeling approaches.

(v) Use open software.

(vi) Set with gold-standards. Standard samples could be agreed upon by the community so that groups adopting a new technique or developing novel methods can have a benchmark to validate and compare their new approaches.

(vii) Establish resources databases. The field would considerably profit from the establishment of resources where genomic and microscopy data can be deposited, which would encourage cross validation (…), encourage the use of machine learning or other emerging technologies to combine data from different sources to unveil novel mechanisms.

From: Marti-Renom et al. Challenges and guidelines toward 4D nucleome data and model standards *Nat Genet. 2018 Oct;50(10):1352-1358.*

Towards standardization of “3D” assays

First aim: to finalize the choice of a common cell line per species as common standard.

One important goal is to use cell lines already characterized by core assays available in DCC

✓**Chicken**: as a possible option :
SL-29 (ATCC® CRL-1590™; fibroblast morphology, from embryo at 11 days gestation)

✓ **Pig:** ?

Whoever is interested to join these and other ASA activities, please write to us:

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ASA Community: faang-sample@animalgenome.org

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