

SAMGD 2015: posters

Room	Id	Name	Title
001	1	Anastasia Yartseva	Use of multivariate predictive modelling to explain Tacrolimus pharmacokinetics inter-patients variability based on a high-throughput genetic screening approach
001	2	Virginie Stanislas	Searching gene-gene interactions in GWAS using a Group Lasso approach
001	3	Safa Aouinti	IMGT/HighV-QUEST and IMGT Clonotype (AA): Identification and Statistical Significance Diversity per Gene for NGS Immunoprofiles of Immunoglobulins and T Cell Receptors
001	4	Jacob Antonsson	Model selection for Genome Wide Association Studies
001	5	Benjamin Sadacca	New insights for drug sensitivity prediction from cancer cell lines data.
001	6	Perrine Soret	High-dimensional longitudinal genomic data : a survey and evaluation of publicly available implementations of machine learning methods
001	7	Solène Julien	Expression of paralogous gene families in the human brain
001	8	Iryna Nikolayeva	Discovery of pairwise monotonic biomarkers for dengue severity
001	9	Margot Correa	Influence of transposable elements on the fate of duplicated genes in human
001	10	Magali Dancette Jaillard	Use of De Bruijn Graphs for Baterial GWAS
005	11	Félix Balazard	Haplotype based estimation of complex diseases.
005	12	Lilia Mesrob	From Exome to Whole Genome sequencing analysis
005	13	Virginie Mournetas	Back to the stemhood: a top-down approach identifying extracellular factors involved in stemness of human embryonic stem cells
005	14	Morgane Pierre-Jean	Change-point detection with kernel methods : Application on the DNA copy number segmentation in cancer studies.
005	15	Norbert Krautenbacher	Predicting from high-dimensional molecular data and environmental variables in stratified samples
005	16	Jean-Michel Bécu	Adaptive ridge regression for variable selection
005	17	Iryna Nikolayeva	Statistical and computational issues in subnetwork analysis of genome-scale data
005	18	Edith Le Floch	Searching for missing heritability using univariate and multivariate approaches on both genotyping and sequencing data.
005	19	Anne-Louise Leutenegger	Estimation of relationships and inbreeding from sequence data in presence of admixture