



LABORATORY OF

GENOMICS AND BIOINFORMATICS

Genomics, transcriptomics, bioinformatics, next-generation sequencing, single-cell approaches

Michal Kolář



In the picture: 1. Labala Rajendra Kumar | 2. Vučinić Kim | 3. Svatoňová Petra | 4. Pfeiferová Lucie | 5. Pačes Jan | 6. Večerková Kateřina | 7. Tichopád Tomáš | 8. Pačes Václav | 9. Hradilová Miluše | 10. Šachová Jana | 11. Ehler Edvard | 12. Kolář Michal | 13. Klianitskaya Marharyta | 14. Kozmik Zbyněk | 15. Krausová Martina | 16. Kocourková Šárka

Activity of our laboratory is based on advanced applications of genomics, transcriptomics and bioinformatics, the most vigorously developing disciplines of contemporary life sciences.

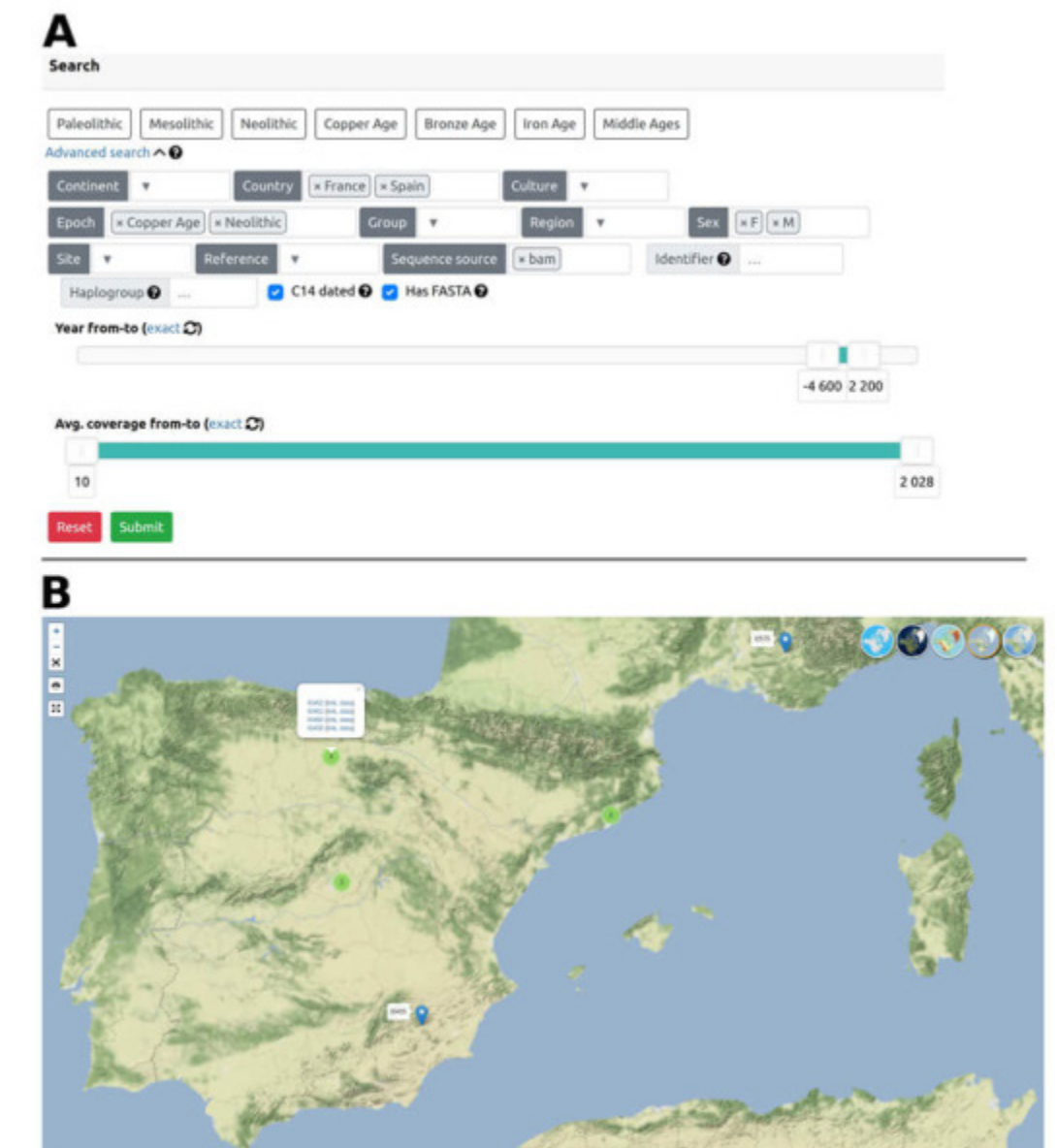
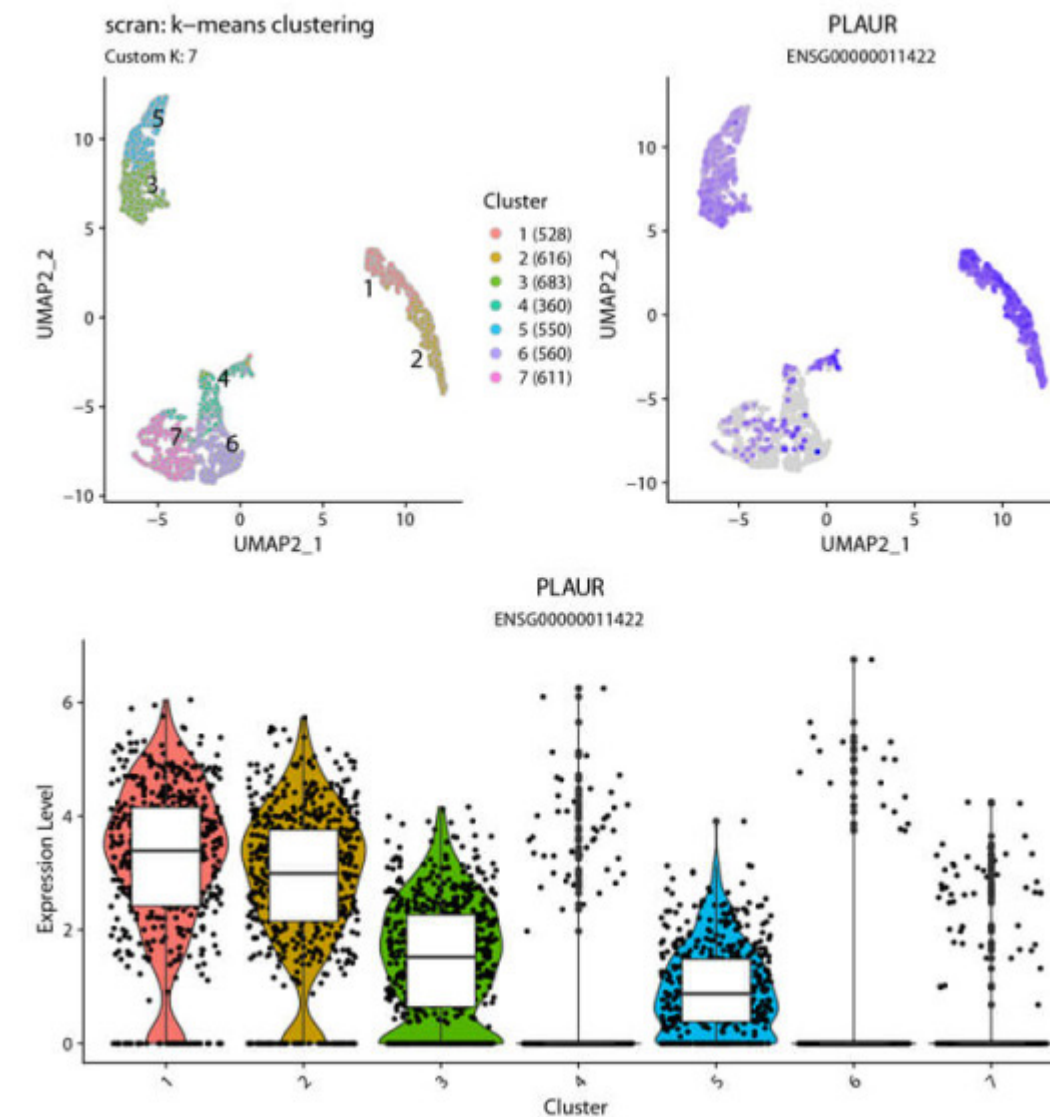
Genomics and bioinformatics: We are equipped with two Illumina sequencers [NextSeq 500 and 2000] and an Oxford Nanopore MinION platform. Since 2019, we have been using single cell transcriptomics and epigenomics technology (10x Genomics) and recently we have established spatially resolved transcriptomics workflow. As a part of our know-how, we develop sophisticated bioinformatical tools and pipelines to analyze produced data sets as well as those available in public databases.

Cancer transcriptomics: We have been involved in a long term-projects focused on head and neck squamous cell carcinoma and skin cancers. We focus on tumor microenvironment and on

interactions between cancer associated fibroblasts and malignant cells. We have collected a large data sets of patient samples (>100 patients) and cancer associated fibroblasts that serve as a basis for our studies.

Bioinformatic databases: The laboratory forms the local node of the Pan-European ELIXIR bioinformatics research infrastructure. We curate and maintain the **database** of mitochondrial sequences coming from the ancient DNA samples, AmtDB, and the database of human endogenous retroviruses, **HERVd**.

We use all these high-throughput and bioinformatic tools to conduct our own scientific projects, for long term collaborations with our colleagues and clinicians, and to support other scientific groups at the Institute. Indeed, an integral part of our laboratory is the Core Facility of Genomics and Bioinformatics.



Left: We created a simplified spheroid model of melanoma. In this model, melanoma cells interact with photodamaged fibroblasts. The cells clearly divide in different functional classes. Right: A screenshot from the web interface of the AmtDB database. The database is a key platform for ancient population genetic studies.

Selected publications:

1. Rasl J, Grušanović J, Klímová Z, Časlavský J, Groušl T, Novotný J, Kolář M, Vomastek T*: ERK2 signaling regulates cell-cell adhesion of epithelial cells and enhances growth factor-induced cell scattering. Cell Signal 2022 99: 110431.
2. Burkartová K, Dresler J, Ridl J*, Falteisek L*: Population Genomics of Microbial Biostalactites: Non-recombinogenic Genome Islands and Microdiversification by Transposons. Front Microbiol 2022 13: 828531.
3. Dupacova N, Antosova B, Pačes J, Kozmik Z*: Meis homeobox genes control progenitor competence in the retina. Proc Natl Acad Sci U S A 2021 118(12).
4. Strnadová K, Pfeiferová L, Příkryl P, Dvořánková B, Vlček E, Frýdlová J, Vokurka M, Novotný J, Šachová J, Hradilová M, Brábek J, Šmígová J, Rösel D, Smetana K, Kolář M*, Lacina L*: Exosomes produced by melanoma cells significantly influence the biological properties of normal and cancer-associated fibroblasts. Histochem Cell Biol 2021.
5. Novotný J, Strnadová K, Dvořánková B, Kocourková Š, Jakša R, Dundr P, Pačes V, Smetana K, Kolář M*, Lacina L*: Single-Cell RNA Sequencing Unravels Heterogeneity of the Stromal Niche in Cutaneous Melanoma Heterogeneous Spheroids. Cancers [Basel] 202012[11].