



GENIGMA: A CITIZEN SCIENCE PROJECT FOR CANCER GENOMES REFERENCE

Elisabetta Broglio, Alessandra Merlotti, Marc A. Martí-Renom, Juan Antonio Rodríguez and Marco Di Stefano





AUNCH IN NOVEMBER 2020 genigma.app

A smartphone game to identify, in a collective way, which fragments of cancer genomes may play a

Each player will analyze various small fragments of cancer cell DNA, that correspond to real data obtained in the lab from cancer cell lines.

Players will receive scientific updates and they will collect pills of knowledge (cards) on genomics, cancer and open science.





THE SCIENTIFIC MISSION

We aim to build cancerspecific genomic references, essential to advance cancer research and explore new medical treatments.

We also expect to train Artificial Intelligence to better identify patterns in cancer genome rearrangements.



CO-CREATIONS AND TESTS

>300 people including gamers, patients. medical doctors, teachers, artists, students and scientists from other disciplines have already collaborated between 2018-19 at different stages of the project.







Co-design and testing events

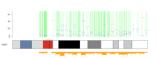
WHY CITIZEN SCIENCE?

- The human genome is big and each cancer is different. Participative research can be more effective in analyzing a sequence which can be up to 3 billion pieces in each cancer line.
- Human eyes perform much better than machines in identifying visual patterns. Currently, cancer genome rearrangements are determined using algorithms that still require manual refinement. Recruiting citizens will bring innovative ways to solve the complex problem.
- From the earliest stages citizen scientists have added a valuable new perspective to the project with their expertise. We'll invest a lot in communicate every achievement to expand the community.

We tested the game using non-cancer cell lines with known genome reference. Preliminary results show we have the strength to identify hotspots (green) for further analysis.

Players can identify central and terminal regions of the chromosomes, that contain repetitive elements where usually algorithms fail to provide a reliable genome reference.

DOES IT WORK?



Chromosome sequence analyzed