CNAG
Website

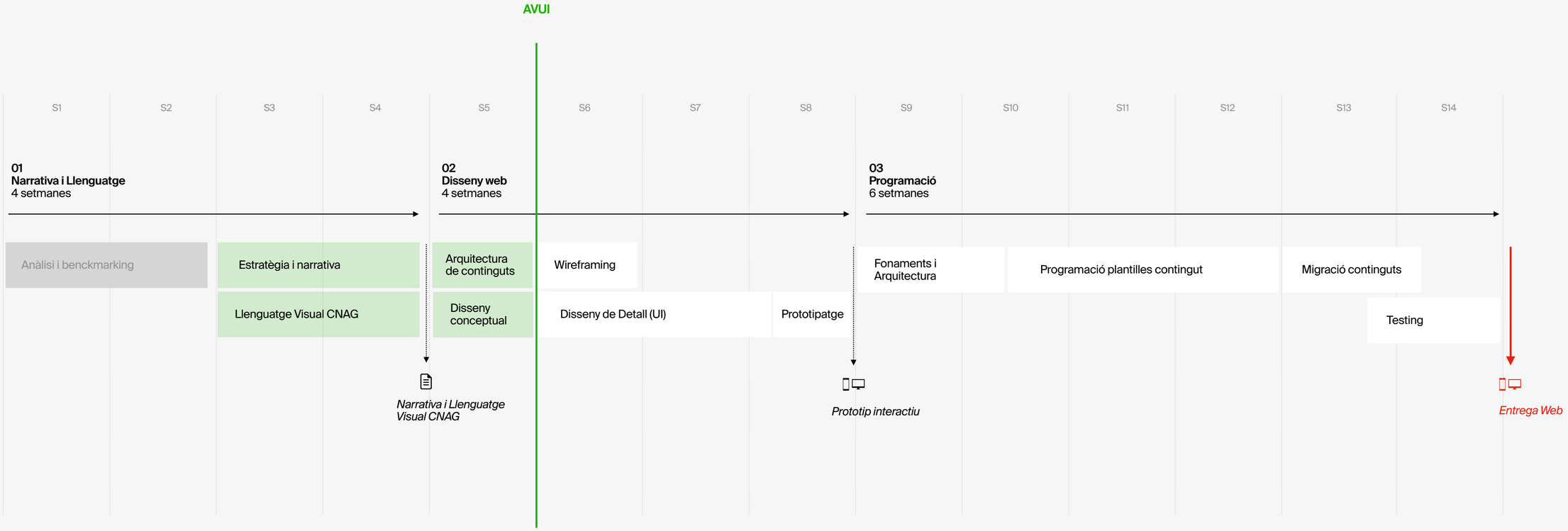
Exit.Design
Setembre 2026

Introducció

Objectius de la reunió

- Revisió del estatus del projecte
- Validar l'estructura i els continguts
- Validar proposta de disseny
- Acordar els següents passos

Estatus del projecte



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The Institution

CNAG Technology Platform
CNAG Research
CNAG International Projects

CNAG Core Value Proposition

Impact
Team
Start Your Project

Estructura web

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01. The Institution

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OVERVIEW

CNAG is one of Europe's leading genome analysis centres: a non-profit research organisation created in 2009 and based in Barcelona, sustained by the Spanish Ministry of Science, Innovation and Universities and the Government of Catalonia.

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VISION (TO BE DEVELOPED)

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MISSION

CNAG's mission is to provide the scientific, clinical and industrial community with a world-class genomics platform in permanent evolution; to pursue innovative research that expands what genomics can do; and to help build the genomics infrastructure network of the future.

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OUR APPROACH

This mission takes shape in three pillars: the platform, open to the scientific, clinical and industrial community; research, pushing the boundaries of genomics; and the infrastructure of the future, which CNAG builds alongside the leading international initiatives. The platform enables the other two; the three together make CNAG.

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LEADERSHIP & ORGANISATION

Director
Dr. Ivo G. Gut

General Manager
Lluís Solà

Organisation

CNAG combines two production units — Sequencing and Bioinformatics — with four Research Groups and four Research and Development Teams, supported by the Scientific & Operations and Corporate Management teams.

Corporate Management

- Finance
- People Management
- Corporate Information Systems
- Corporate Communication
- Legal
- Facility and Sustainability

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GOVERNANCE

Board of Trustees (Patronat)

President
Eva Ortega Paíno (Secretària General, MICIU)

Vice-President
Núria Montserrat Pulido (Generalitat de Catalunya)

Membres en representació del MICIU i de la Generalitat.

Executive Commission

President
Teresa Sanchis Estruch (Directora General de Recerca, MICIU)

Vice-President
José I. Doncel Morales (Sotsdirector, MICIU)

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HISTORY

Founded in 2009 to give Spain competitive, large-scale genome sequencing and analysis capacity, CNAG has grown into one of Europe's principal genomics infrastructures.

Pendent: timeline de 6–8 fites

Narrativa i continguts
02. CNAG Technology Platform

OVERVIEW

CNAG offers a leading-edge genome sequencing platform and a data platform for managing genomic information at massive scale — both in permanent renewal, always at the forefront.

Genomic technologies are the foundation of CNAG. By integrating advanced sequencing technologies with high-performance data processing, we generate, analyse and interpret genomic data at scale. Our technological infrastructure supports applications ranging from fundamental research and precision medicine to population genomics and biodiversity studies.

SEQUENCING PLATFORM

CNAG operates one of Europe's most advanced sequencing platforms, integrating short-read, long-read, single-cell and spatial genomics technologies.

The platform supports a wide range of genomic, transcriptomic, epigenomic and multi-omics applications.

Core Technologies

- **Short-read sequencing** — precision and volume for large-scale genomics
- **Long-read sequencing** — complete genomes and complex structural variation
- **Single-cell genomics** — biology read cell by cell
- **Spatial genomics & advanced imaging** — not just what happens in each cell, but where
- **Multi-omics** — genome, transcriptome, epigenome and proteome combined into one integrated view

With a sequencing capacity of up to 20,000 gigabases per day, equivalent to approximately 200 human whole genomes every 24 hours, CNAG can support high-throughput projects across precision medicine, population genomics, functional genomics and biodiversity research.

High-Throughput Short-Read Sequencing
Illumina platforms for large-scale genomic, transcriptomic and epigenomic studies.
- 2 × Illumina NovaSeq X Plus
- 1 × Illumina NovaSeq 6000
- 1 × Illumina MiSeq i100 Plus
- 1 × Illumina MiSeq

Long-Read Sequencing
Third-generation sequencing technologies for genome assembly, structural variant detection and complex genome analysis.
- 1 × PacBio Revio
- 3 × Oxford Nanopore PromethION
- 1 × Oxford Nanopore GridION

Single-Cell Genomics
High-throughput single-cell sequencing technologies.
- 1 × 10x Genomics Chromium X

Spatial Genomics & Advanced Imaging
Platforms for spatial transcriptomics and high-resolution tissue analysis.
- 1 × 10x Genomics Xenium
- 1 × Bruker NanoString CosMx
- 1 × Bruker Vutara 3D Super-Resolution Microscope

Sequencing Services

Biorepository
Sample Preparation
High-Throughput Sequencing
Long-Read Sequencing
Single-Cell Genomics
Spatial Genomics
Laboratory Support

DATA PROCESSING PLATFORM

CNAG's Data Processing Platform provides the computational infrastructure required to securely store, process and analyse large-scale genomic data.

By combining high-performance computing, large-capacity storage and advanced bioinformatics, the platform enables the analysis and interpretation of increasingly complex genomic datasets.

Core Infrastructure
- **High-performance computing**
- **Large-scale storage**
- **Bioinformatics**
- **AI-ready computing**

Core Capabilities
- **Genome analysis**
- **Variant detection**
- **Genome assembly**
- **Multi-omics integration**
- **AI-enabled computing**
- **Clinical interpretation**

CNAG operates a large-scale computational environment designed to support the processing, analysis and long-term storage of genomic data.

Current Capacity

- 10,000 computing cores
- 22 PB total storage capacity
- 14 PB high-performance disk storage
- 8 PB archival tape storage

Bioinformatic Services

Production Bioinformatics
Variant Calling & Analysis
Functional Genomics
Human Genetics
Data Processing & Management
GPAP Platform

PLATFORM EVOLUTION

Continuous investment in emerging technologies ensures that CNAG remains at the forefront of genomic research and provides the scientific community with access to increasingly advanced capabilities.

Planned Sequencing Technologies

- SBX (Roche) — next-generation sequencing platform introducing an innovative expanded-DNA sequencing approach for fast, highly accurate and scalable sequencing.
- BD Rhapsody HT Xpress — high-throughput single-cell genomics platform.
- Pyxa (Stellaromics) — 3D spatial multiomics platform for high-resolution tissue analysis.

Planned Data Processing Infrastructure

- New 8 PB archival storage system, combining object storage and an LTO-9 tape archive
- Expanded capacity for large-scale sequencing and genomic analysis

SAMPLE REQUIREMENTS

To ensure high-quality results, samples submitted to CNAG must meet specific quality and preparation standards, which vary depending on the sequencing technology used.

General Sample Requirements (link)
Sample Req. for PacBio HiFi Sequencing (link)
Sample Req. for Oxford Nanopore Sequencing DNA (link)
Sample Req. for Oxford Nanopore Sequencing RNA (link)

The Biorepository team works closely with collaborators to determine extraction procedures, verify sample quality upon arrival, and coordinate shipment.

INSTRUMENT CATALOGUE

Short-Read Sequencing

- Illumina NovaSeq X Plus — Generates up to 16–21 terabases per run—more than 128 human genomes—with onboard analysis that reduces cost and turnaround time. https://www.illumina.com/content/dam/illumina/gcs/assembled-assets/marketing-literature/novaseq-x-series-spec-sheet-m-us-00197/novaseq-x-series-specification-sheet-m-us-00197.pdf
- Illumina NovaSeq 6000 — Flexible flow-cell configurations deliver from 80 gigabases to 6 terabases per run. https://www.illumina.com/content/dam/illumina/gcs/assembled-assets/marketing-literature/novaseq-6000-spec-sheet-m-gl-00271/novaseq-6000-spec-sheet-m-gl-00271.pdf
- Illumina MiSeq i100 Plus — Delivers same-day results for targeted applications, with run times as fast as four hours. https://www.illumina.com/content/dam/illumina/gcs/assembled-assets/marketing-literature/miseq-i100-specification-sheet-m-gl-02244/miseq-i100-specification-sheet-m-gl-02244.pdf
- Illumina MiSeq — Integrates cluster generation, sequencing and data analysis in a single instrument, going from DNA to results in about eight hours. https://www.illumina.com/content/dam/illumina/gcs/assembled-assets/marketing-literature/miseq-system-data-sheet-m-gl-00006/miseq-data-sheet-m-gl-00006.pdf

Long-Read Sequencing

- Oxford Nanopore PromethION — Multiple independent flow cells generate terabases of long-read DNA and RNA data in real time. · https://nanoporetech.com/resource-centre/minion-and-gridion-brochure
- Oxford Nanopore GridION — Runs up to five independent flow cells, with integrated computing for real-time data analysis. https://nanoporetech.com/resource-centre/promethion-brochure
- PacBio Revio — Delivers highly accurate HiFi reads with methylation detection in every run, providing genomic and epigenetic information simultaneously. https://www.pacb.com/wp-content/uploads/Revio-specification-sheet.pdf

Single-Cell Genomics

- 10x Genomics Chromium X — Partitions from hundreds to a million cells in a single-day workflow and supports the full portfolio of Chromium single-cell assays. https://cdn.10xgenomics.com/image/upload/v1725314283/support-documents/CG000415_ChromiumX-Specifications_Rev_E.pdf
- Mission Bio Tapestri — Reads genotype and immunophenotype from the same cell across thousands of cells. https://www.missionbio.com/products/platform
- MACS Cell Separator (Miltenyi Biotec) — Cell enrichment ahead of single-cell workflows. (Pendent)

Spatial Genomics and Imaging

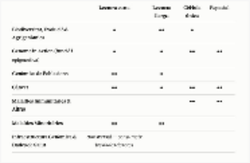
- 10x Genomics Xenium — Maps up to 5,000 genes, alongside proteins, at subcellular resolution directly within tissue. https://www.10xgenomics.com/platforms/xenium
- 10x Genomics Visium — Provides unbiased, whole-transcriptome spatial gene-expression analysis in frozen and fixed tissue sections. https://www.10xgenomics.com/platforms/visium
- Bruker NanoString CosMx — Detects more than 19,000 RNAs and 72 proteins in the same tissue section at cellular and subcellular resolution. https://nanostring.com/resources/cosmx-smi-brochure/
- Bruker Vutara 3D Super-Resolution Microscope — Uses bi-plane detection to image cellular structures in 3D at nanometre-scale resolution and depths of up to 100 µm. https://www.bruker.com/en/products-and-solutions/fluorescence-microscopy/super-resolution-microscopes/vutara-vxl.html
- BGI Stereo-seq — Provides subcellular detail across tissue sections of up to 13 × 13 cm, enabling whole-organ mapping. https://www.completegenomics.com/stereo-seq-technology/

Narrativa i continguts
03. CNAG Research (1/2)

OVERVIEW

CNAG conducts research across the genomic discovery-to-healthcare continuum — from fundamental biology to the genomic basis of disease and its translation into clinical practice.

Our Research Groups and Teams combine genomic technologies, computational methods and biological expertise to turn genomic knowledge into solutions for research, healthcare and biodiversity conservation.



RESEARCH GROUPS AND TEAMS

Research Groups lead broad scientific programmes, while Research and Development Teams provide specialised technological and analytical expertise across specific areas of genomics.

Research Groups
- Biomedical Genomics
- Structural Genomics
- Single-Cell Genomics
- Comparative Genomics

Research and Development Teams
- Genome Assembly and Annotation
- Bioinformatics Dev. and Statistical Genomics
- Functional Genomics
- Spatial Genomics

RESEARCH GROUPS

BIOMEDICAL GENOMICS GROUP

Overview
The Biomedical Genomics Group investigates how genomic variation contributes to human disease and how genomic information can be translated into better prevention, diagnosis and treatment.

Group Leader
Dr. Ivo Gut

Research Focus
- Cancer Genomics
- Genomic Analysis Tools and Data Infrastructures
- Personalised and Genomic Medicine

Selected Projects and Initiatives
- B1MGPlus / 1+ Million Genomes Initiative — interoperable frameworks for secure access to genomic, clinical and phenotypic data across Europe.
- BCLL@las — chronic lymphocytic leukaemia through advanced genomic and immune-cell analysis.
- IMPaCT Genomics — implementation of genomic medicine within the Spanish National Health System.

Selected Publications
- Pheno-Ranker: a toolkit for comparison of phenotypic data stored in GA4GH standards and beyond — BMC Bioinformatics, 2024.
- Multi-organ single-cell transcriptomics of immune cells — Scientific Data, 2024.
- Benchmarking single-cell RNA-sequencing protocols for cell atlas projects — Nature Biotechnology, 2020.

Team Members.
- Ivo G. Gut (Group Leader)
- Gabriela Aguileta (Bioinformatician)
- Ivo Leist (PhD Student)
- Claudia Buhigas Novoa (Postdoc)
- Dietmar Fernández (Postdoc)
- Manuel Rueda (Bioinformatician)
- Miranda Stobbe (Postdoctoral Fellow)

Contact (pendent)

STRUCTURAL GENOMICS GROUP

Overview
The Structural Genomics Group studies the three-dimensional organisation of the genome and its role in gene regulation, from chromosome conformation to super-resolution imaging.

Group Leader
Dr. Marc A. Marti-Renom

Research Focus
- 3D Genome Architecture and Gene Regulation
- Computational Modelling Tools
- Genome Visualisation by Super-Resolution Microscopy (OligoSTORM, OligoFISSEQ)

Selected Projects and Initiatives
- 3D'omics (Horizon 2020) — population variability of the 3D genome in livestock.
- HoloGen — spatial visualisation of the microbiome in complex tissues, including tumours.
- CEGS-CGI (NIH) — centre-scale programme on genome structure and function.

Publications
- Three-dimensional genome architecture persists in a 52,000-year-old woolly mammoth skin sample — Cell, 2024
- LATS1 controls CTCF chromatin occupancy and hormonal response of 3D-grown breast cancer cells — EMBO Journal, 2024
- Enhancer-driven 3D chromatin domain folding modulates transcription in human mammary tumor cells — Life Science Alliance, 2024

Members
- Marc A. Martí-Renom (Group Leader)
- Alexander Barclay (PhD Student)
- Iana Kim (Postdoctoral Fellow)
- María Martí (Postdoctoral Fellow)
- Meritxell Novillo (Postdoctoral Researcher)
- Leo Zuber (PhD Student)
- Anastasiia Nikitina (Postdoctoral Researcher)
- Zoe Horisberger (PhD Student)
- Mireia Novell (Lab Technician)
- John Markham (Specialised Technician)
- Ana Nikolovsca (PhD Student)

Contact (pendent)

SINGLE-CELL GENOMICS GROUP

Overview
The Single-Cell Genomics Group develops and applies single-cell and spatial genomics technologies to study cellular heterogeneity in health and disease, with an emphasis on cancer, immunology and autoimmune conditions.

Group Leader
Dr. Holger Heyn

Research Focus
- Single-Cell and Spatial Technology Development
- Tumour Microenvironment and Immuno-Oncology
- Autoimmune and Cardiovascular Disease

Selected Projects and Initiatives
- Human Cell Atlas (CZI) — coordinating a working group on technologies and computational frameworks for the atlas.
- ERC Synergy BCLL@las — B-cell lineage, premalignant transformation and tumour subclonality in CLL.
- LIMECOP — paired spatial transcriptomics of colorectal tumours and liver metastases (VHIO, AstraZeneca, KU Leuven, BMS).

Publications
- An atlas of cells in the human tonsil — Immunity, 2024
- Adaptation in human immune cells residing in tissues at the frontline of infections — Nature Communications, 2024
- FixNCut: single-cell genomics through reversible tissue fixation and dissociation — Genome Biology, 2024

Members
- Holger Heyn (Group Leader)
- Giulia Lunazzi (Project Manager)
- Ginevra Caratù (Single Cell Laboratory Team Manager)
- Elena Domènech (Lab Manager)
- Patricia Lordén (Lab Technician)
- Davide Maspero (Postdoctoral Fellow)
- Juan Nieto (Postdoctoral Fellow)
- Paula Nieto (PhD Student)
- Sam Morabito (Postdoctoral Computational Biologist)
- Max Ruiz (Lab Technician)
- Miren Berasategui (Lab Technician)
- Pedro Rocha (Visiting Medical Researcher)
- Gerard Deuner (Data Analyst)
- Emanuele Pitino (PhD Student)
- Ivo Borkus (Data Analyst)
- Nerea Martín (Laboratory Technician)
- Francesco Craighero (Senior Computational Biologist)

Contact (pendent)

COMPARATIVE GENOMICS GROUP

Overview
The Comparative Genomics Group studies how genomes vary and evolve across species and populations, connecting evolutionary insight with biodiversity and human genomics.

Group Leader
Dr. Tomàs Marquès

Research Focus
- Genome Evolution
- Population and Comparative Genomics
- Biodiversity Genomics

Selected Projects and Initiatives (pendent)
- ApeGenomeDiversity (ERC Consolidator Grant) — ancestral diversity of great apes from the fossil record and extant genomes.
- Global catalog of primate genome diversity — genome sequencing of 233 primate species, with Illumina and Baylor College of Medicine.
- Barcelona Zoo Cryozoo — biobank of cell lines from endangered species, with UPF, EMBL and the Museu Nacional de Ciències Naturals.

Publications
- Enamel proteins reveal biological sex and genetic variability in southern African Paranthropus — Science, 2025
- Local genetic adaptation to habitat in wild chimpanzees — Science, 2025
- Identification of constrained sequence elements across 239 primate genomes — Nature, 2024

Members
- Tomàs Marquès (Group Leader)
- Esther Lizano (Senior Researcher)
- Javier Prado (Post-Doctoral Researcher)
- Sebastian Hans Cuadros (Post-Doctoral Researcher)
- Lucas Esteban Wange (Post-Doctoral Researcher)
- Alba Duch (Project Manager)
- Lídia Altimiras (Laboratory Manager)
- Johanna Krueger (PhD Student)
- Cira Martínez (Coordinator of Criozoo)
- Irune Ruiz (PhD Student)
- Mar Crego (PhD Student)
- Harvinder Kaur Pawar (PhD Student)
- Núria Hermosilla (PhD Student)
- Maria Torralvo (PhD Student)
- Guillermo Carrillo (PhD Student)
- Sandra Ruibal (Laboratory Technician)
- Pol Alentorn (Laboratory Technician)
- Sandra Martín (Laboratory Technician)
- Albert Bañeras (Laboratory Technician)

Contact (pendent)

Narrativa i continguts
03. CNAG Research (2/2)

RESEARCH AND DEVELOPMENT TEAMS

GENOME ASSEMBLY & ANNOTATION TEAM

Overview
The Genome Assembly and Annotation Team produces chromosome-level reference genomes — the "books of life" of each species — supporting biodiversity research and conservation worldwide.

Group Leader
Dr. Tyler Alioto

Research Focus
- Chromosome-Level Genome Assembly
- Genome Annotation
- Biodiversity Gen. and Assembly Benchmarking

Selected Projects and Initiatives
- Earth BioGenome Project — 47 new reference genomes produced at CNAG in 2025.
- European Reference Genome Atlas (ERGA) — 24 European species assembled in 2025.
- Catalan Initiative for the Earth BioGenome Project (CBP) — reference genomes for Catalan biodiversity.

Publications
- The European Reference Genome Atlas: piloting a decentralised approach to equitable biodiversity genomics — npj Biodiversity, 2024
- The Catalan initiative for the Earth BioGenome Project — NAR Genomics and Bioinformatics, 2024
- Chromosome-Level Genome Assembly and Annotation of Corallium rubrum — Genome Biology and Evolution, 2025

Members
- Tyler Alioto (Team Leader)
- Francisco Camara (Bioinformatics Technician)
- Fernando Cruz (Data Analyst)
- Jèssica Gómez (Bioinformatics Technician)

Contact (pendent)

BIOINFORMATICS DEVELOPMENT AND STATISTICAL GENOMICS TEAM

Overview
The Bioinformatics Development and Statistical Genomics Team builds the pipelines and analytical platforms that extract the maximum information from large-scale genomic, transcriptomic and epigenomic datasets.

Group Leader
Dr. Simon Heath

Research Focus
- Statistical Genomics and Analysis Pipelines
- DNA Methylation and Epigenomic Analysis Methods
- Computational Efficiency and Pangenome References

Selected Projects and Initiatives
- LUCIA — low-coverage nanopore sequencing of 2,500 samples for population genomic and methylation variation.
- Methylation analysis toolkit — open-source methods for differential (modiff) and allele-specific (asms)methylation.
- Pangenome evaluation — adopting pangenome references in CNAG's genomic analyses.

Publications
- Fluctuating DNA methylation tracks cancer evolution at clinical scale — Nature, 2025 (destacada per la mateixa CNAG com a notícia pròpia)
- cvlr: finding heterogeneously methylated genomic regions using ONT reads — Bioinformatics Advances, 2023

Members
- Simon Heath (Team Leader)
- Emanuele Raineri (Staff Scientist)

Contact (pendent)

FUNCTIONAL GENOMICS TEAM

Overview
The Functional Genomics Team applies transcriptomics and epigenomics to the diagnosis of rare diseases and familial cancer, and to understanding the role of transposable elements in neurodegenerative disease.

Group Leader
Dr. Anna Esteve-Codina

Research Focus
- Transcriptomics for Rare-Disease and Cancer Diagnostics
- Epigenomics and Long-Read Methylation Analysis
- Transposable Elements in Neurodegeneration (HERVarium)

Selected Projects and Initiatives
- ERDERA — co-leading the RNA-seq working group of the European Rare Diseases Research Alliance.
- IMPaCT Genomics — national RNA-seq working group detecting RNA outliers in undiagnosed patients.
- SEED-ALS — coordinating the WGS core of the national ALS monitoring project (14 regions).

Publications
- High content of nuclei-free low-quality cells in reference single-cell atlases: a call for more stringent quality control using nuclear fraction — BMC Genomics, 2024 (aquesta és exactament la que la Memòria anomenava "highlight 2024")
- Phenotype-driven genomics enhance diagnosis in children with unresolved neuromuscular diseases — European Journal of Human Genetics, 2024
- Unraveling undiagnosed rare disease cases by HiFi long-read genome sequencing — Genome Research, 2025

Members
- Anna Esteve (Team Leader)
- Marc Dabad (Bioinformatics Technician)
- Eloi Casals (Software Engineer)
- Beatriz Martín (Bioinformatics Technician)
- Tomàs Montserrat (PhD Student)
- Matteo Orlandi (Bioinformatics Technician)

Contact (pendent)

SPATIAL GENOMICS TEAM

Overview
The Spatial Genomics Team develops spatial transcriptomics platforms as digital pathology tools, generating single-cell-resolution maps of tissues to identify diagnostic and therapeutic biomarkers.

Group Leader
Dr. Anna Pascual-Reguant

Research Focus
- Spatial Transcriptomics Platforms (Sequencing- and Imaging-Based)
- Digital Pathology
- Computational Tools for Spatial Data Analysis

Selected Projects and Initiatives
- Dynamite — predictive biomarkers for immune-checkpoint therapy in colorectal cancer via spatial TCR sequencing.
- LIMECOP — paired spatial transcriptomics of colorectal tumours and metastases (VHIO, AstraZeneca).
- COLORSCAPE — spatial transcriptomics of colorectal cancer (KU Leuven, BMS).

Publications
- An atlas of cells in the human tonsil — Immunity, 2024
- Harnessing STING Signaling and Natural Killer Cells Overcomes PARP Inhibitor Resistance in Homologous Recombination-Deficient Breast Cancer — Cancer Research, 2025
- Spatial transcriptomics and in situ immune cell profiling of the host ectocervical landscape of HIV infected Kenyan sex working women — Frontiers in Immunology, 2024

Members
- Anna Pascual (Spatial Genomics Team Leader)
- Helena Crowell (Postdoctoral Fellow)
- Irene Ruano (Specialised Technician)
- Ines Parreira (PhD Student)
- Jessica Chevallier (Postdoctoral Researcher)

Contact (pendent)

Narrativa i continguts
04. CNAG International Projects

OVERVIEW

CNAG contributes to international research and infrastructure projects through advanced sequencing, bioinformatics
and genomic data analysis.

INTERNATIONAL RESEARCH PROJECTS

Collaborative projects that generate new scientific knowledge and advance genomic research, biomedical innovation and precision medicine. CNAG currently participates in twelve active research projects, spanning cancer, rare diseases, immunology, population genomics and biodiversity.

Cancer

- **BCLL@las** — single-cell genomics to understand the development and transformation of B cells into chronic lymphocytic leukaemia.
- **LUCIA** — research into the genetic, environmental and lifestyle factors associated with lung cancer.
- **CATALYST** — study of the evolution of the immune microenvironment in metastatic colorectal cancer.

Rare Diseases

- **BRIDGING-RD** — bridging the research and innovation gap for rare diseases.
- **HEREDITARY ATAXIA** — investigating hereditary ataxias in underrepresented West African populations.
- **SCREEN4CARE** — newborn genetic screening and digital approaches to accelerate rare disease diagnosis.

Immunology and Other Conditions

- **3TR** — taxonomy, treatment, targets and remission in autoimmune, inflammatory and allergic disease.
- **SIGNATURE** — single cells in autoimmune inflammatory diseases.

Population Genomics

- **Genome of Europe (GoE)** — a European reference resource representing the genomic diversity of populations across Europe.

Biodiversity and Evolutionary Genomics

- **Biodiversity Genomics Europe (BGE)** — genomic data and technologies to improve biodiversity research, monitoring and conservation across Europe.
- **3D'omics** — three-dimensional host–microbiota interactions and their influence on animal health and production.
- **Mut-Scales** — the factors that determine mutation rates across cellular and evolutionary scales.

INTERNATIONAL INFRASTRUCTURE PROJECTS

Projects focused on building the shared infrastructures, platforms, standards and systems on which genomic research and data access depend. Through them, CNAG helps build the genomics infrastructure network of the future.

- **GDI — Genomic Data Infrastructure** — a federated European infrastructure for the secure access, discovery and reuse of genomic, clinical and phenotypic data. (featured)
- **EASIGEN-DS** — a design study for a future European infrastructure dedicated to advanced genomic technologies, coordinated by CNAG. (featured)
- **B1MGplus — Beyond 1 Million Genomes Plus** — building on the 1+ Million Genomes initiative to strengthen cross-border access to genomic data. (featured)
- **ERDERA — European Rare Diseases Research Alliance** — the European partnership aligning rare-disease research across more than 170 organisations in 37 countries.
- **CGI-Clinics —** data-driven cancer genome interpretation for personalised cancer treatment.
- **CEGS-CGI —** Center for Genome Imaging — NIH centre-scale programme on genome imaging.

PROJECT PAGES (EXAMPLES)

LUCIA

One-line definition
Lung Cancer-related Risk Factors and Their Impact Assessment

Overview
LUCIA is a Horizon Europe project that seeks to improve understanding of the factors contributing to lung cancer. It brings together clinical, biological, environmental and technological expertise to develop a toolbox for identifying new risk factors and assessing their impact on lung cancer development.

Key Information
- Programme: Horizon Europe
- Duration: January 2023 – December 2026
- Coordinator: Technion – Israel Institute of Technology
- Consortium: 20 partners from nine countries

Official website
https://luciaeuproject.technion.ac.il/

BCLL@las

One-line definition
B-cell Chronic Lymphocytic Leukaemia Atlas — resolving the genomic and epigenomic hallmarks of chronic lymphocytic leukaemia at single-cell resolution.

Overview
BCLL@las is an ERC Synergy project that maps the cellular diversity of chronic lymphocytic leukaemia, from the development of healthy B cells to their transformation into leukaemia. By reading the disease cell by cell, the project aims to better predict its progression and response to treatment.

Key Information
- Programme: ERC Synergy Grant (€8.3 million)
- PIs: Ivo Gut and Holger Heyn (CNAG), Elías Campo and Iñaki Martín-Subero (IDIBAPS)
- Duration: (pendent)

Official website
(pendent de confirmar)

EASIGEN-DS

One-line definition
Design Study for a European Infrastructure on Advanced Genomics Technologies.

Overview
EASIGEN-DS lays the groundwork for a new distributed European research infrastructure uniting the continent's leading genomics facilities. Following the ESFRI lifecycle, it designs a Technology Platform — single-cell, spatial, long-read and population-scale genomics — and a Support Platform for standardisation and training, addressing the fragmentation of Europe's sequencing capacity.

Key Information
- Programme: Horizon Europe
- Duration: 2025 – January 2028
- Coordinator: CNAG
- Consortium: leading European genomics facilities and expert partners

Official website
https://easigen.eu/

GDI — Genomic Data Infrastructure

One-line definition
A federated European infrastructure for the secure access, discovery and reuse of genomic, clinical and phenotypic data.

Overview
GDI builds the data infrastructure of the 1+ Million Genomes initiative: a federated network connecting national genomic data collections, so that clinicians, researchers and innovators can discover and analyse genomic and associated clinical data securely across borders.

Key Information
Programme: Digital Europe Programme, co-funded by Member States
Duration: November 2022– October 2026
Coordinator: ELIXIR
Consortium: 70 institutes from 24 European countries

Official website
https://gdi.onemilliongenomes.eu/

Purpose / Claim

Opció 1

Unlocking the full potential of genomics and transform healthcare worldwide

Opció 2

Reading the code of life to unlock the future it holds

Manifesto

The genome is the language of life

To sequence it is to read it
— a first step toward discovering the future it holds.

We don’t do this alone.
We are a platform open to the scientific, clinical and industrial community — instruments at the frontier, data at scale, knowledge held in common.

Our strength isn’t having every answer: it’s building the place where answers can be found.

Disseny web

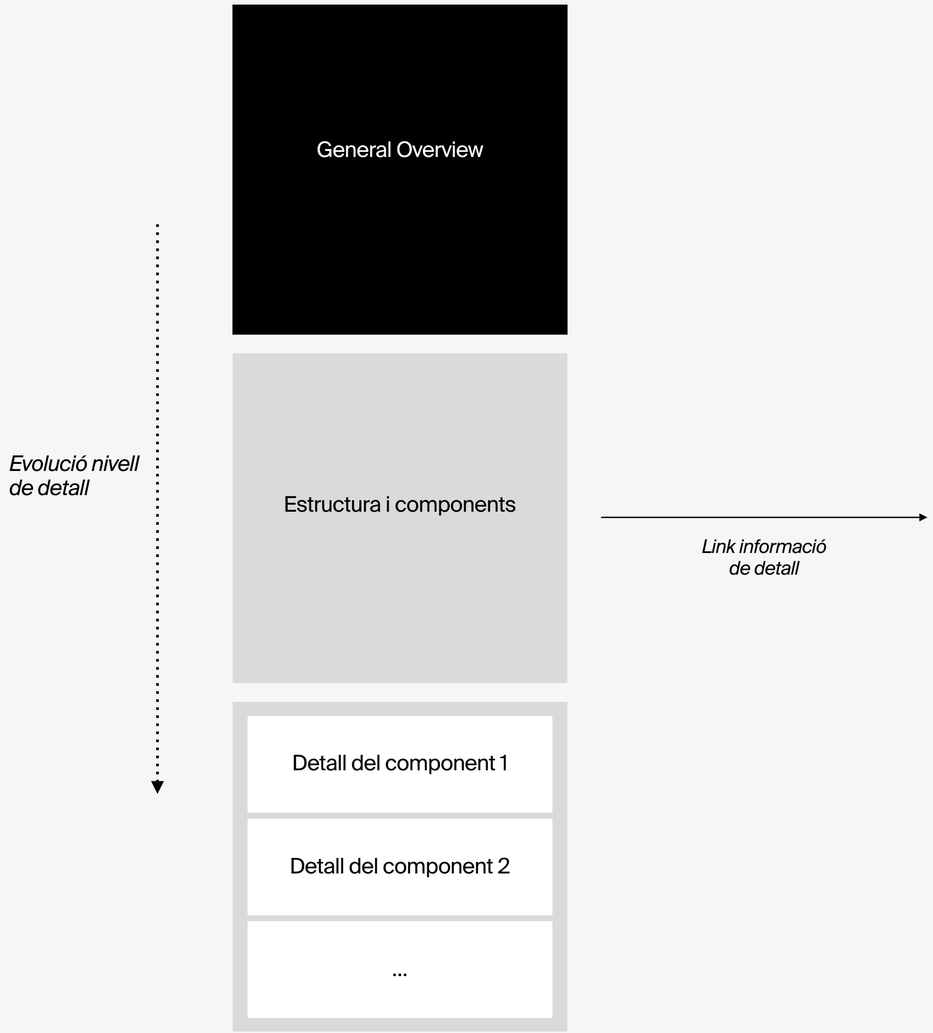
Criteris de disseny

- Claredat i simplificació gràfica
- Densitat progressiva / Overview → Informació de detall
- Llenguatge visual contemporani
- Mobile-first

Densitat progressiva

La informació es presenta per capes: primer l'essencial, després el detall, a mesura que l'usuari vulgui aprofundir.

- Permet lectura ràpida i i lectura detallada
- Apte per diferents audiències



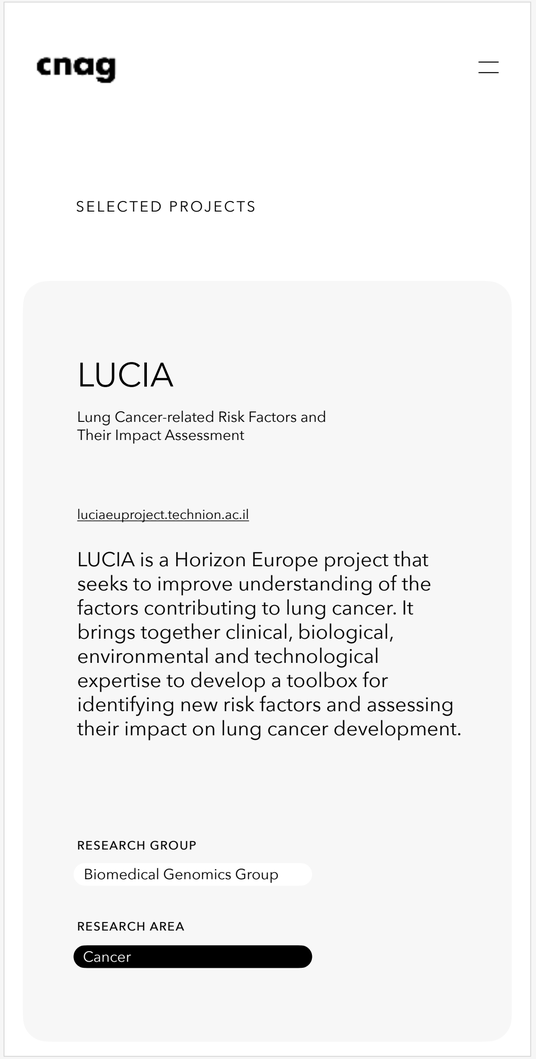
Cada contingut viu en un sol lloc.

Si ha d'aparèixer en un segon lloc, el segon lloc és un enllaç, mai una còpia.

Exemple:
Pàgina de projecte
Publicacions
...

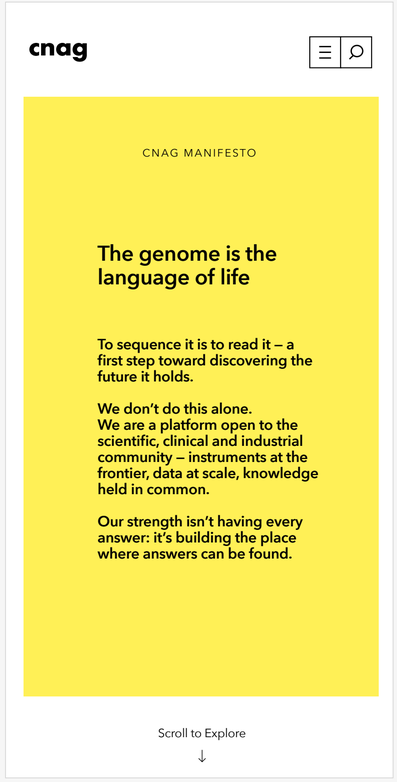
Convivència de dos llenguatges visuals complementaris:

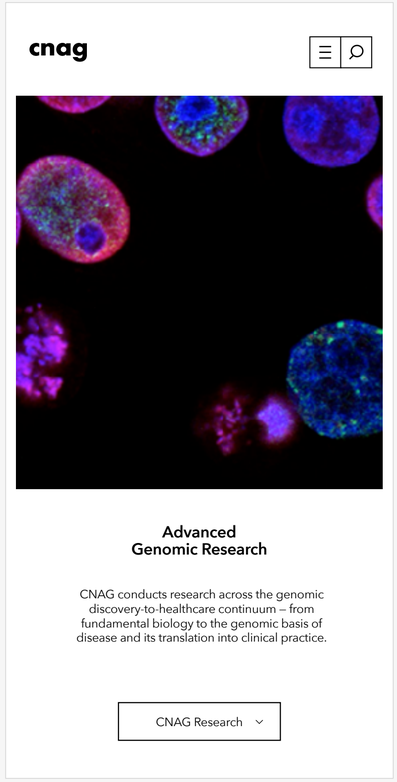
1. Llenguatge molt visual i d'impacte
2. Llenguatge tècnic i de detall

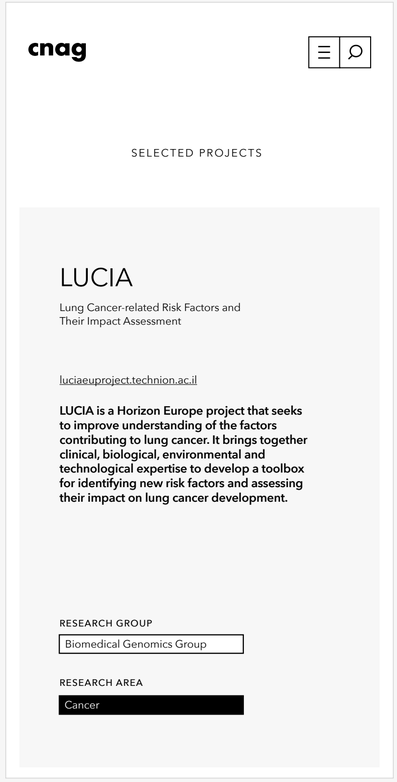


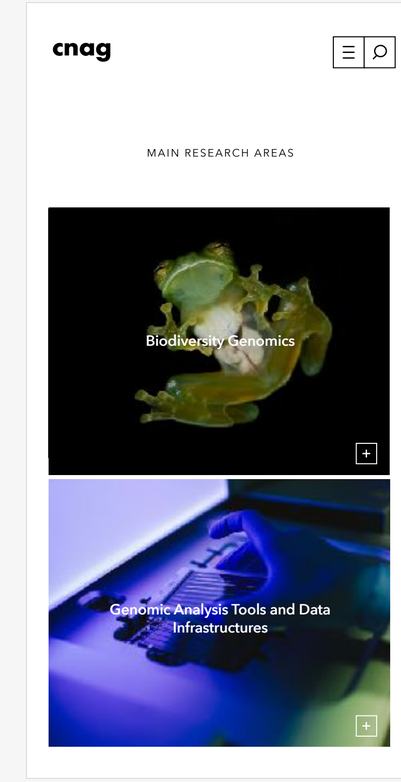
Variant 1
Basada en la proposta presentada en la fase anterior

- Ús del color
- Geometria rectilínia (botons, imatges...)
- Tipografia bold









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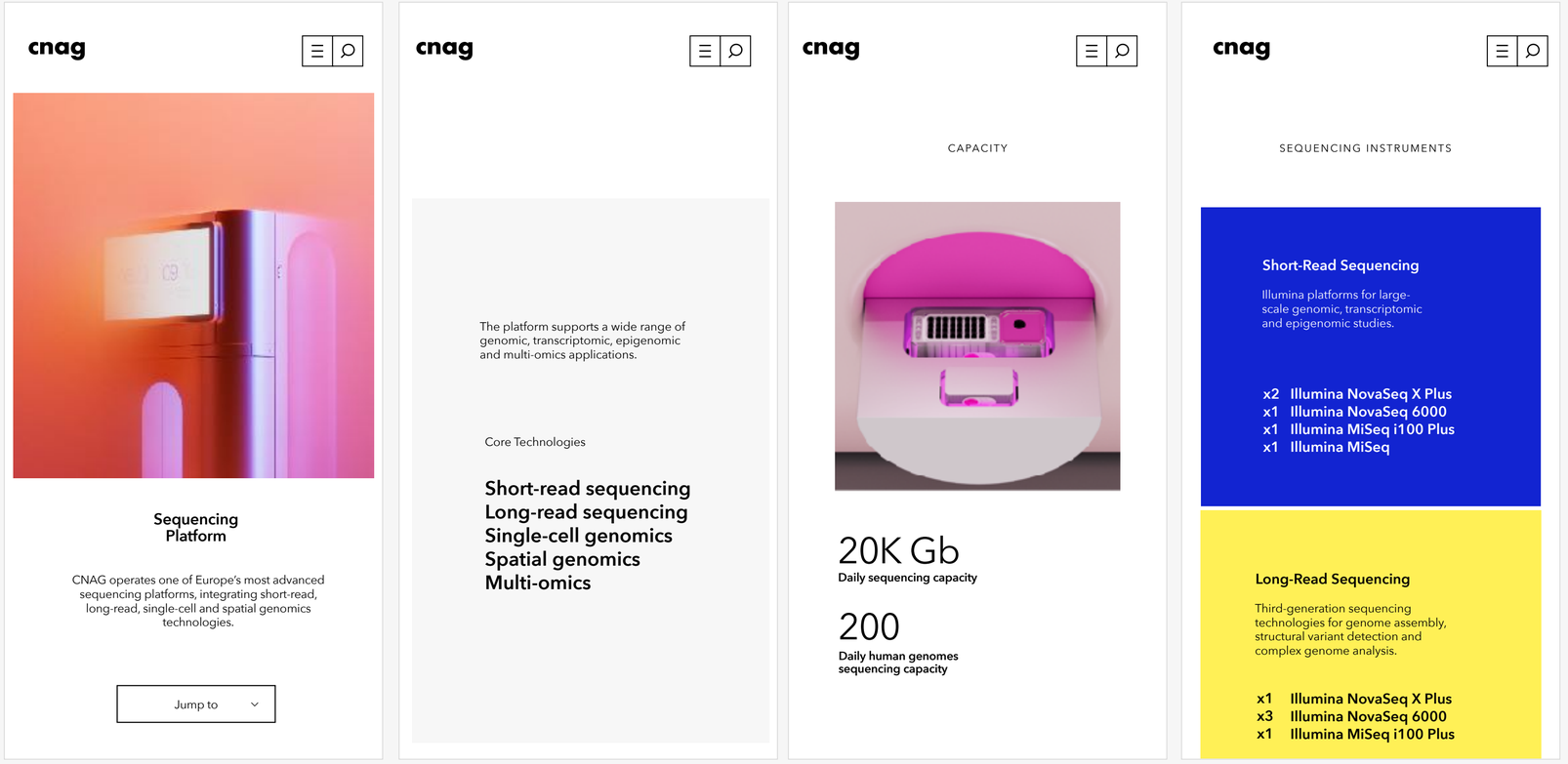
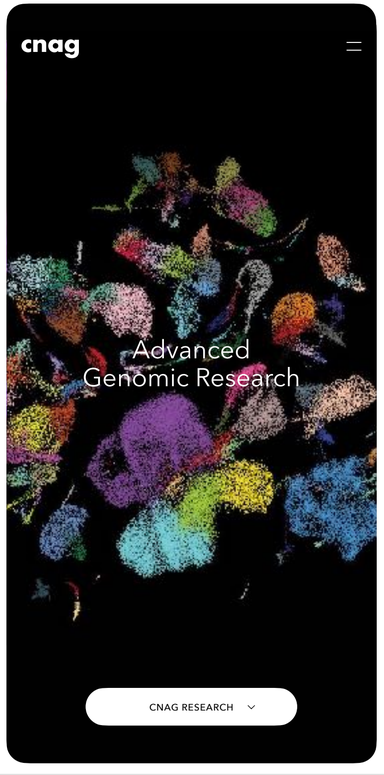
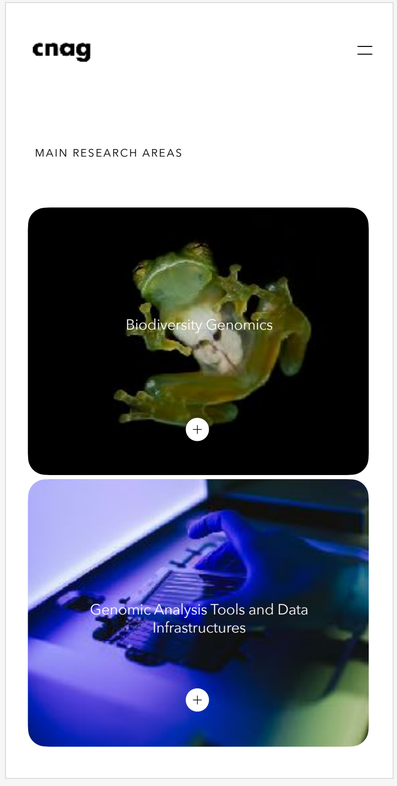


Variant 2
Evolució

- Blanc i negre
- Geometria arrodonida (botons, imatges...)
- Tipografia light





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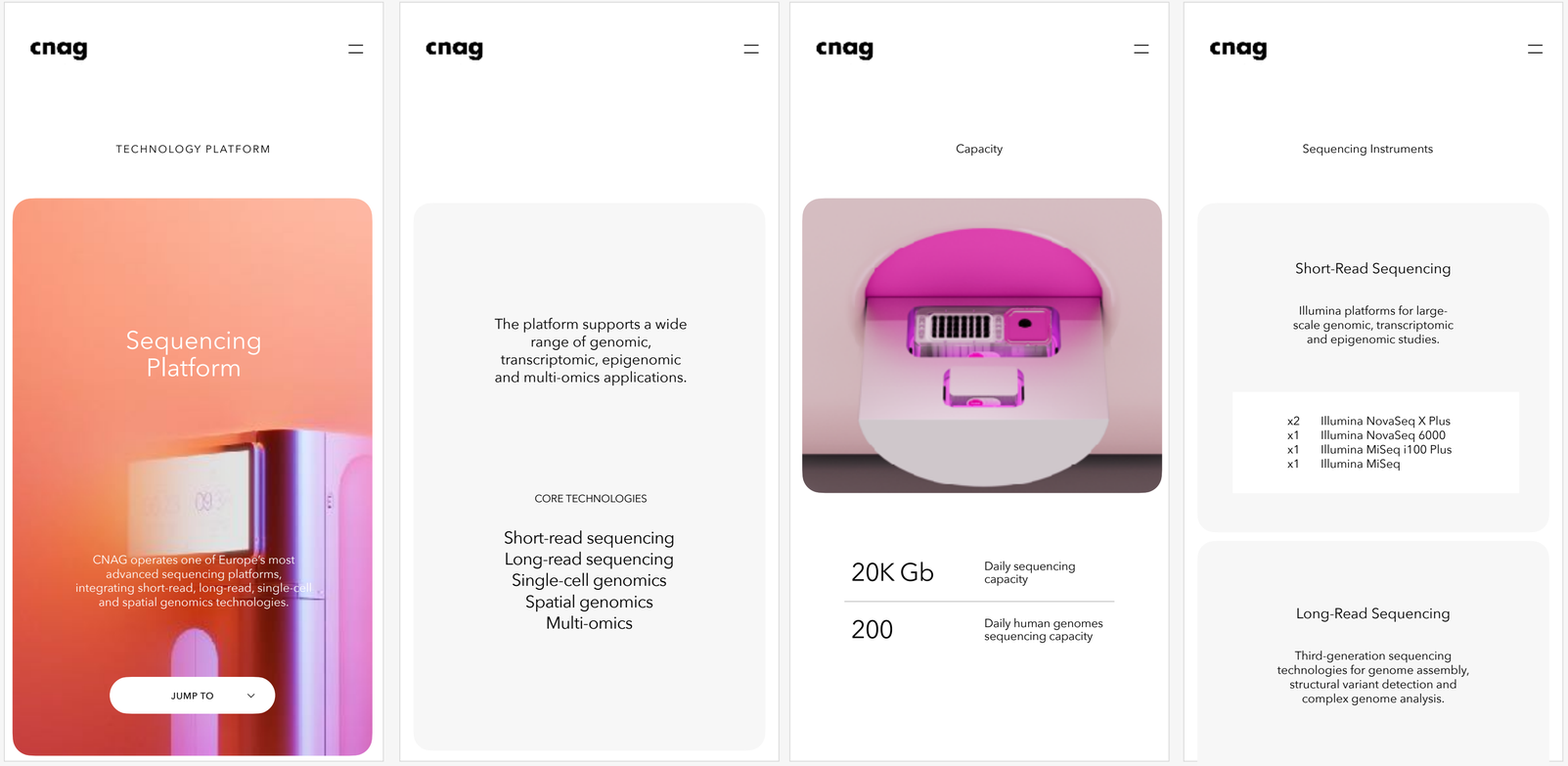


Disseny web

Selecció de pàgines desenvolupades (variant 2)

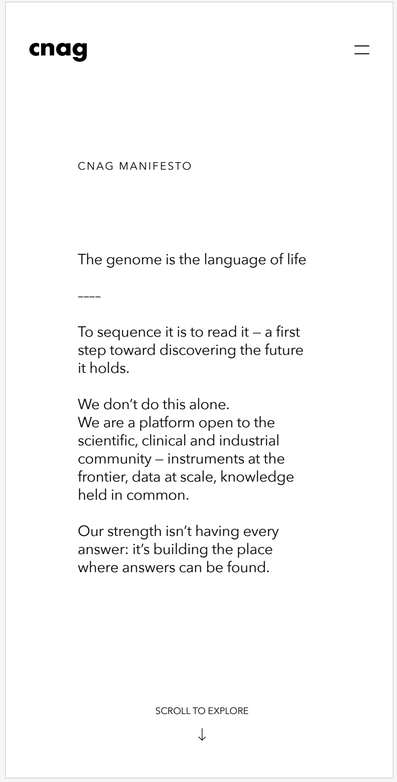
- Homepage
- Menú
- CNAG Research (Group)
- CNAG Technology Platform

Home

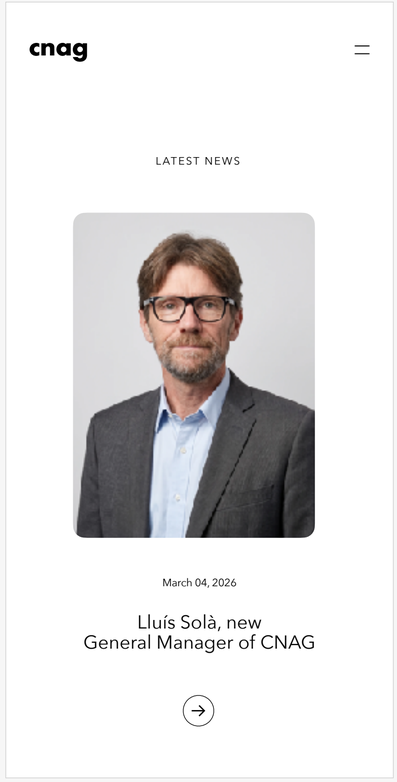
- Scroll visual pels principals components del CNAG i destacats
- Ús de video
- Accés directe a seccions

Home

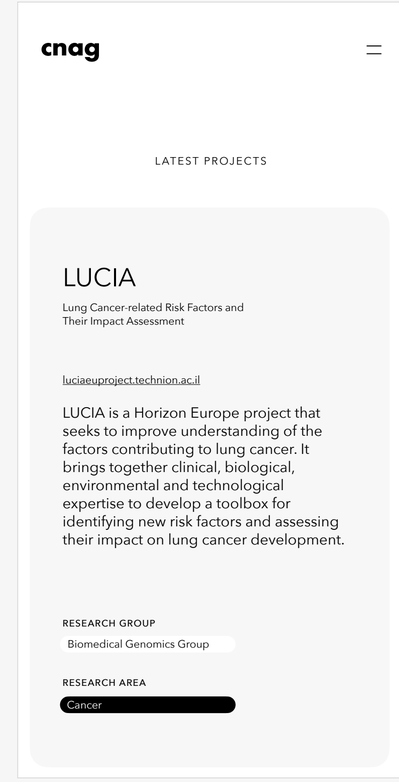
El sistema de la home permet visualitzar una gran varietat de continguts i formats



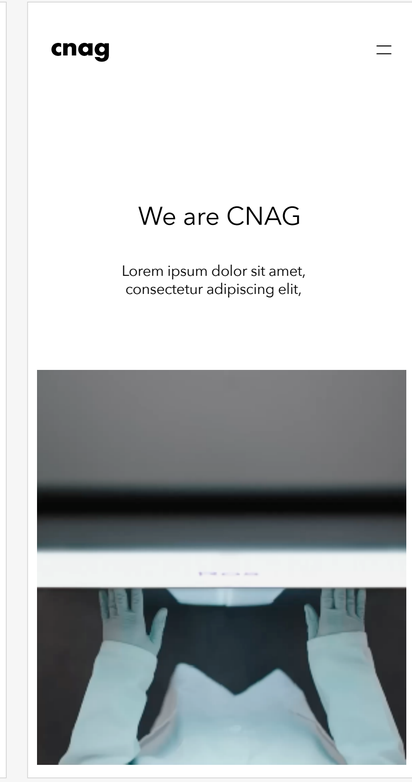
Manifesto



Institutional News



Highlighted projects



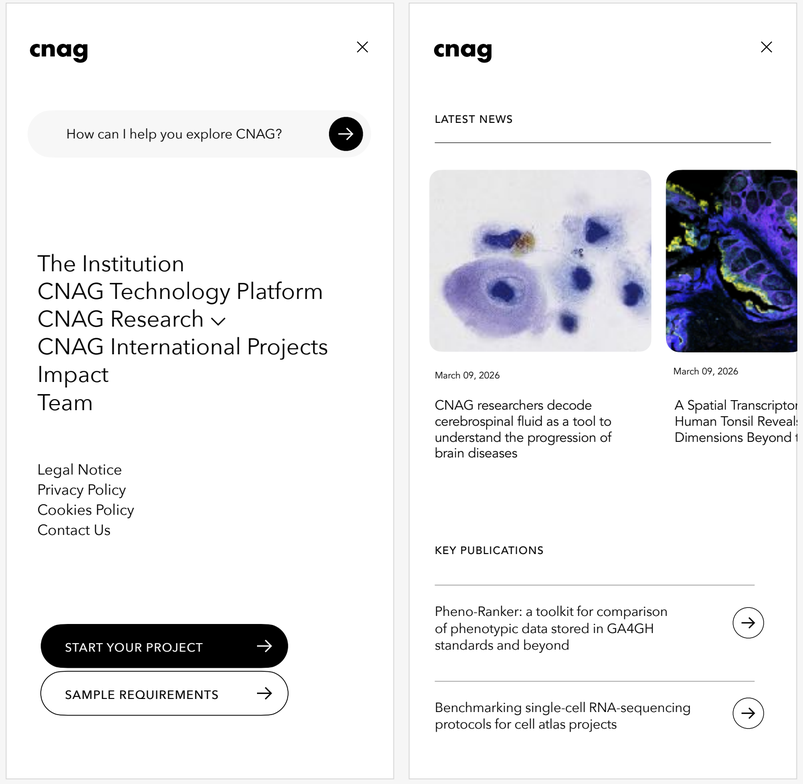
Campaign

Menú

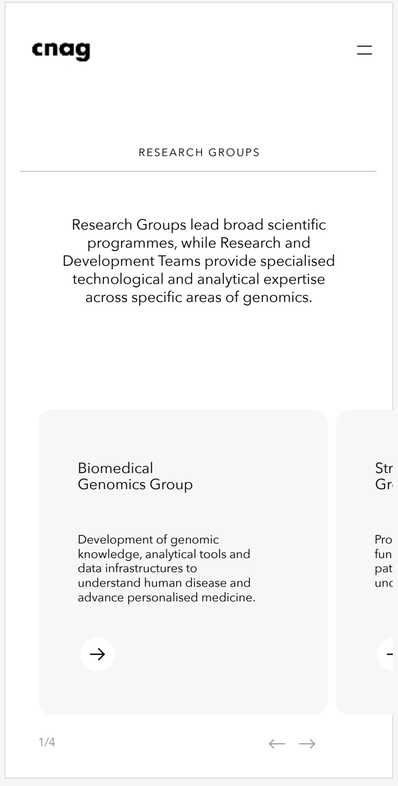
Sistema de menú enriquit amb:

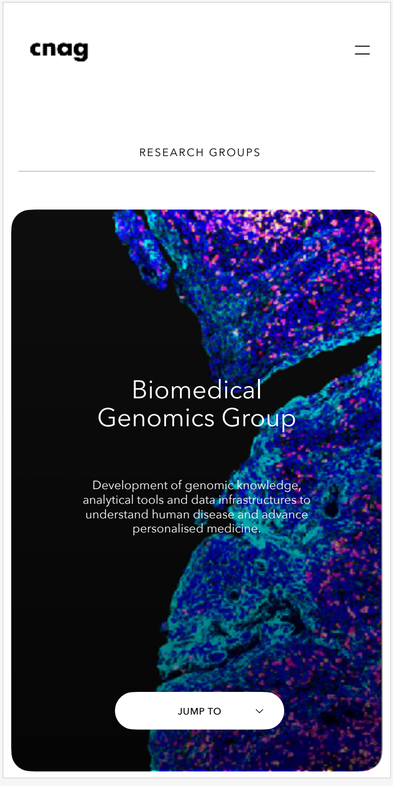
- Accés directe a infromació d'interès (sample requirements)
- Visualització de novetats (projectes, news...)
- CTA

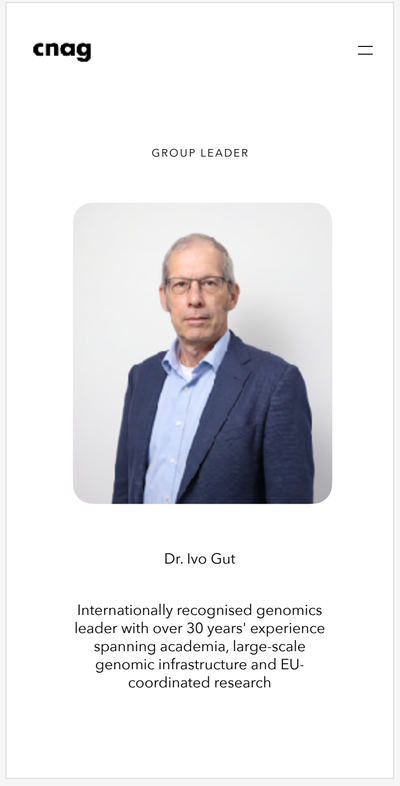
...

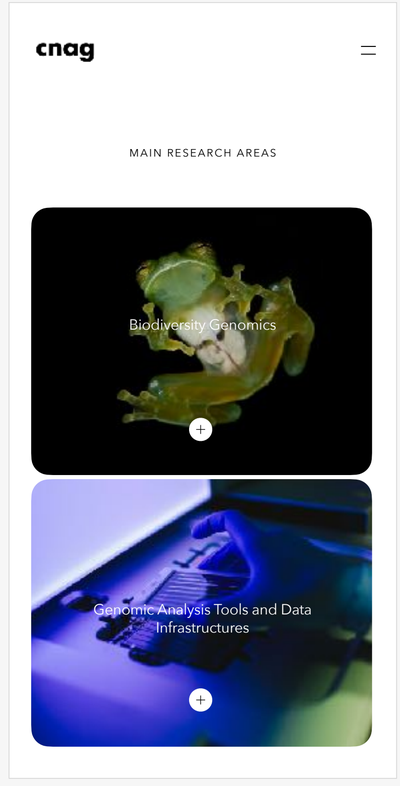


CNAG Research









CNAG Research

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SELECTED PROJECTS

EASIGEN-DS

Designing the concept for a European research infrastructure dedicated to advanced genomic technologies.

BCLL@las

Studying chronic lymphocytic leukaemia through advanced genomic and immune-cell analysis

LUCIA

Lung Cancer-related Risk Factors and Their Impact Assessment

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SELECTED PROJECTS

LUCIA

Lung Cancer-related Risk Factors and Their Impact Assessment

luciaeuproject.technion.ac.il

LUCIA is a Horizon Europe project that seeks to improve understanding of the factors contributing to lung cancer. It brings together clinical, biological, environmental and technological expertise to develop a toolbox for identifying new risk factors and assessing their impact on lung cancer development.

RESEARCH GROUP

Biomedical Genomics Group

RESEARCH AREA

Cancer

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SELECTED PUBLICATIONS

Pheno-Ranker: a toolkit for comparison of phenotypic data stored in GA4GH standards and beyond

04 December 2024

Leist IC, Rivas-Torrubia M, Alarcón-Riquelme ME, et al.
BMC Bioinformatics

Multi-organ single-cell transcriptomics of immune cells uncovered organ-specific gene expression and functions

04 December 2024

Tsagiopoulou M, Rashmi S, Aguilar-Fernandez S, Nieto J, Gut IG.
Scientific Data

Benchmarking single-cell RNA-sequencing protocols for cell atlas projects

04 December 2024

Mereu E, Lafzi A, Moutinho C, et al.
Nature Biotechnology,

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TEAM MEMBERS

Ivo G. Gut	Group Leader
Gabriela Aguileta	Bioinformatician
Ivo Leist	PhD Student
Claudia Buhigas	Postdoctoral Researcher
Dietmar Fernández	Postdoctoral Researcher
Manuel Rueda	Bioinformatician
Miranda Stobbe	Postdoctoral Fellow

CNAG Technology Platform

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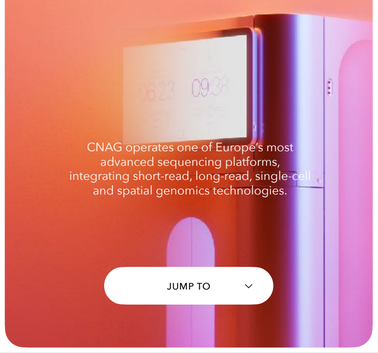
TECHNOLOGY PLATFORM

Sequencing Platform



CNAG operates one of Europe's most advanced sequencing platforms, integrating short-read, long-read, single-cell and spatial genomics technologies.

JUMP TO

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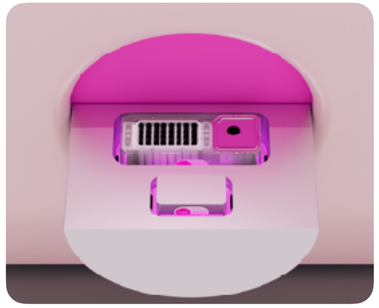
CAPACITY



20K Gb	Daily sequencing capacity
200	Daily human genomes sequencing capacity

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SEQUENCING INSTRUMENTS

Short-Read Sequencing

Illumina platforms for large-scale genomic, transcriptomic and epigenomic studies.

x2	Illumina NovaSeq X Plus
x1	Illumina NovaSeq 6000
x1	Illumina MiSeq i100 Plus
x1	Illumina MiSeq

Long-Read Sequencing

Third-generation sequencing technologies for genome assembly, structural variant detection and complex genome analysis.

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INSTRUMENTS CATALOGUE

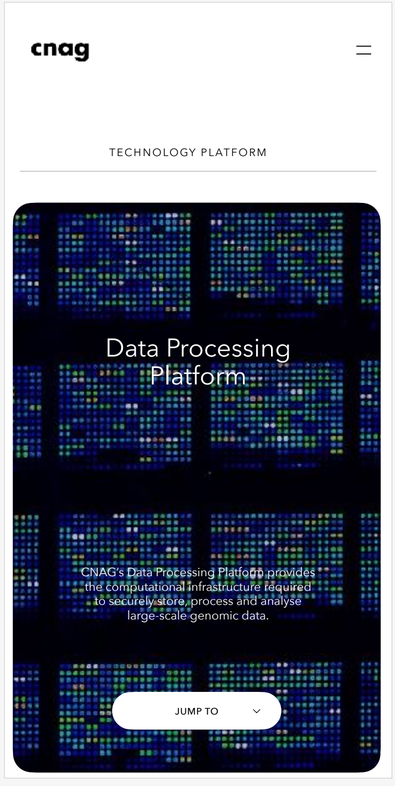
Illumina NovaSeq X Plus

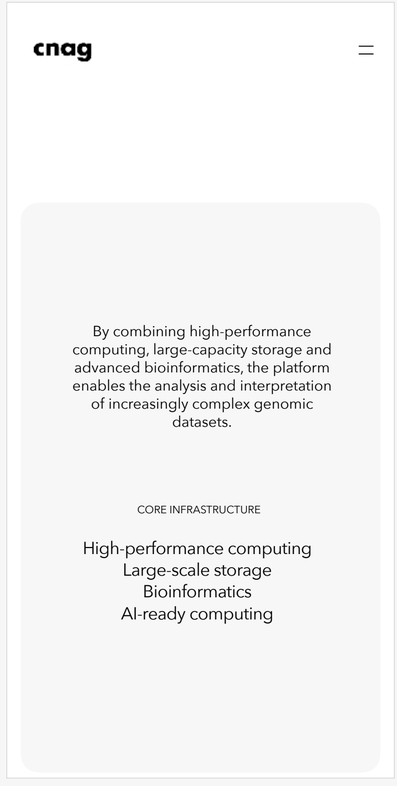
High-throughput short-read sequencing (XLEAP sequencing-by-synthesis chemistry, ultra-high-density patterned flow cells)

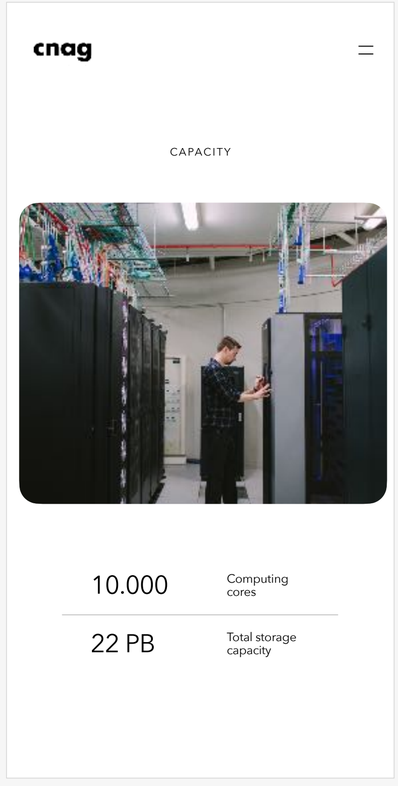
Throughput	16-21 TB per run
Flow-cell formats	1.5B, 5B, 10B, 25B
Accuracy	≥85% bases Q30

DOWNLOAD SPECS

CNAG Technology Platform







Disseny web
Experiència d’usuari

CNAG AI Assistant

Cercador conversacional integrat al web (LLM propi del CNAG) que dóna accés a qualsevol contingut del CNAG

- Assistent IA basat en RAG
- Interacció per veu
- Qualsevol idioma
- Qualsevol registre (científic, informal...)

RAG (CNAG)

Retrieval-Augmented Generation

Una arquitectura d'IA que combina un model de llenguatge (LLM) ja existent amb una base de coneixement pròpia, per produir respostes precises i acotades al contingut real del CNAG.

Model d'IA general LLM
+ base de dades a mida

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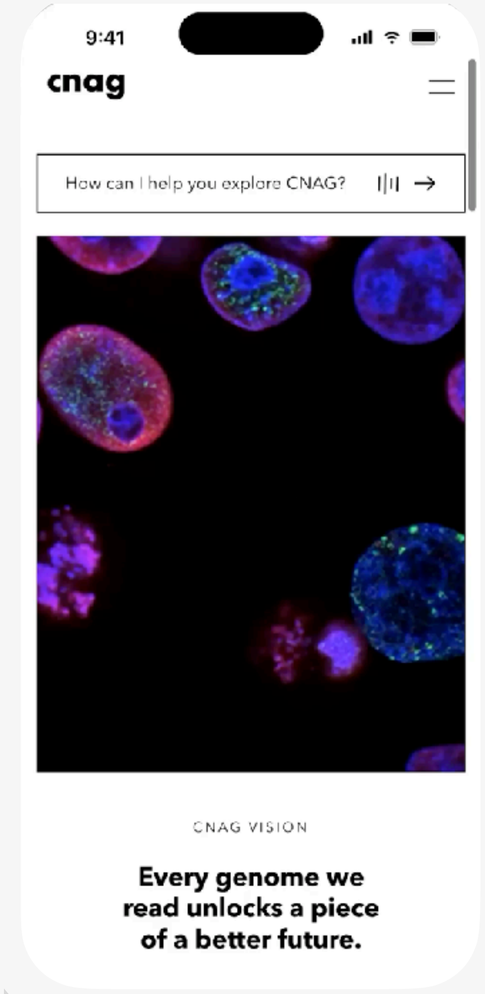

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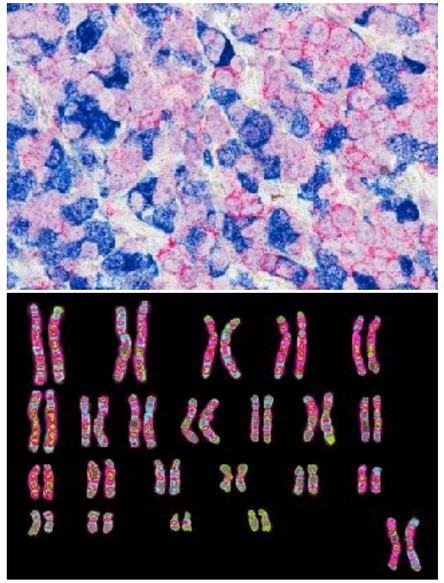
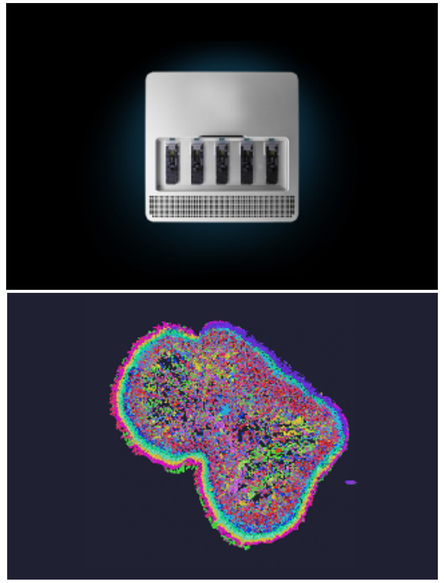
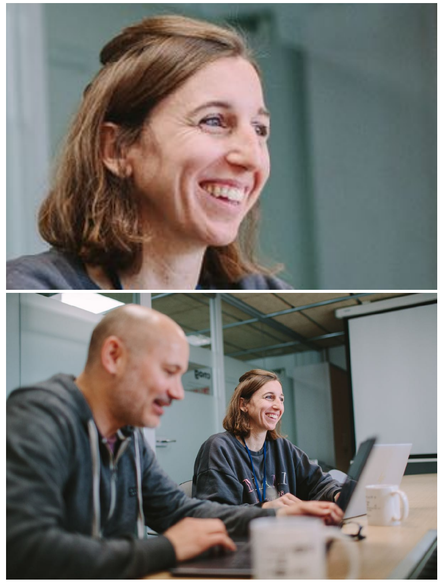
Disseny web
Banc d’imatges



Research



Technology



Institutional

Next steps

CNAG	• Validació de la proposta d’estructura i continguts • Validació de la proposta de disseny • Enviament de bancs d’imatges temàtics (research i technology)
Exit.Design	• Disseny de totes les plantilles web (desktop i mobile) • Desenvolupament del prototip web (desktop i mobile)