IFB task force vs Covid-19

https://frama.link/ifb-ag20-covid19

Noms

Started in March 2020

Goals

1. *Acute Phase*
   Quick and effective support to researchers engaged in the fight against Covid-19

2. *Chronic phase*
   Participate to the European effort, together with our partners in ELIXIR and EBI

IFB SUPPORTS THE TEAMS INVOLVED IN THE FIGHT AGAINST COVID-19

To address the COVID-19 outbreak, the Institut Français de Bioinformatique (IFB) launches an action to identify the needs in computing and data analysis, and offers expertise and computing facilities to support the involved teams.

Facilities

- **Skills** in computing, statistical analysis, databases, data science and bioinformatics. IFB federates 30 platforms of services spread over all the French regions, and gathering 400 experts in the different domains of bioinformatics.
- **A high-performance computing infrastructure**. The National Network of Computing Resources (NNCR) regroups 22 000 computing cores and 115 Tb RAM on national and regional servers (HPC clusters andclouds, https://www.france-bioinformatique.fr/en/infrastructure-0), including very high memory servers (3 Tb RAM, powered with 48 à 256 cores per server).
- **Software environments suited** to the needs of life and health sciences: bioinformatics tools, databases, packages, containers, virtual machines, workflows and a national Galaxy instance (https://usegalaxy.fr).
- **A community forum** to share experience and provide mutual support between users and experts (https://community.france-bioinformatique.fr/).
- Importantly, our actions include but are not restricted to our bioinformatics-specific skills. We interact with the teams involved in the fight against COVID-19, to identify their needs and provide concrete and efficient support.

COVID-19 Data Portal
- The European Commission and the EBI have launched the European COVID-19 Data Portal. This brings together relevant datasets for sharing and analysis in an effort to accelerate coronavirus research.

- Finally, IFB is part of the international effort led by EBI to create a European **COVID19 Data Portal** (https://www.covid19dataportal.org/)

In action

We interact with the teams involved in the fight against COVID-19, to identify their needs and propose them a concrete and efficient support; We also make the link between the different COVID-19 targeting actions at the national and international level (ELIXIR, EBI).

French

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Ongoing and achieved IFB actions

Some other actions to support bioinformatics against COVID-19
- In France
- In Europe
- Internationally

france-bioinformatique.fr/covid-19-en/

1. *Quick and effective support to the French Covid-19 researchers*

Compute & Storage

- **Molecular docking** to screen a library for drug candidates
- **Covidstress server**: Impact of COVID-19 on Human psychology

Tools & Databases

- **VirHostNet** SARS-CoV-2 release
- **Viromedb**: a complete viral genome database
- COVID-19 **Workflows Hub**
- **COVIDScan**: Thoracic CT scan results database
- **PIPprofileR**: viral genome comparisons
- Biomarker discovery in exhaled air

COVID-19 TASK FORCE

Bioinfo Expertise

- Statistical support for **drug repositioning** study
- **VirHostSeq**: dual RNA-seq metatranscriptome analysis of Covid-19 patients.
- Tracing the **origins of SARS-CoV-2** in coronavirus phylogenies [FR][EN]

Training & Outreach

- Home Learning (lessons about COVID-19)
- Bioinfo course (FR): investigating SARS-CoV-2 origins
- Public communication: The great adventure of Science

A Centralized Help Desk

- Handling of covid-19 related requests on the community support platform

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ELIXIR support to COVID-19 research

ELIXIR provides a range of services that you can use for studying the SARS-CoV-2 coronavirus and the COVID-19 disease. If you have questions about our COVID-19 related services, please contact Kathi at katharina.lauer@elixir-europe.org.
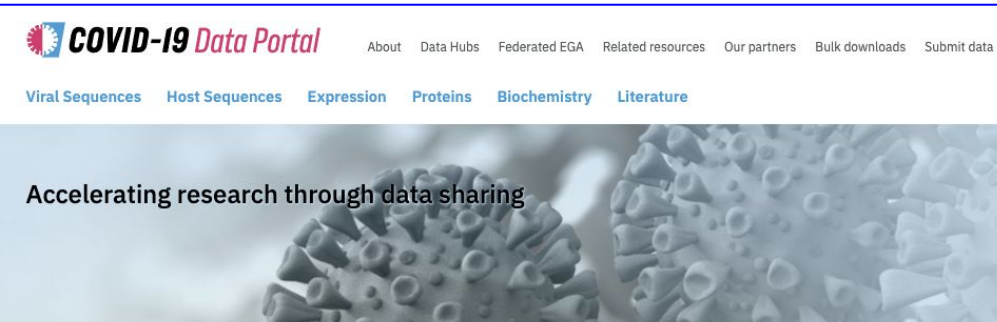
- Find a database to store your data
- Access data relevant to COVID-19
- Make your data easier to find and share
- Find software and workflows to analyse your data
- Find computing resources to help you analyse datasets
- Contribute to ELIXIR's work on COVID-19
- Find COVID-19 publications from ELIXIR
- Services offered by other European infrastructures
- Find out more

Use our interactive map to find out what each country in ELIXIR is doing in response to COVID-19.

- A federation of the national initiatives against Covid-19.

- Specification of annotation standards

elixir-europe.org/services/covid-19

COVID-19 Data Portal

- https://www.covid19dataportal.org/
- An **EMBL-EBI** initiative
- ELIXIR requested the national nodes to participate to the data portal

Viral sequences ➜
Raw and assembled sequence and analysis of SARS-CoV-2.

82,163 records >

Host sequences ➜
Raw and assembled sequence and analysis of human and other hosts.

961 records >

Expression ➜
Gene and protein expression data of human genes implicated in the virus infection of the host cells. Identifying cell types and genes with highest expression in SARS-CoV-2 infections.

65 records >

Proteins ➜
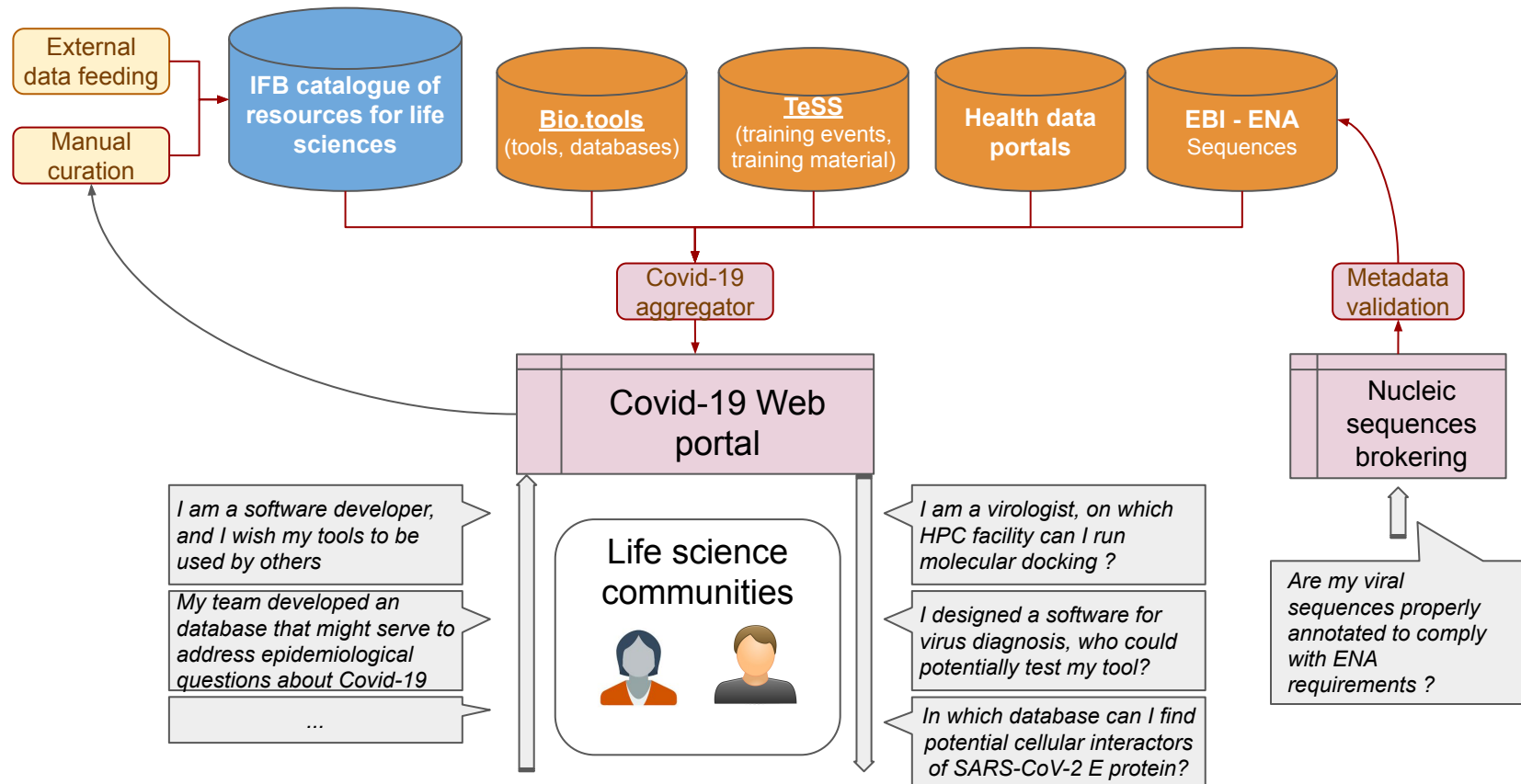Curated functional and classification data on the SARS-CoV-2 protein entries and associated protein receptors.

587 records >

Biochemistry ➜
COVID-19 pathways, interactions, complexes, targets and compounds.

1,463 records >

Literature ➜
Search for the latest literature about SARS-CoV-2.

163,284 publications >

Related resources ➜
A range of related resources for studying the SARS-CoV-2 coronavirus and the COVID-19 disease

- IFB data broker for ENA
- Thomas Denecker (started on Oct 1st)
- First mission: accompanying virologists for the FAIRification and submission of viral genomes
  - Promote early sharing of Covid-19 relevant data
  - Define standards and profiles of annotation to make the metadata re-usable
- Develop tools to
  - Facilitate metadata collection
  - Validate the metadata before submission
  - Facilitate the submission of the data and metadata to ENA

Data broker

ENA
European Nucleotide Archive

PRIDE
PRoteomics IDEntifications Database

...
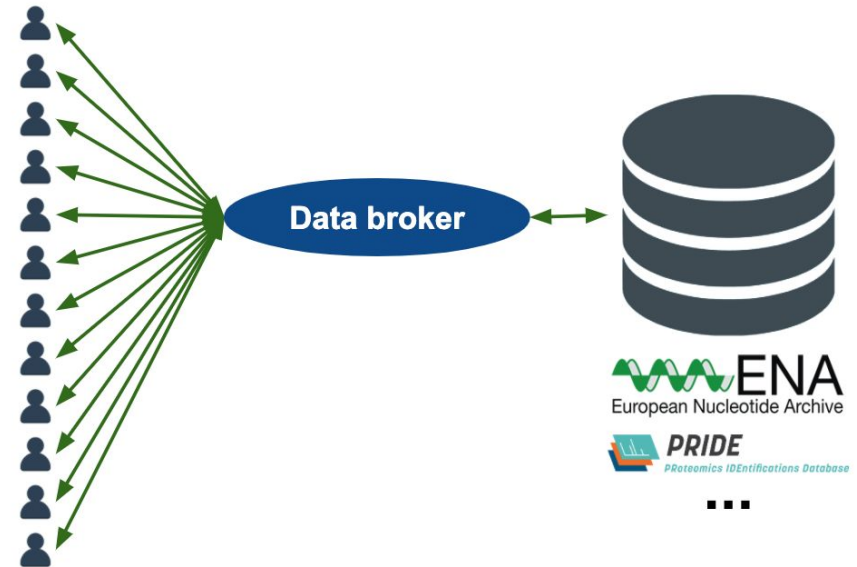
Task force members

Christophe Antoniewski

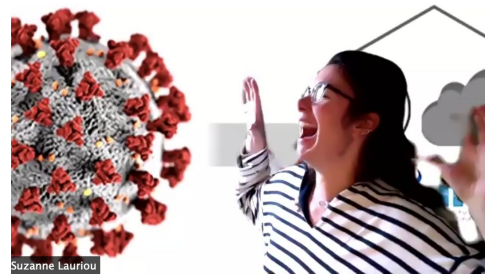Victoria Dominguez del Angel

Olivier Sand

Jacques van Helden

David Salgado

Sam Keuchkerian

Who's this?

Suzanne Lauriou
Oh là là pas de masque...

Thomas Denecker

Nicolas Geysse

Alban Gaignard

Thomas Rosnet

… vous …

How to improve accessibility of Covid-19 related resources?

- Developing a portal of French resources for Covid-19
    - databases, cohorts, tools, training material, expertises, publications, …
    - Federated with ELIXIR resources and EBI COVID-19 Data Portal
    - In link with international resources (bio.tools, TeSS).
- Fostering collaborations between the relevant actors: Inserm, CNRS, Aviesan, CARE, HAL, IFB, ...
- FAIRifying the data
    - Specifying annotation standards
    - Quality control
    - Data brokering: supporting researchers to facilitate data submission
- Training: data management, FAIRification, data submission, bioinformatics analysis, ...
- Hackathons to develop resources
- Annotathons to boost the annotation
- Bioinformatics support to research projects
- ...

ACTION	CATEGORY	DESCRIPTION	RESULT
Docking on the bigmem cluster	Compute	Installation of a Java **docking tool** on the IFB-core-cluster, support for the use of the cluster, and access to the bigmem node for the screening of a molecular library in order to identify ligands potentially useful to fight SARS-CoV-2 infection.	*In vitro* tests of the candidates started
In vitro screening for SARS-CoV-2 inhibitors	Statistics	Support to Bruno Coutard's virology team for the **statistical analysis** of an in vitro screening with a library of 1520 antiviral molecules, in order to identify inhibitor of SARS-CoV-2 infection.	PMID 32753646
VirHostNet SARS-CoV-2 release	Databases	Update of the **VirHostNet knowledge base** (protein-protein interactions) dedicated to SARS-CoV-2 and to systems biology-based research against COVID-19.	PMID 25392406
Analysis of SARS-CoV-2 envelope protein	Compute	The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) envelope (E) protein harbors a c**onserved BH3-like motif**	
COVIDScan: Thoracic CT scan results database of COVID suspected patients	Databases	This resource was developed to facilitate the creation of structured reports concerning thoracic scanners for patients suspected of COVID pneumonia. The tool can be integrated into Radiological Information Systems and allows the extraction of data.	
VirHostSeq: dual RNA-seq metatranscriptome analysis of Covid-19 patients.	Analysis	In the context of the VibraFlu project (PIA ECOFECT) and in collaboration with Laurence Josset team at HCL, we have developed a bioinformatics pipeline called VirHostSeq for the analysis of dual RNA-seq transcriptome/metatranscriptomes. This pipeline is applied to **real-time analysis of metatranscriptome of Covid-19 patients** from HCL.	
Viromedb: a complete viral genome database	Databases	In the context of the VibraFlu project (PIA ECOFECT) and in collaboration with Laurence Josset team at HCL, we have developed **Viromedb a database of complete viral genome** including SARS-CoV-2 referenced in GenBank and Refseq database.	
Home Learning (lessons about COVID-19)	Training	This project, set up during the Virtual Biohackathon, aimed to develop beginner's **lessons in bioinformatics around the Covid-19**.	

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ACTION	CATEGORY	DESCRIPTION	RESULT
COVID-19 Workflows Hub	Workflows	WorkflowHub is a European-wide registry of scientific workflows funded by EOSC-Life, which involves ELIXIR nodes: UK (lead), NL, BE, FR, DE and ES. COVID-19 Workflows Hub is a fast tracked instance resulting from the COVID-19 Biohackathon (from 5 to 11 April 2020).	
SARS-CoV-2 origins	Phylogeny	Analysis of genomic and proteic sequences in various coronavirus strains in order to infer the **evolutionary events at the origin of SARS-CoV-2,** and to understand the mechanisms of virulence.	PMID 32773024
Impact of COVID-19 on Human psychology	Psychology and neurosciences	Deployment of a Shiny app enabling to visualise the results of a study about the **impact of COVID-19 pandemy on Human psychology** (stress, confidence, observance of sanitary rules), let by an international consortium of psychologists and neurobiologists.	Nature Scientific Data, In press
PIPprofileR: a web tool to generate profiles of percent identical positions	Tools	A Shiny-based Web tool enabling to generate profiles of Percent Identical Positions (PIP), which are widely used to compare coronavirus genomes and etect recombinant regions.	SOURCE CODE
Biomarker discovery in exhaled air	Tools, Signal Processing, Statistics	Bioinformatic and biostatistical methods for the treatment and analysis of expired air by mass spectrometry and electronic nose developed by CEA in partnership with the Exhalomics platform of the Foch Hospital/University Versailles Saint-Quentin. In particular the ptairMS R package for processing PTR-TOF-MS spectrometry data, available on github.	SOURCE CODE
The great adventure of Science	Public communication	A series of four 1-hour sessions on the French radio France Culture about scientific approaches to the Covid-19 pandemic, opening wider questions about the world of science: publication, handling of uncertainty, public communication, competitiveness, political issues, frauds, power games, ...	
Development of a universal quality control kit	Sequence analysis	At the current stage only already commercialized RNA fragments are used, in order to ensure rapid product development; first evaluation of the corresponding quality tests was already performed at the CHU Bordeaux in September 2020. Next stage will concern the development of an universal quality control kit and will involve the analysis of possible RNA sequence combinatorics; the corresponding test kits will be validated at a national reference center.	
docking on grid	Compute	Installing nodes for docking compute on biomed VO	