

## Title page

# Toward an observatory of the evolution of COVID-19 vaccines trials through phylomemy reconstruction

### Authors:

Quentin Lobbé<sup>1\*</sup>  
David Chavalarias<sup>1</sup>  
Alexandre Delanoë<sup>1</sup>  
Gabriel Ferrand<sup>2,3,4</sup>  
Sarah Cohen-Boulakia<sup>5</sup>  
Philippe Ravaud<sup>2,3,4</sup>  
Isabelle Boutron<sup>2,3,4</sup>

- 1) CNRS, Complex Systems Institute of Paris Île-de-France
- 2) Université de Paris, INSERM, INRAE, CNAM, CRESS, F-75004 Paris, France
- 3) Centre d'Épidémiologie Clinique, AP-HP, Hôpital Hôtel-Dieu, F-75004 Paris, France
- 4) Cochrane France, F-75004 Paris, France
- 5) Université Paris-Saclay, France

### Corresponding author:

Quentin Lobbé  
Complex Systems Institute of Paris Île-de-France, 113 Rue Nationale, 75013 Paris, France  
quentin.lobbe@gmail.com

### Guarantor:

David Chavalarias  
Complex Systems Institute of Paris Île-de-France, 113 Rue Nationale, 75013 Paris, France  
david.chavalarias@iscpif.fr

### Authors contributions:

All authors contributed equally to the paper. G Ferrand was responsible for the data collection process. Q Lobbé, D Chavalarias and A Delanoë were responsible for the text mining and data visualization processes. S Cohen-Boulakia, P Ravaud and A Boutron were responsible for the data interpretation process.

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## KEYWORDS

COVID-19  
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## ABSTRACT

This paper aims at reconstructing the evolution of all the available COVID-19 vaccines trials extracted from the *COVID-NMA database* by applying the *phylomemy reconstruction process*. We visualize the textual contents of 1,794 trials descriptions and explore their collective structure along with their semantic dynamics. We map the continuous progress of the main COVID-19 vaccine platforms from their early-stage trials in February 2020 to their most recent combinations driven by the rise of variants of concern, third dose issues and heterologous vaccinations. This paper brings insights for the global coordination between research teams especially in crisis situations such as the COVID-19 pandemic.

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## WHAT IS NEW

- We use a new text mining method to synthesize the overwhelming amount of information about current COVID-19 research
- We analyze the textual content of 1,794 COVID-19 vaccines trials descriptions
- We reconstruct the temporal evolution of the main vaccines platforms and thus visualize the emergence of upcoming research questions
- We bring insights for the global coordination between research teams toward the creation of an observatory of the evolution of clinical trials

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## 1. Introduction

Over the past two years, the ongoing COVID-19 pandemic has impacted a wide number of human domains: from economy to education, from public health to politics. Among others, Science swung early on into action to find both a cure and an effective vaccine. This has resulted in an unprecedented volume of publications that have generated an information overload for the medical community. One of today's challenges is to synthesize this overwhelming amount of information about current COVID-19 research in order to improve coordination between the different research streams.

**While related works have so far focused on visualizing structured data or meta-data to follow the mutation of the virus [8], the worldwide evolution of the pandemic [5] or the discovery of new treatments [11], we here propose to explore the richness of unstructured data (textual content) extracted from the *COVID-NMA database*: an international initiative for mapping and reviewing trials registries. Because curating clinical registries is an highly time-consuming task, we think that visualizing the content of not yet annotated textual fields (such as full trials descriptions) can improve our global comprehension of the way science progresses in pandemic time. In particular, the analysis of semantic inheritance processes can reveal temporal structures hidden within trials registries that are still out of the reach of any meta-data driven visualization systems. We thus choose to make us of a new visualization method designed to reconstruct the dynamics of unstructured elements of knowledge: the *phylomemy reconstruction process* [3]. By using phylomemies, one can reconstruct the temporal evolution of the semantic landscape of timestamped corpora of textual documents. With trials registries as input data, we aim at reconstructing the way researchers converge trial by trial towards the discovery of new treatments.**

**In this paper, we will focus on COVID-19 vaccines trials extracted the *COVID-NMA database*. The *COVID-NMA database* stores the curated dataset of all the clinical trials available in the set of international primary and secondary trial registries [1, 11] ( *i.e.*, all trials registered in the International Clinical Trials Registry Platform (ICTRP), Clinicaltrials.gov and the EU clinical trials registry – see 2.1).**

**The use of such data challenges us in two ways (see 2.2): How can we deal with mutable and ever-growing databases? How can we combine the expertise of epidemiologists and *Complex Systems* researchers to create and interpret the resulting visualizations?**

## 2. Materials and method

Our paper aims at applying a new text mining method – the *phylomemy reconstruction process* – to reconstruct the temporal evolution of COVID-19 vaccines research. To that end, we choose to analyze a set of 1,794 clinical trials descriptions extracted from the *COVID-NMA database*. Our data set has been collected and curated by the combined effort of epidemiologists, data integration and complex systems researchers.

### 2.1. The COVID-NMA database

The COVID-NMA project is an international initiative aimed at providing a living mapping and a living systematic review of all trials assessing treatments and preventive interventions for COVID-19 [1, 11]. The development of the COVID-NMA database relies on a full methodology designed to generate and make available a complete, comprehensive, integrated, non-redundant and carefully annotated data sets on clinical trials. We automatically extract data from clinical registries on a weekly basis and provide assistance to epidemiologists on the curation and annotation process. Raw data is extracted from the EU clinical trials register, from the ClinicalTrial registry managed by the U.S. National Library of Medicine, from the IRCT registry and from the WHO International Clinical Trials Registry Platform (ICTRP) – an international registry that assembles information on clinical trials registered in 17 primary registries to identify new trial assessing COVID-19 vaccine and update of previously registered trial records. Data are extracted from registries, annotated **and enriched** by epidemiologists, then stored and made available through the COVID-NMA database.

### 2.2. Pre-processing the COVID-NMA database

**In order to be used as input data, the COVID-NMA database need to be pre-processed. But the unprecedented volume of trials related to COVID-19 has challenged our capacity to build a time-consistent and insightful visualization. We thus faced two main issues: dealing with the mutable nature of trials registries and collaboratively curating a core vocabulary from the trials descriptions.**

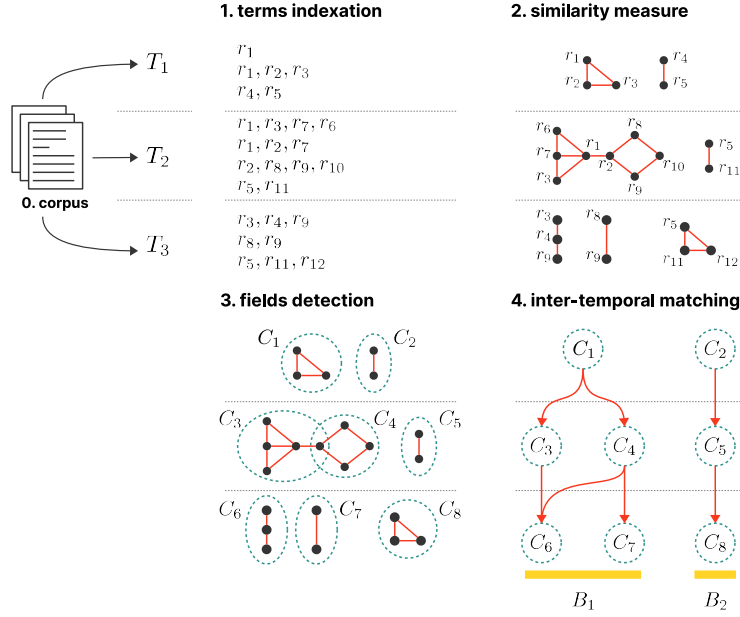
We first note that international trials registries can be post-updated by research teams. **Contrary to regular scientific publications, their textual contents are mutable by nature: the description of a given trial can be post-updated weeks after having been recorded. One can detail an experimental protocol or simply link some results to a trial. Usually, researchers can manually deal with such updates, but in our case, the tight temporality of the COVID-19 pandemic forced us to monthly reconstruct our visualization on top of hundreds of changeable trials. We have thus developed a time-consistent strategy: for each recorded trial, we have made the decision not to update its textual description. By doing so, we don't break the temporal continuity of the phylomemy reconstruction process as we preserve the natural evolution of the descriptions. However, we have kept the meta-data (i.e, trial phases, funding, associated publications, etc.) up-to-date with their most recent version.**

**The phylomemy reconstruction process requires the creation of a core vocabulary to visualize the evolution of the trials descriptions.** To that end, we have first filtered from the COVID-NMA database a set of 1,794 records exclusively related to vaccination. Within each selected trial, we have merged the sections '*pharmacological treatment*', '*treatment type*' and '*treatment name*' together to create **a normalized** description. The resulting corpus  $D_{vt}$  has latter been collectively and collaboratively curated by epidemiologists thanks to the free software *Gargantext* [6]. This software, allow us to follow a human-driven approach where epidemiologists can validate and annotate each term they want to extract from the descriptions. We have thus created a core vocabulary as a list of 175 root terms.

### 2.3. The phylomemy reconstruction process

The phylomemy reconstruction process [2, 3] combines advanced text-mining methods, scientometrics and methods for the reconstruction of evolving complex networks in order to reconstruct the latent semantic structures of an unstructured – but timestamped – set of textual documents. Applied to a scientific corpus, it results in an inheritance network of research areas covered by all the collected publications. The phylomemy reconstruction process can be described as a combination of four subsequent operators of summarized by the Figure 1:

1. **Terms indexation.** By means of natural language processing (NLP) algorithms and human validations – NLP algorithms and human validations are handled by the free software *Gargantext* [6] –, we first extract from an original corpus of documents (Figure 1.0) a core vocabulary as a list  $\mathcal{L} = \{r_i | i \in \mathcal{I}\}$  of sets  $r_i$  of equivalent expressions called *roots* (Figure 1.1).



**Figure 1:** The four operators of the phylomemy reconstruction process: 1. terms indexation, 2. similarity measures, 3. fields detection, 4. inter-temporal matching

In our case study, the corpus is a set of 1,794 trials descriptions. The *roots* are all the technical and equivalent names (including characteristics variations and any misspelling) given for a same vaccine. For instance, the technical expressions “rad5” and “rad26” were aggregated into “gam-covid-vac”.

The corpus is then sliced into periods of interest  $\mathcal{T}^* = \{T_i\}_{1 \leq i \leq K}$ ,  $T_i \subset \mathcal{T}$  for which roots’ co-occurrences are computed.

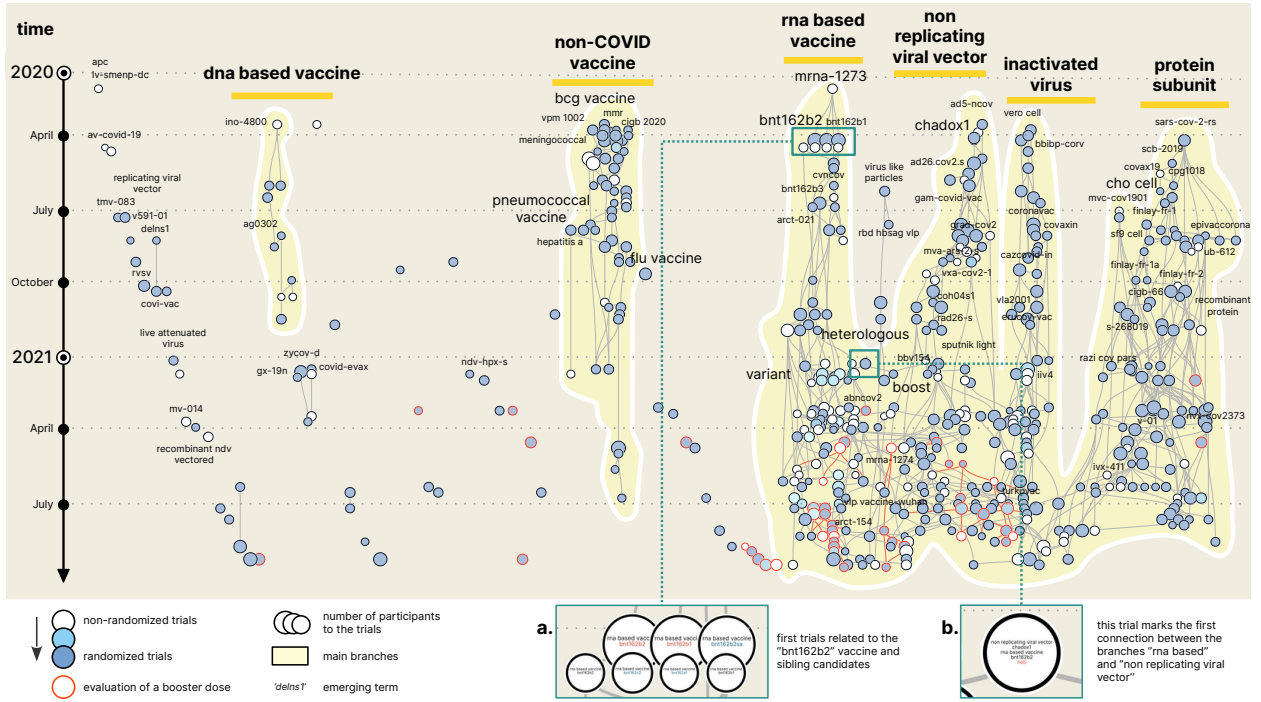
In our case study, we consider two weeks periods starting every monday from February 2020 to October 2021 and the output is a series of matrices of roots co-occurrences.

- 2. Similarity measure.** Within each period of time and on the basis of its co-occurrences matrix, we estimate the semantic similarity between roots using the *confidence* measure [7]. The completion of this task results in a temporal series of graphs of similarity (Figure 1.2).
- 3. Fields detection.** For each period, a community detection algorithm – the *frequent item set* method [12] – is applied to detect subsets of densely connected roots within the graphs of similarity. Theses subsets  $C^T$  are called *fields* (Figure 1.3) and their aggregated root expressions describe consistent research topics that were explored at a given period.

In our case study, the *fields* correspond to one or more descriptions of clinical trials sharing the same vaccine strategy. The output of this field detection step is a temporal series of clustering  $C^* = \{C^T | T \in \mathcal{T}^*\}$  with  $C^T = \{C_j | j \in J^T\}$  and  $C_j = \{r_i | r_i \in \mathcal{L}, i \in I_j \subset I\}$  computed over all the periods. It describes all the research directions explored from February 2020 to October 2021.

- 4. Inter-temporal matching.** A temporal matching algorithm is then applied to identify meaningful kinship connections between fields from one period of time to another, *i.e.* fields that belong to the same research stream. We finally highlight the different research steams  $B_k$  over time and called them *branches of knowledge* (Figure 1.4).

The phylomemy reconstruction process makes it possible to draw the knowledge lineages at different resolutions through the tuning of a *level of observation* [3]. The complexity of the resulting semantic landscape can range from a wide ‘continent’ to an ‘archipelago’ of specialized branches of knowledge.



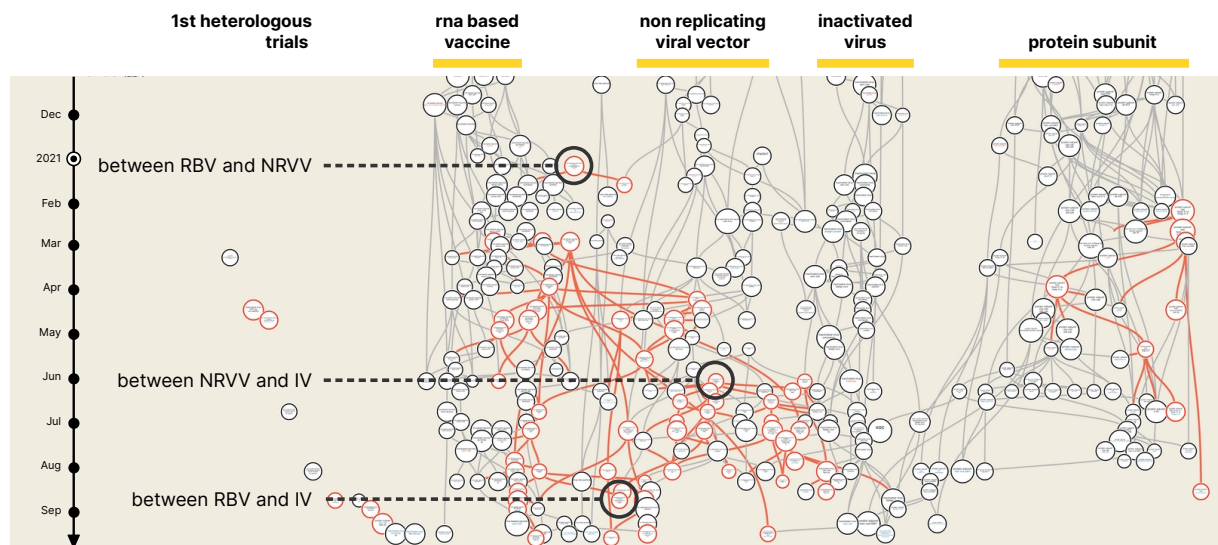
**Figure 2:** Phylomemy of 1,794 COVID-19 vaccines trials recorded between February 2020 and October 2021 in the COVID-NMA database. Online and interactive version available at [maps.gargantext.org/publications](https://maps.gargantext.org/publications)

## 2.4. Visualizing phylomemies

The structures highlighted by a phylomemy reconstruction process synthesize the complexity of the knowledge produced by a research community. In order to make this newly reconstructed knowledge actionable and explorable, a phylomemy can be visualized as a temporal network with time going by from top to bottom [10]. Fields are represented by full circles and solid dark lines translate their kinship connections. *Emerging terms* (ie, terms appearing for the first time in the phylomemy) are displayed over the whole structure according to the combined coordinates of their period and fields of appearance. Term's size depends on their frequencies in the original corpus of trials. Branches are sorted from left to right so that closely related ones lie side by side. Interactive features can be used to reveal the entire fields' content, follow the dissemination of a given term throughout the phylomemy or simplify the *scale of description* of a selected branch.

## 3. Description of the resulting phylomemy

For our case study, we have used the corpus  $D_{vt}$  of 1,794 COVID-19 vaccines clinical trials (see 2.1) in order to reconstruct the weekly evolution of the research on COVID-19 vaccines between February 2020 and October 2021. Key expressions are extracted from the original descriptions of the tested vaccines, grouped into roots and then into fields. The reconstructed fields thus embody a set of trials at a given period of time. We here choose a level of observation  $\lambda = 0.5$  to shape quite precise branches. The resulting phylomemy (Figure 2) contains 175 roots and 550 fields distributed among 55 branches. The largest ones '*dna based vaccine*', '*non-COVID vaccines*', '*rna based vaccine*', '*non-replicating viral vector*', '*inactivated virus*' and '*protein sub-unit*' are highlighted by yellow shades. Shades of blue indicate the proportion of randomized clinical trials among the total number of trials on which the corresponding field has been reconstructed. The visualization of a phylomemy can also offer its user to interactively highlight some key information, as for example the research paths addressing vaccine boost issues, highlighted in red at the bottom of this figure.



**Figure 3:** A focus of Figure 2. In red are highlighted all the trials evaluating heterologous primary vaccination and heterologous booster. We circle the first heterologous trials involving different platforms.

## 4. Following the worldwide tracks of COVID-19 vaccines

### 4.1. General observations

After having explored and analyzed Figure 2 alongside epidemiologists, we noticed that the reconstructed phylomemy clearly retrieves five major COVID-19 vaccine platforms in the form of complete branches. These platforms include the classical vaccine platforms i.e., ‘non-replicating viral vector’, ‘inactivated virus’ and ‘protein subunit’ as well as the next-generation vaccine platform i.e., ‘dna based vaccines’ and ‘rna based vaccines’. The visualization shows the continuous development of each branch and the way some of them started to interact and eventually blended while others stopped. Interestingly, trials of ‘rna based vaccines’ were registered very early in the course of the pandemic (February 2020) with trials evaluating the vaccine developed by Moderna TX (mRNA-1273) followed by the vaccine developed by Pfizer/BioNTech (BNT162b2) and sibling ones like BNT162b1 or BNT162b2sa that were not much longer tested (see Figure 2.a). The number of trials increased rapidly and interactions with other widely explored techniques were observed shortly afterwards: notably with the ‘non-replicating viral vector’ family (ChAdOx1 – AstraZeneca – see Figure 2.b). The latest interaction involved the ‘protein subunit’ branch in July 2021. In contrast, ‘dna based vaccines’, with a first trial registered in April 2020, had a very limited number of trials planned and the whole branch stopped rapidly in 2020. Similarly, other platforms of ‘replicating viral vector vaccine’, ‘virus-like particle vaccine’ and ‘live attenuated virus vaccine’ showed a very limited development.

### 4.2. Repurposing non-COVID vaccines

As the development and approval of COVID-19 vaccines was expected to take time, researchers also explored repurposing non-COVID vaccines. Considering the lower severity of the disease in children and young adults, some researchers hypothesized the possible heterologous protective effect of these vaccines. Some evidence shows that live-attenuated vaccines such as Bacille Calmette–Guerin (BCG), Measles, Mumps, Rubella (MMR) can induce protective innate immunity, which could be central in controlling SARS-CoV-2 [4]. While this hypothesis was appealing, it did not seem to expand into a wider research domain. The branch of ‘non-COVID vaccines’ appears and expands at the beginning of the pandemic but progressively decreases towards the end of 2020 as other more promising vaccines arose. Nevertheless, some researchers highlighted the need to adequately assess the use of non-COVID live-attenuated vaccines as they could potentially boost response in high-risk populations, be used in addition to COVID-vaccines to increase effectiveness and durability of their effect, or be used to protect people exposed to COVID-19 patients [4].



### 4.3. Heterologous vaccination

The branches interactions reflect the exploration of a new approach to vaccine implementation moving from homologous prime vaccination (i.e., injections of two doses of the same vaccine) to heterologous prime vaccination (i.e., injection of the first dose of a given vaccine and the second dose of another vaccine). This is clearly shown in Figure 3 with the assessment of the heterologous prime vaccination of ‘*rna based vaccine*’ (BNT162b2-Pfizer/BioNTech) and ‘*non-replicating viral vector*’ (ChAdOx1-AstraZeneca) in early 2021. This new approach was motivated by concerns about waning vaccine immunity, but also by practical considerations. Following concerns about the safety of the AstraZeneca ChAdOx1 vaccine, the EMA recommended giving a second dose Pfizer BNT162b2 vaccine to patients under the age of 55 years old who received one dose of ChAdOx1-S-nCoV-19. Furthermore, decision makers needed flexibility to overcome the issue of vaccine availabilities during the vaccine rollout. This new approach proved to be relevant and other associations were evaluated: ‘*non replicating viral vector*’ and ‘*inactivated virus*’ in June 2021 and later ‘*rna based vaccine*’ and ‘*inactivated virus*’ in September 2021.

### 4.4. Boosters

Phylomemies are essential in identifying shifts in research questions. While evidence of the beneficial effect of vaccines is mounting, research questions are moving toward exploring the effect of booster to overcome the waning of vaccine efficacy over time. Early in 2021, new trials assessing the impact of administering a third dose (see Figure 2, red outline at the bottom) have been registered particularly for ‘*rna based vaccines*’ and ‘*non-replicating viral vector*’ [9]. An important part of the research on boosters’ effects is considering heterologous boosters.

### 4.5. Filters and **specific** research questions

By using meta-data from the trials registries, we can filter the current phylomemy and thus push faceted observations to the fore or identify **current main** research questions. Phylomemies also provides important information on research planning and reporting. As shown in Figure 2, most trials registered are randomized controlled trials. Early in the pandemic, non-randomized trials were primarily early phase trials while those registered in 2021 include both early phase trials exploring new vaccines and phase 4 trials assessing vaccines safety.

We can explore the visualization to better understand how different countries participated in the overall research effort over time. For example, when filtering on the country (see [maps.gargantext.org/phylo/vaccines/countries](https://maps.gargantext.org/phylo/vaccines/countries)), we see that trials conducted in the USA explored all vaccine platforms and that first registered trials frequently involved a center in the USA, confirming their leading role in clinical research (e.g., ‘*dna based vaccine*’, ‘*rna based vaccine*’, ‘*protein subunit*’). Other important trials characteristics such as funding sources can also be highlighted (see [maps.gargantext.org/phylo/vaccines/fundings](https://maps.gargantext.org/phylo/vaccines/fundings)).

We also address the question of the publication of trial results (i.e., preprint or peer-reviewed articles). As shown in Figure 4, we currently have access to the results of a very limited number of planned trials. While most of the COVID vaccine trials registered in early 2020 are published, most of the non-COVID vaccine trials are still unpublished. Understanding whether these trials were actually conducted with unpublished results or were unable to recruit is an important issue.

**Using meta-data and filters is a way to address specific questions through the phylomemy by highlighting and quickly finding subsets of trials within the registries. For instance, we can make use of the ‘type of patient’ field to push trials related to specific public (‘younglings’, ‘pregnant women’, ‘immunosuppressed’, etc.) to the fore of the visualization. A dedicated phylomemy can be explored at [maps.gargantext.org/phylo/vaccines/publics](https://maps.gargantext.org/phylo/vaccines/publics).**

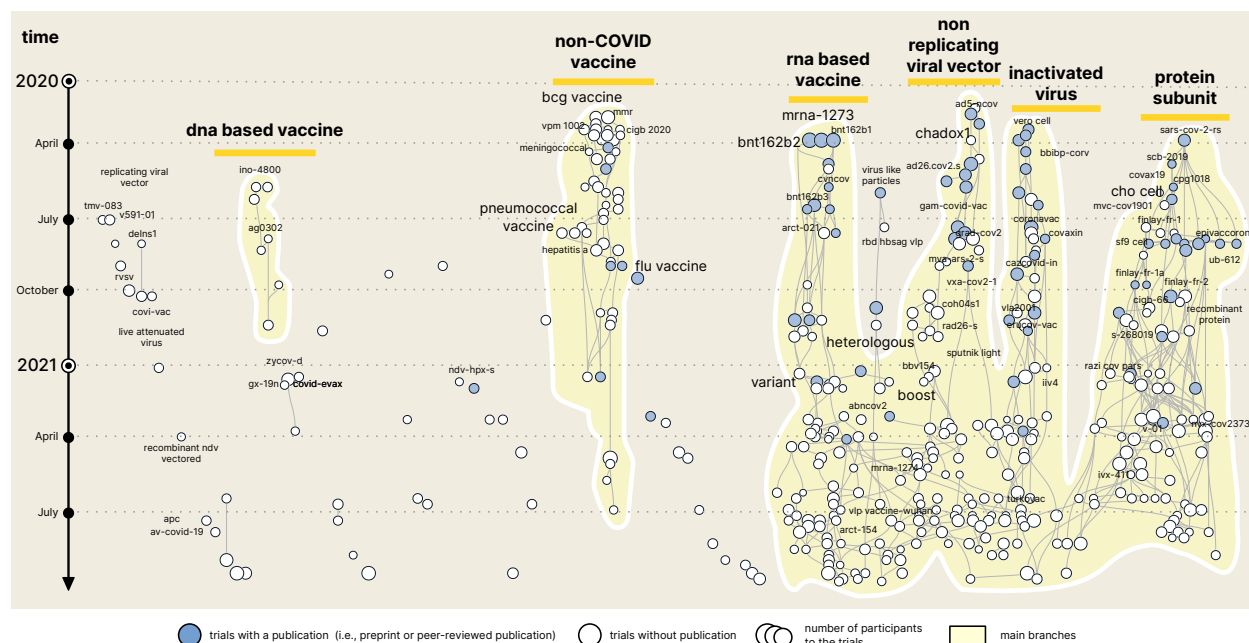
## 5. Discussion

**At this stage, two main questions arise from our work: Is our method generalizable? Can we infer or predict future trends from the visualizations?**

### 5.1. Generalization

**The scope of our paper is entirely related to COVID-19 vaccines trials. But we defend that our approach is now generalizable to various contexts without extra effort. In the following, we develop this point by incrementally generalizing future domains of application:**

- **integrating other COVID-NMA meta-data: in consultation with epidemiologists, we have enriched our visualizations with the possibility to filter on a selected set of meta-data (see 4.5). This list can be extended**



**Figure 4:** Phylomemy of the randomized only COVID-19 vaccines trials. In blue, we highlight all the trials with an associated publication (i.e., preprint or peer-reviewed articles).

to all the structured fields of the COVID-NMA database by simply changing the pre-processing script (see 2.2). Furthermore, as phylomemories are designed to reveal structure out of un-structured data, the COVID-NMA database could even be enriched with new fields such as sub-categories of vaccine trials: *‘heterologous’*, *‘boosters’*, etc. In due time, our approach could influence the way scientists share trials information in registries by standardizing new meta-data and un-structured textual content.

- **working on COVID-19 treatments instead of vaccines:** choosing between visualizing COVID-19 vaccines or treatments is also a matter of selecting the right field in the COVID-NMA database. Yet, we will still have to create a new core vocabulary (see 2.2). But thanks to GarganText, it will only take a few days to collaboratively achieve this task and annotate hundreds of trials descriptions. A first draft can be found in [3].
- **visualizing trials related to another disease:** since the beginning of this study, the COVID-NMA database as evolved and is now able to integrate registries data related to different diseases (Sarah ...). As an example, we have reconstructed the phylomemy of 1,798 trials related to Alzheimer disease and extracted from the WHO international registries. The resulting visualization can be explored at [maps.gargantext.org/phylo/alzheimer/](https://maps.gargantext.org/phylo/alzheimer/).
- **analyzing publication data:** phylomemies have been first designed to visualize the content of scientific publications. Thanks to the recent integration of phylomemies to the free software GarganText, one can already reconstruct the temporal structure of various corpora of thousands of papers extracted from *PubMed* or from *the Web of Science* (GarganText is now connected to the *API* of scientific databases). In the context of COVID-19 pandemic, it would be interesting to visualize both the results of trials and the results of papers or pre-print to explore the entire scientific landscape. A first exploration of COVID-19 literature can be found at [/maps.gargantext.org/maps/covid-19/](https://maps.gargantext.org/maps/covid-19/).
- **monitoring various type of clinical trials on the fly:** if all placed end to end, the continuous integration of WHO international registries within the COVID-NMA enrichment pipeline and through the phylomemy reconstruction process would enable the dynamic analysis of any kind of trials content as they arise. Such



**analytical workflow will require the creation of two teams: an integration team able to deal with the possible evolution of the registries and an annotation team dedicated to the creation and update of core vocabularies.**

## 5.2. Prediction

**Phylomemies are not yet designed to predict future trends on their own. They help us to understand the present states of dynamical processes regarding their former evolution. Inferring upcoming developments can be pursued by combining the knowledge of field's experts (like epidemiologists) and the comprehension of hidden dynamics relieved by the phylomemies. But in the case of this paper, we think that the nature of the input data already place us ahead of regular scientific time by visualizing registries data instead of publications data. Indeed, except for pandemic time, there usually is a gap of five years between the first trial and the publication of a new treatment. Phylomemies associated to trials registries might consequently be scientific tools for understanding possible future treatments.**

## 6. Perspectives and insights for COVID-19 research

Global coordination between research teams is a key for accelerating innovation in Science, especially during crisis situations such as the COVID-19 pandemics. Reducing redundancies and providing heuristics to find new search paths as they arise can save time and lives [11]. We claim that phylomemy reconstruction could be instrumental to guide trialists, funders and decision makers in biomedical research. In times of crises, it would enable them to better adapt to the evolution of the situation by following **main** research questions and identify less promising domains. It could also facilitate the identification of research gaps, research questions that may have been abandoned prematurely and redundancy in research.

In a world where experts are increasingly specialized, our approach could draw attention to alternative solutions developed in other branches of science or to problems already encountered in research direction to be explored. It could also lead to new conceptual operations to be performed on a knowledge database, such as "give me all the branches of knowledge that are merging" or "suggest a promising combination of compounds to test". This could both accelerate research by making tangible the latent structure of innovation, and promote collaborations between teams that would not otherwise be interested in each other's work. Phylomemy reconstructions may thus become collective and reflective tools to foster the worldwide collective coordination between researchers. This revolution in clinical trial processing is within reach. Nevertheless, it would imply having access to high quality data on research planning and protocol.

Our case study focuses on a single disease, but this approach is fully generic and we call for a worldwide observatory for monitoring the dynamics of clinical trials. As it scales up, our approach could be implemented for any disease or research field.

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## Data Availability

The original COVID-NMA database can be downloaded at [covid-nma.com](https://covid-nma.com). The pre-processing script can be downloaded at <https://doi.org/10.7910/DVN/JTRI7A>. The full list of root terms is available at <https://doi.org/10.7910/DVN/JTRI7A>. The reconstructed phylomemy is available for live explorations at [maps.gargantext.org/phylo/vaccines/publications](https://maps.gargantext.org/phylo/vaccines/publications) and downloadable at <https://doi.org/10.7910/DVN/JTRI7A>.

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