

University of Groningen

## The ELIXIR Human Copy Number Variations Community

Salgado, David; Armean, Irina M; Baudis, Michael; Beltran, Sergi; Capella-Gutierrez, Salvador; Carvalho-Silva, Denise; Dominguez Del Angel, Victoria; Dopazo, Joaquin; Furlong, Laura I; Gao, Bo

*Published in:*  
 F1000Research

*DOI:*  
[10.12688/f1000research.24887.1](https://doi.org/10.12688/f1000research.24887.1)

**IMPORTANT NOTE:** You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

*Document Version*  
 Publisher's PDF, also known as Version of record

*Publication date:*  
 2020

[Link to publication in University of Groningen/UMCG research database](#)

*Citation for published version (APA):*

Salgado, D., Armean, I. M., Baudis, M., Beltran, S., Capella-Gutierrez, S., Carvalho-Silva, D., Dominguez Del Angel, V., Dopazo, J., Furlong, L. I., Gao, B., Garcia, L., Gerloff, D., Gut, I., Gyenesei, A., Habermann, N., Hancock, J. M., Hanauer, M., Hovig, E., Johansson, L. F., ... Bérout, C. (2020). The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. *F1000Research*, 9, [1229]. <https://doi.org/10.12688/f1000research.24887.1>

### Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: <https://www.rug.nl/library/open-access/self-archiving-pure/taverne-amendment>.

### Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.



## OPINION ARTICLE

# The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research [version 1; peer review: 2 approved]

David Salgado <sup>1</sup>, Irina M. Armean<sup>2</sup>, Michael Baudis <sup>3</sup>, Sergi Beltran<sup>4,5</sup>, Salvador Capella-Gutierrez <sup>6,7</sup>, Denise Carvalho-Silva <sup>2,8</sup>, Victoria Dominguez Del Angel <sup>9</sup>, Joaquin Dopazo <sup>10</sup>, Laura I. Furlong <sup>11</sup>, Bo Gao <sup>3</sup>, Leyla Garcia <sup>2,12,13</sup>, Dietlind Gerloff<sup>14</sup>, Ivo Gut<sup>4,5</sup>, Attila Gyenesi<sup>15</sup>, Nina Habermann<sup>16</sup>, John M. Hancock <sup>13</sup>, Marc Hanauer<sup>17</sup>, Eivind Hovig <sup>18,19</sup>, Lennart F. Johansson<sup>20</sup>, Thomas Keane<sup>2</sup>, Jan Korbel<sup>16</sup>, Katharina B. Lauer <sup>13</sup>, Steve Laurie<sup>4</sup>, Brane Leskošek<sup>21</sup>, David Lloyd <sup>13</sup>, Tomas Marques-Bonet<sup>22</sup>, Hailiang Mei<sup>23</sup>, Katalin Monostory<sup>24</sup>, Janet Piñero <sup>11</sup>, Krzysztof Poterlowicz <sup>25</sup>, Ana Rath<sup>17</sup>, Pubudu Samarakoon<sup>26</sup>, Ferran Sanz<sup>11</sup>, Gary Saunders <sup>13</sup>, Daoud Sie<sup>27</sup>, Morris A. Swertz<sup>20</sup>, Kirill Tsukanov <sup>2</sup>, Alfonso Valencia<sup>6,7,28</sup>, Marko Vidak<sup>21</sup>, Cristina Yenyxe González<sup>2</sup>, Bauke Ylstra<sup>29</sup>, Christophe Bérout<sup>1,30</sup>

<sup>1</sup>Aix Marseille Univ, INSERM, MMG, Marseille, France

<sup>2</sup>European Molecular Biology Laboratory, European Bioinformatics Institute, Wellcome Genome Campus, Hinxton, UK

<sup>3</sup>Department of Molecular Life Sciences and Swiss Institute of Bioinformatics, University of Zurich, Zurich, Switzerland

<sup>4</sup>CNAG-CRG, Centre for Genomic Regulation (CRG), Barcelona Institute of Science and Technology (BIST), Baldiri Reixac 4, Barcelona 08028, Spain

<sup>5</sup>Universitat Pompeu Fabra (UPF), Barcelona, Spain

<sup>6</sup>Barcelona Supercomputing Center (BSC), Barcelona, Spain

<sup>7</sup>Spanish National Bioinformatics Institute (INB)/ELIXIR-ES, Barcelona, Spain

<sup>8</sup>Open Targets, Wellcome Genome Campus, Hinxton, Cambridgeshire, CB10 1SD, UK

<sup>9</sup>Institut Français de Bioinformatique, UMS3601-CNRS, CNRS, Paris, France

<sup>10</sup>Clinical Bioinformatics Area, Fundación Progreso y Salud, CDCA, Hospital Virgen del Rocío, Sevilla, Spain

<sup>11</sup>Research Programme on Biomedical Informatics (GRIB), Hospital del Mar Medical Research Institute (IMIM), Department of Experimental and Health Sciences, Pompeu Fabra University (UPF), Barcelona, Spain

<sup>12</sup>ZB MED Information Centre for Life Sciences, Cologne, Germany

<sup>13</sup>ELIXIR Hub, Hinxton, UK

<sup>14</sup>Luxembourg Centre for Systems Biomedicine, University of Luxembourg, Belvaux, Luxembourg

<sup>15</sup>Szentágothai Research Center, University of Pécs, Pécs, Hungary

<sup>16</sup>Genome Biology, European Molecular Biological Laboratory, Heidelberg, Germany

<sup>17</sup>Orphanet, INSERM, Paris, France

<sup>18</sup>Department of Tumor Biology, Institute for Cancer Research, Oslo University Hospital, Oslo, Norway

<sup>19</sup>Centre for bioinformatics, Department of Informatics, University of Oslo, Oslo, Norway

<sup>20</sup>Department of Genetics, University of Groningen, University Medical Center Groningen, Groningen, The Netherlands

<sup>21</sup>Faculty of Medicine - ELIXIR Slovenia, University of Ljubljana, Ljubljana, Slovenia

<sup>22</sup>Institute of Evolutionary Biology (UPF-CSIC), Catalan Institution for Research and Advanced Studies, Barcelona, Spain

<sup>23</sup>Sequencing Analysis Support Core, Leiden University Medical Center, Leiden, The Netherlands

<sup>24</sup>Institute of Enzymology, Research Centre for Natural Sciences, Budapest, Hungary

<sup>25</sup>Centre for Skin Sciences, University of Bradford, Bradford, UK

<sup>26</sup>

Department of Medical Genetics, Oslo University Hospital, Oslo, Norway

<sup>27</sup>Department of Clinical Genetics, Cancer Center Amsterdam, Amsterdam UMC, Vrije Universiteit Amsterdam, Amsterdam, The Netherlands

<sup>28</sup>Catalan Institution of Research and Advanced Studies, Barcelona, Spain

<sup>29</sup>Department of Pathology, Cancer Center Amsterdam, Amsterdam UMC, Vrije Universiteit Amsterdam, Amsterdam, The Netherlands

<sup>30</sup>Département de Génétique Médicale et de Biologie Cellulaire, APHM, Hôpital d'enfants de la Timone, 13385 Marseille, France

**V1** First published: 13 Oct 2020, 9(ELIXIR):1229  
<https://doi.org/10.12688/f1000research.24887.1>

Latest published: 13 Oct 2020, 9(ELIXIR):1229  
<https://doi.org/10.12688/f1000research.24887.1>

### Abstract

Copy number variations (CNVs) are major causative contributors both in the genesis of genetic diseases and human neoplasias. While “High-Throughput” sequencing technologies are increasingly becoming the primary choice for genomic screening analysis, their ability to efficiently detect CNVs is still heterogeneous and remains to be developed. The aim of this white paper is to provide a guiding framework for the future contributions of ELIXIR’s recently established *human CNV Community*, with implications beyond human disease diagnostics and population genomics. This white paper is the direct result of a strategy meeting that took place in September 2018 in Hinxton (UK) and involved representatives of 11 ELIXIR Nodes. The meeting led to the definition of priority objectives and tasks, to address a wide range of CNV-related challenges ranging from detection and interpretation to sharing and training. Here, we provide suggestions on how to align these tasks within the ELIXIR Platforms strategy, and on how to frame the activities of this new ELIXIR Community in the international context.

### Keywords

Copy Number Variation, Data analysis, next-generation sequencing, whole genome sequencing, Human Genetics, Oncogenetics, Common Diseases, Federated Human Data



This article is included in the **ELIXIR** gateway.

### Open Peer Review

Reviewer Status  

Invited Reviewers

1

2

version 1



13 Oct 2020



report



report

1. **Antonio Rausell** , Université de Paris, INSERM UMR1163, Imagine Institute, Clinical Bioinformatics Laboratory, Paris, France AP-HP, Necker Hospital for Sick Children, F-75015, France
2. **Andrew Lonie** , University of Melbourne, Melbourne, Australia

Any reports and responses or comments on the article can be found at the end of the article.

**Corresponding authors:** David Salgado ([david.salgado@univ-amu.fr](mailto:david.salgado@univ-amu.fr)), Christophe Bérout ([christophe.beroud@inserm.fr](mailto:christophe.beroud@inserm.fr))

**Author roles:** **Salgado D:** Conceptualization, Funding Acquisition, Methodology, Project Administration, Resources, Software, Supervision, Validation, Writing – Original Draft Preparation, Writing – Review & Editing; **Armean IM:** Methodology, Writing – Review & Editing; **Baudis M:** Conceptualization, Funding Acquisition, Investigation, Methodology, Project Administration, Resources, Software, Supervision, Validation, Writing – Original Draft Preparation, Writing – Review & Editing; **Beltran S:** Methodology, Writing – Review & Editing; **Capella-Gutierrez S:** Conceptualization, Methodology, Writing – Review & Editing; **Carvalho-Silva D:** Conceptualization, Methodology, Writing – Review & Editing; **Dominguez Del Angel V:** Conceptualization, Methodology, Writing – Review & Editing; **Dopazo J:** Conceptualization, Methodology, Writing – Review & Editing; **Furlong LI:** Conceptualization, Methodology, Writing – Review & Editing; **Gao B:** Conceptualization, Methodology, Writing – Review & Editing; **Garcia L:** Conceptualization, Methodology, Writing – Review & Editing; **Gerloff D:** Conceptualization, Methodology, Writing – Review & Editing; **Gut I:** Conceptualization, Methodology, Writing – Review & Editing; **Gyenesi A:** Conceptualization, Methodology, Writing – Review & Editing; **Habermann N:** Conceptualization, Methodology, Writing – Review & Editing; **Hancock JM:** Conceptualization, Methodology, Writing – Review & Editing; **Hanauer M:** Conceptualization, Methodology, Writing – Review & Editing; **Hovig E:** Conceptualization, Methodology, Writing – Review & Editing; **Johansson LF:** Conceptualization, Methodology, Writing – Review & Editing; **Keane T:** Conceptualization, Methodology, Writing – Review & Editing; **Korbel J:** Conceptualization, Methodology, Writing – Review & Editing; **Lauer KB:** Conceptualization, Methodology, Writing – Review & Editing; **Laurie S:** Conceptualization, Methodology, Writing – Review & Editing; **Leskošek B:** Conceptualization, Methodology, Writing – Review & Editing; **Lloyd D:** Conceptualization, Methodology, Writing – Review & Editing; **Marques-Bonet T:** Conceptualization, Methodology, Writing – Review & Editing; **Mei H:** Conceptualization, Methodology, Writing – Review & Editing; **Monostory K:** Conceptualization, Methodology, Writing – Review & Editing; **Piñero J:** Conceptualization, Methodology, Writing – Review & Editing; **Poterlowicz K:** Conceptualization, Methodology, Writing – Review & Editing; **Rath A:** Conceptualization, Methodology, Writing – Review & Editing; **Samarakoon P:** Conceptualization, Methodology, Writing – Review & Editing; **Sanz F:** Conceptualization, Methodology, Writing – Review & Editing; **Saunders G:** Conceptualization, Funding Acquisition, Investigation, Methodology, Project Administration, Resources, Software, Supervision, Writing – Original Draft Preparation, Writing – Review & Editing; **Sie D:** Conceptualization, Methodology, Writing – Review & Editing; **Swertz MA:** Conceptualization, Methodology, Writing – Review & Editing; **Tsukanov K:** Conceptualization, Methodology, Writing – Review & Editing; **Valencia A:** Conceptualization, Methodology, Writing – Review & Editing; **Vidak M:** Conceptualization, Methodology, Writing – Review & Editing; **Yenyxe González C:** Conceptualization, Methodology, Writing – Review & Editing; **Ylstra B:** Conceptualization, Methodology, Writing – Review & Editing; **Bérout C:** Conceptualization, Funding Acquisition, Investigation, Methodology, Project Administration, Resources, Software, Supervision, Validation, Writing – Original Draft Preparation, Writing – Review & Editing

**Competing interests:** No competing interests were disclosed.

**Grant information:** The first ELIXIR hCNV Community meeting held in Hinxton (UK) was supported by ELIXIR. The authors declare that no grants were involved in supporting this work.

*The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.*

**Copyright:** © 2020 Salgado D *et al.* This is an open access article distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

**How to cite this article:** Salgado D, Armean IM, Baudis M *et al.* **The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research [version 1; peer review: 2 approved]** F1000Research 2020, 9(ELIXIR):1229 <https://doi.org/10.12688/f1000research.24887.1>

**First published:** 13 Oct 2020, 9(ELIXIR):1229 <https://doi.org/10.12688/f1000research.24887.1>

## Introduction

In the late 1950s, Tjio and Levan established that the human karyotype consists of 46 chromosomes<sup>1</sup>. This was promptly followed by the description of numerical chromosomal abnormalities in Down syndrome and, in less than one year, a new discipline emerged in the field of human genetics: “cytogenetics”<sup>2</sup>. Shortly after, somatic karyotype alterations were attributed to the identification of “Philadelphia chromosome” in the blood of Chronic Myeloid Leukemia patients<sup>3</sup>, which were found to be the result of specific underlying chromosomal rearrangements<sup>4</sup>. From then on, cytogenetics was not only applied to identify heritable chromosomal aberrations, but also established the field of “Cancer Cytogenetics”<sup>5</sup>, which led to a leap forward in approaching the molecular mechanisms of malignant diseases.

Since these early discoveries, multiple links between chromosomal alterations and diseases have been described. In parallel to those microscopic observations, the identification of the first genomic mutation in humans occurred in 1949 with the discovery of an amino acid change responsible for sickle cell anemia<sup>6</sup>, while the genetic alteration itself was identified only a few years later by Ingram<sup>7</sup>. Thanks to the rapidly advancing Sanger sequencing technology<sup>8</sup>, disease-causing genome variations are now routinely identified and confirmed. However, while both “cytogenetic” and “genomic” alterations in heritable human diseases and cancer are based on alterations of DNA sequence or structure, an epistemological dichotomy remained between the fields of molecular biology and genetics (targeting specific sequence alterations) and cytogenetics (focusing on genetic alterations detected by cytogenetic methods).

In the late 1980s, the development of DNA labeling techniques using the direct or indirect incorporation of fluorescent dyes<sup>9,10</sup> helped to establish the field of “molecular cytogenetics”, in which the hybridization of labeled DNA probes informs about characteristics of chromosomal substrates. Variations of the Fluorescent *In-Situ* Hybridization (FISH)<sup>11</sup> technology include interphase FISH (i.e. the hybridization of specific fluorescent probes on interphase nuclei) and reverse *in-situ* hybridization techniques<sup>8</sup>, in which the labeled DNA sample of interest is hybridized against a substrate consisting of normal metaphase chromosomes. While overall these technologies helped to put “the Genetics back into Cytogenetics”<sup>12</sup>, the development of Comparative Genomic Hybridization (CGH), a dual-color, whole-genome extension of the reverse *in-situ* hybridization concept was particularly instrumental in the delineation of a type of structural genome variations termed “Copy Number Variations” (CNVs). This category of genome variants encompasses those that range from a few hundred DNA base pairs to such affecting several megabases up to duplications or deletions involving whole chromosomes.

While abundant CNVs have been demonstrated to affect virtually every type of cancer<sup>13,14</sup>, they have also been shown to be a large contributor to inherited genome variation and have been shown to impact both genic and intergenic regions alike<sup>15</sup>.

Since the recognition of CNVs as contributors to the genomic variation landscape, multiple CNVs have been associated with

human traits and diseases. Recently, a review by Srebnik *et al.*<sup>16</sup> reported, in a meta-analysis of data from 10,314 fetuses, that CNVs were associated with an early-onset syndromic disorder in 0.37% (95% CI, 0.27-0.52%) of cases; with late-onset disease in 0.11% (95% CI, 0.05%-0.21%); and with diseases susceptibility in 0.30% (95% CI, 0.14-0.67%). The prevalence of early-onset syndromic disorders caused by CNVs was thus calculated to be 1:270<sup>16</sup>. In parallel, it has been known for years that CNVs account for the majority of disease-causing variation of some genes, as illustrated for example by the *DMD* gene, for which up to 74% and 87% of mutations are deletions or duplications of one or more exons, respectively, for Duchenne and Becker patients<sup>17</sup>. Additionally to their role in syndromic disorders, CNVs have also been associated with common, polygenic diseases such as obesity<sup>13,14</sup>, and mental disorders<sup>15,16</sup>.

CNVs are also a major contributor to the somatic mutation landscape in cancer. Specific deletion CNVs may lead to loss of heterozygosity events involving tumor suppressor genes, with a tumor promoting effect demonstrated early on for the somatic loss of wild-type alleles in many inherited cancer syndromes<sup>18</sup>. In contrast, proto-oncogenes, such as *MYCN* and *ERBB2*, are frequently deregulated through chromosomal amplification events, leading to over-expression of the gene products due to a highly increased genomic dosage<sup>19</sup>. However, while the association between individual duplication and deletion CNVs and tumor-related genes has been determined for many types of cancer, most types of malignancies show recurring CNV patterns with involvement of large genomic regions, beyond a limited number of cancer-associated gene loci.

CNV detection has been performed since the early 1990s using various generations of chromosomal (cCGH)<sup>20,21</sup> and array-based (aCGH)<sup>22,23</sup> CGH technologies, including high-density oligonucleotide arrays and Single Nucleotide Polymorphism (SNP) genotyping arrays<sup>24,25</sup>. The current generation of these hybridization technologies is still considered as ‘gold standard’ in order to fulfill the diagnostic needs of clinical cytogenetics laboratories. Their use is highly flexible, as it is easy to design custom arrays, including hundreds of thousands to millions of probes. It is thus possible to use the technology for genome-scale analysis through to region specific analysis.

However, these technologies also have limitations: for example, their inability to distinguish chromosomal abnormalities as tandem, inverted, or translocated duplications; and the probe hybridization process itself which may result in poor sensitivity and precision, depending on probe design and the quality of analyzed DNA. In parallel, it is not currently possible to simultaneously achieve a genome-wide level and a high resolution because of the limited density of the array probes. In addition, as was shown by Haraksingh *et al.*, the current generation of arrays still requires careful quantitative comparative analysis for researchers and clinicians to be able to select the appropriate tool for a given application<sup>26</sup>.

Today, emerging Next-Generation Sequencing (NGS) technologies, especially deep coverage Whole Genome Sequencing (WGS),

is quickly becoming the primary strategy for CNV detection in the study of human disease. Because of the ability of this technology to provide a nucleotide level resolution, it can theoretically solve the limitations observed for array-based technologies, and also provide the exact boundaries and localization for a given CNV.

Nevertheless, due to the demanding data analysis workflows and high costs of deep coverage WGS experiments, many laboratories have implemented either low coverage WGS, or the Whole Exome Sequencing (WES) based approach for CNV detection (which stands between array-based approaches and deep WGS). Thus, when targeting the classes of inherited and somatic genome alterations subsumed as CNV for research and clinical applications, one faces a heterogeneous field encompassing different experimental technologies and related bioinformatics methods for data analysis, without a clear ‘gold standard’ serving all heterogeneous applications. Despite these technical challenges, the CNV field is of primary importance for human disease diagnosis and research, including the field of cancer genetics.

In this context, in February 2018, ELIXIR-FR and ELIXIR-ES initiated the creation of the “ELIXIR human CNV Community” (hCNV Community) as a starting point for consolidating this field at the European level, and beyond. The first hCNV Community meeting “The future of hCNV in ELIXIR” took place in Hinxton (UK), as a general, strategically focused, meeting to discuss, prioritize, and map the future of hCNV related activities in ELIXIR. In this white paper, we first summarize the main conclusions of the meeting, and then explain possible future directions for the incorporation of human CNV activities across ELIXIR.

### Meeting: “The Elixir Human Cnv Community”

The initial face-to-face meeting of the ELIXIR human CNV Community took place on September 28<sup>th</sup>, 2018 in Hinxton (UK). Attendance was open to any member from any ELIXIR Node, with the limitation of 25 participants at maximum. Remote participation (via teleconference) was offered to those that wished to attend but could not do so in person. There were 21 attendees at the meeting, representing 11 ELIXIR Nodes: EMBL-EBI, France, Germany, Hungary, Luxembourg, Netherlands, Norway, Slovenia, Spain, Switzerland, United Kingdom, and there were also two representatives from the ELIXIR Hub. The meeting started with a presentation from Gary Saunders (ELIXIR Human Data Communities coordinator) who provided a general overview of the current ELIXIR Communities and activities. This initial talk was followed by a series of presentations where each Node summarized their ongoing activities and expertise related to hCNV research. The remainder of the meeting was devoted to an open discussion on the challenges of CNVs and how to address them through activities and tasks building on ELIXIR partners’ experience(s). Each activity was mapped to at least one of the five ELIXIR Platforms (Data, Tools, Interoperability, Compute, and Training). In addition, the potential interaction of the hCNV Community with the other ELIXIR Communities and international initiatives was discussed.

## Outcomes and discussion

### Identification of key activities to address CNV challenges

The field of human CNV research is complex and evolving; activities range from CNV detection to their interpretation as potentially pathogenic to common genomic background variation. To simplify this process analysis, seven objectives have been defined by the ELIXIR hCNV Community:

#### **Objective #1: optimal CNV detection pipelines**

Multiple publications have reported pipelines to detect CNV using micro-array, WES or WGS data<sup>27,28</sup>. Nevertheless, as reported by Zare *et al.*<sup>29</sup>, who evaluated the performance of various CNV detection tools in cancer, there is a low consensus among the tools in calling CNVs, especially from widely used WES experiments: a moderate sensitivity (50 to 80%); a fair specificity (70 to 94%) and a poor false discovery rate (27 to 60%). Similar results were reported by Yao *et al.*<sup>30</sup> who concluded that read-depth based programs are still immature for WES-based CNV detection with a low sensitivity and an uncertain specificity. Comparable experiences were revealed by participants of the ELIXIR hCNV workshop, and it was concluded that, even if micro-array technologies provide overall better CNV detection parameters, the wide adoption of NGS technologies represents a true challenge for the accurate detection of CNV. Based on these observations, the need for an extensive assessment and benchmarking of existing tools was established as one of the working areas of the hCNV Community. The objective will be to release a set of sensitive and reliable pipelines, optimized and validated to detect CNV from various high throughput datasets. These pipelines will be available either through ELIXIR compute nodes and/or as stand-alone solutions. Considering the actual performances of available systems, it is anticipated that we will provide a portfolio of tools, each being useful for a specific situation: CNV type; detection technology; disease context.

To reach this objective, three tasks are proposed:

*Task #1.1* will establish the list of available pipelines/software as well as partners’ local solutions to detect CNV from gene panels, WES, low and deep coverage WGS, array CGH, and SNP arrays.

*Task #1.2* will benchmark these systems using datasets from Objective #2 to select the most sensitive, specific, reliable, and rapid systems for each dataset for germline and somatic CNVs. Note that if no system is efficient enough for some conditions, the hCNV partners will develop new system(s) to address community needs. The CNV field is very dynamic and multiple systems are released monthly. We therefore expect to be able to select a combination of tools that will provide enough efficiency to be used for research purposes and eventually diagnostics.

*Task #1.3* will optimize the selected pipelines from Task #1.2 to increase performance on ELIXIR compute nodes and define optimal parameters and guidelines to help end-users to efficiently and reliably detect CNV in various situations through the ELIXIR training platform.

**Objective #2: definition of reference datasets**

The ambition is to produce reference datasets of fully validated somatic and germline CNVs representing a wide range of sample types and experimental technologies. The aim is to provide reference materials available to the community for the comparison and evaluation of pipelines and/or NGS technologies and/or for quality assurance. This will include both digital raw data and, potentially, biomaterials.

To do so, the hCNV Community will establish reference datasets including various CNV (deletions and duplications) of various sizes ranging from a single exon CNV to large genomic rearrangements. Two subsets will be defined for germline and somatic CNVs. These datasets will contain samples with fully validated CNVs by other approaches such as multiplex ligation-dependent probe amplification and quantitative or semi-quantitative PCR. Four tasks are proposed:

*Task #2.1* will be dedicated to WES reference datasets.

*Task #2.2* will be dedicated to WGS reference datasets.

*Task #2.3* will be dedicated to gene panels reference datasets.

*Task #2.4* will be dedicated to CGH/SNP microarrays reference datasets.

During the strategic workshop in Hinxton, participants discussed the GDPR and its impact on reference human datasets. The participation of lawyers and ethics specialists is therefore needed, and this was proposed to be addressed at a more global level by the ELIXIR Human Data Communities as a whole. In case no human reference dataset could be exchanged at a community level, alternatives using other model organisms have been proposed.

As previously mentioned, the NGS technologies are rapidly evolving and therefore the reference datasets will need to be regularly updated.

In the context of tools metrology, i.e. efficiency evaluation and improvement of detection, the Genome in a Bottle initiative has released a set of reference materials which has already been largely used for Short Nucleotide Variation(s) (SNV)<sup>28,29</sup>. In a recent paper, Zook *et al.*<sup>31</sup> reported the use of a new reference dataset for germline structural variant detection including CNV<sup>32,33</sup>. We will therefore adopt these reference samples and use them with all technologies to produce reference datasets.

**Objective #3: data exchange formats**

International collaborative projects require harmonization and standardization of results in order to ensure efficient data aggregation and comparison. Although various international initiatives, such as the GA4GH Genomic Knowledge Standards and Large Scale Genomics Work Streams, are currently addressing aspects of this issue, no robust and exhaustive standard CNV annotation format has emerged so far. To address this issue, the hCNV community identified two tasks:

*Task #3.1* will establish the list of existing formats to describe CNVs and list common and specific features.

*Task #3.2* will develop recommendations to use a standardized format to report CNVs. If a few alternative formats are frequently used, it will provide bioinformatics resources to convert data into the common data exchange format.

hCNV partners notably discussed the adoption of the VCF format and its current limitations for the CNV field. It was concluded that, although this format is well-known by molecular biologists and could therefore be a starting point, it is less frequently used by cytogeneticists. There is therefore a strong need to improve this format and identify other nomenclatures and widely used formats in other communities. It is being recognized that any development or improvement of standards for CNV annotation should be performed in alignment with existing efforts, notably GA4GH work streams and the ELIXIR Interoperability Platform.

**Objective #4: identification of patients with similar genotypes and phenotypes**

Finding similar cases at the clinical level is a key component of clinical diagnosis and research to identify disease-causing genes and to explain genotype/phenotype correlations and intermediate clinical phenotypes. Although perhaps straightforward in the case of common diseases, this is much more of a challenge for the millions of patients affected by a rare disease, as routinely each case is similar only to a handful of patients across Europe. Within the Discovery Work Stream of GA4GH there are standards, such as Beacon<sup>34</sup>, to establish a federated data discovery network that is able to connect databases of genomic variations and phenotypic data using a common application programming interface (API). The GA4GH Driver Project “ELIXIR Beacons” provides a schema definition and API, together with a reference implementation to allow data owners to add their resources to the Beacon Network, as simply as possible (<https://beacon-project.io>). With the recent addition of CNV representation to the Beacon API and planned ontology-based phenotype queries the Beacon ecosystem represents a prime target for the implementation of (CNV related) genotype-phenotype representation and querying. The hCNV group will work towards enabling its use for the envisioned patient discovery, through the support of extended clinical descriptions including enabling and testing of relevant annotation standards (e.g. HPO, NCI, additional ontologies). To do so:

*Task #4.1* will select ontologies required to efficiently capture phenotypic description useful for data interpretation for any genetic disease.

*Task #4.2* will provide lists of common data elements that should be provided in various situations such as rare disease, oncology, or common diseases.

Various ELIXIR hCNV partners are already strongly involved in the development of ontologies, such as HPO<sup>35</sup> and ORDO<sup>36</sup> and in the mapping of various ontologies, medical

terminologies, vocabularies and nomenclatures. In addition, national databases described in Objective #6, will not only be FAIRified (see below) but also adopt the recommendations from Objective #4 to ensure cross queries and the identification of similar patients.

#### **Objective #5: creation of innovative tools**

CNVs often involve large genomic regions encompassing multiple genes. In addition, in recessive diseases, CNVs can alter one allele of a specific locus, whilst the second could be altered by SNV. In many situations, it is therefore difficult to identify the single, or multiple, genes harboring variation that is directly associated with a particular phenotype.

The hCNV Community will develop innovative tools to: annotate CNV; facilitate their interpretation through a combinatorial approach; and help to pinpoint key genes in regions of interest. The following tasks have been identified and will most likely evolve as more data become available and as technologies evolve:

*Task #5.1* will define CNV annotations including: type; genotype; genes and transcripts; expression level; exons; regulatory elements; breakpoints/ fusion fragments for WGS only (allowing detection of tandem duplications vs. inverted duplications and translocations).

*Task #5.2* will develop a specific pipeline to interpret duplications as tandem, inverted or translocation duplications may result in very different phenotypes.

*Task #5.3* will develop specific bioinformatics tools to select candidate genes localized in the CNV region by combining genes' annotations and patients' phenotype.

#### **Objective #6: FAIRification of hCNV services and datasets**

Various CNV national databases, ELIXIR Core Data Resources, and ELIXIR Deposition Databases are currently being developed by ELIXIR hCNV partners. In order to allow interoperability (including discovery), the FAIR principles (Findable, Accessible, Interoperable, Reusable)<sup>37,38</sup> will be applied to those systems to demonstrate the feasibility and utility of distributed CNV databases. This will respect databases' ownerships and national regulations' compliance while allowing searching for similar patients across the network. To respect and follow these principles, we will ensure that data are:

##### (i) Findable:

- The data should contain globally unique, resolvable and persistent identifiers.
- Include machine-readable descriptions to support structured search and filtering.

##### (ii) Accessible:

- Metadata has to be accessible beyond the lifetime of the digital resource (e.g. using BioSchemas).

- Clearly defined regarding the condition for access and security protocols for sharing and accessing data.

##### (iii) Interoperable:

- Usage of a specific file format
- Extensible machine interpretable formats for data and metadata (e.g. YAML files, JSON-LD)
- Use vocabularies (ontologies) and link with other robust resources
- Integration with FAIR resources

##### (iv) Reusable:

- Provide licensing, provenance and description on community-standards.

*Task #6.1* will use the French BANCCO database (<http://bancco.fr>) developed at Aix Marseille University and the CIB-ERER (Spanish network for research in rare diseases) database developed at the Fundación Progreso y Salud of Sevilla prototypes to demonstrate the benefits of using the FAIR data principles for CNV in diagnostic and research contexts.

*Task #6.2* will extend the FAIRification to other non-specific CNV databases such as the European Variation Archive (EVA), RD-CONNECT, arrayMap<sup>39</sup> and Database of Genomics Variants Archive (DGVa).

#### **Objective #7: dissemination**

The global adoption of tools and guidelines is strongly linked to the ability to communicate, produce training materials, and train actors as well as patients and the general public.

*Task #7.1* will set-up Jamborees to gather experts' point of view on the various objectives and related tasks and developments.

*Task #7.2* will set-up regular hackathons to ensure smooth developments and benchmarks by various ELIXIR Nodes.

*Task #7.3* will promote the ELIXIR hCNV Community through participation at international meetings, such as GA4GH Plenary. A contact has already been established with the Human Genome Variation Society (HGVS) (see below).

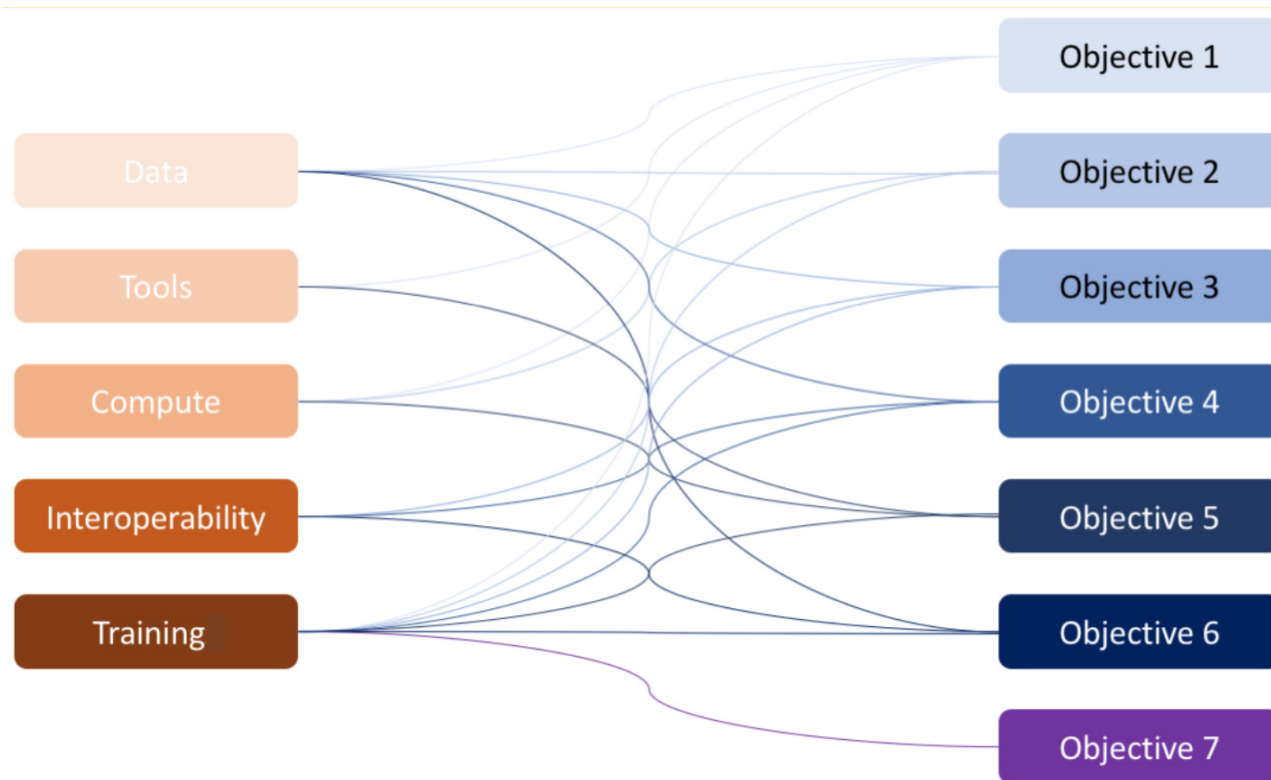
#### **Alignment with ELIXIR Platforms**

The ELIXIR hCNV Community's objectives have many links to the activities of the ELIXIR Platforms (Figure 1).

#### **Data Platform**

The aims of this Platform have been described as to drive the use, re-use, and value of life science data. It aims to do this by providing users with robust, long-term sustainable data resources within a coordinated, scalable and connected data ecosystem. Thus, the ELIXIR hCNV Community that will collect





**Figure 1. Interactions of the hCNV Community objectives with the ELIXIR platforms.** Left: ELIXIR Platforms; Right: ELIXIR hCNV Community objectives.

high quality genetic and phenotypic data will establish strong links with the ELIXIR Data Platform by providing Deposition Databases for CNV; and by benefiting from literature data integration and scalable curation provided by the Platform.

#### Tools and Compute Platforms

As described in Objectives #1 and #5, various reference tools will be validated and/or created by the ELIXIR hCNV Community. Their promotion will be facilitated by inclusion in the “Tools and services registry” bio.tools (<https://bio.tools>)<sup>40</sup>. The activity related to benchmarking will be carried out within the “scientific benchmark and technical monitoring” infrastructure (OpenEbench) (<https://openebench.bsc.es>) and the ELIXIR Compute Platform. In addition, tools will be made interoperable and shall be included as Galaxy workflows<sup>41</sup> and available to the community through the “Cloud and Computing Resources” from the ELIXIR Compute Platform.

#### Interoperability Platform

Key to ELIXIR hCNV Community Objective #3 is the development of recommendations to use standardized format(s) to report CNVs. Additionally, Objective #4 will work to extend and harmonize the use of ontologies across the ELIXIR hCNV Community. Both of these objectives align with the “Interoperability with a Purpose at Source” task of the ELIXIR Interoperability Platform Programme for 2019-23.

More generally, in Objective #6, interoperability will be a major component of the hCNV Community. CNV FAIR databases will therefore strongly interact with the ELIXIR Interoperability Platform at multiple levels.

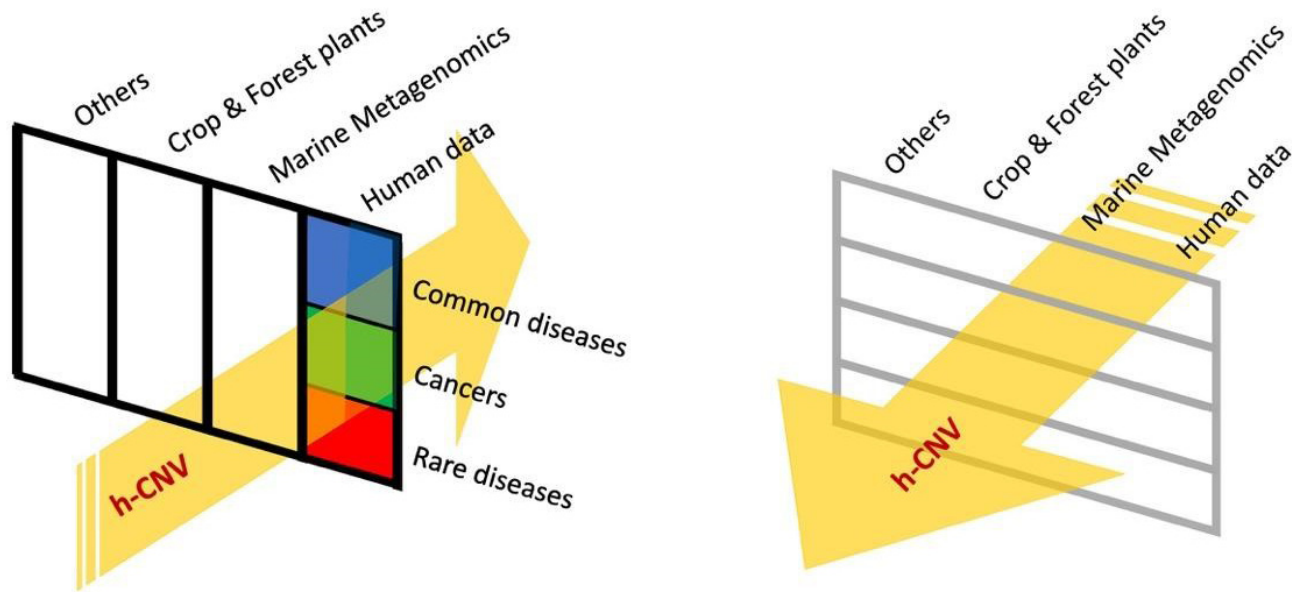
#### Training Platform

Finally, the global recognition of the ELIXIR hCNV Community’s achievements will only be made possible through training, capacity building, and dissemination. A strong link has already been established with this ELIXIR Platform for training coordination and additional collaborations including capacity building will be established as systems, databases and tools are released.

#### Alignment with other ELIXIR Communities

CNVs are genetic mutations found in all organisms. The ELIXIR hCNV Community will naturally strongly interact with the “Federated Human Data” and “Rare Diseases” ELIXIR Communities (Figure 2). Moreover, the hCNV community will benefit from the “Federated Human Data” Community thanks to its experience in human data secure access (GDPR) and ethical aspects (ELSI).

Going beyond these, interactions could be established with the ELIXIR Marine Metagenomics and Plant Sciences Communities in the longer term (Figure 2). In fact, the hCNV



**Figure 2. Interactions of the hCNV Community with the ELIXIR Communities.** Left: vertical interaction with all of the current ELIXIR Human Data Communities (Federated Human Data and Rare Diseases). Right: It is predicted that the ELIXIR hCNV Community will interact with other ELIXIR Communities, such as Marine Metagenomics and Plant Sciences; relationships to other ELIXIR Communities will be investigated and developed over time.

detection tools might allow the handling of CNV in plants and marine organisms. Its feasibility will be discussed with these Communities to allow optimal interactions.

In addition, the creation of pipelines and tools will link to the ELIXIR's Galaxy Community through the implementation of tools and training materials in their platform.

#### *Alignment with the ELIXIR Industry Programme*

Due to the known involvement in human disease, the topic hCNV is of considerable interest to the scientific industry, for example in the field of personalized medicine. It is therefore of critical importance to ensure that the services we provide are of sufficient quality and fit for purpose for adoption in industry as well as in academia. To facilitate knowledge exchange, we will continue to encourage the participation of industrial partners in the ELIXIR hCNV Community in the role of Community Partner(s). This novel form of engagement is anchored in the ELIXIR Scientific Programme 2019–23 and is part of a comprehensive initiative to embed ELIXIR into the wider ecosystem. Furthermore, we propose to use the ELIXIR Industry Staff Exchange program to allow members of the ELIXIR hCNV Community to work with industry partners on projects of mutual interest in the form of short-term staff exchanges.

#### *Integration at a global level*

As already described, the use of ontologies, nomenclatures and data exchange formats should be viewed in a more global context. In fact, this dimension has already been addressed by the ELIXIR hCNV Community's partners who have identified international projects and organizations with which

relationships will be established. Thus, the GA4GH organization will interact and benefit from the hCNV community at various levels. The International Rare Disease Research Consortium (IRDiRC) will not only benefit from the Community but will also be able to promote its achievements through its members and the "IRDiRC Recognized Resources" labeling program. HGVS has also been approached to participate to their scientific meetings to disseminate the community's achievements.

## **Conclusions**

We believe that this white paper demonstrates the global need for ELIXIR to establish the human Copy Number Variation Community (hCNV) as it responds to a major challenge of NGS data interpretation in the era of whole genome sequencing both for research and in clinical settings. To do so, we have identified seven objectives ranging from CNV detection to data interpretation and sharing, for which various tasks have been described. The interactions with ELIXIR Platforms and Communities, and worldwide integration in the complex landscape of societies, initiatives and projects, has been addressed to avoid duplication of efforts and ensure fruitful collaborations.

Finally, the growing interest for CNV detection and interpretation in human diseases will ensure the global recognition and expansion of the community and will trigger many interactions both for other ELIXIR Communities (such as Marine Metagenomics and Plant Sciences), and industry.

## **Data availability**

No data is associated with this article.

## References

1. Tjio JH, Levan A: **The Chromosome Number of Man.** *Hereditas.* 1956; **42**(1–2): 1–6.  
[PubMed Abstract](#) | [Publisher Full Text](#)
2. Jacobs PA: **An Opportune Life: 50 Years in Human Cytogenetics.** *Annu Rev Genomics Hum Genet.* 2014; **15**(1): 29–46.  
[PubMed Abstract](#) | [Publisher Full Text](#)
3. Nowell C: **The minute chromosome (Ph<sup>1</sup>) in chronic granulocytic leukemia.** *Blut Z Für Gesamte Blutforsch.* 1962; **8**(2): 65–6.  
[PubMed Abstract](#) | [Publisher Full Text](#)
4. Rowley JD: **A New Consistent Chromosomal Abnormality in Chronic Myelogenous Leukaemia identified by Quinacrine Fluorescence and Giemsa Staining.** *Nature.* 1973; **243**(5405): 290–3.  
[PubMed Abstract](#) | [Publisher Full Text](#)
5. Levan A: **Some Current Problems of Cancer Cytogenetics.** *Hereditas.* 1967; **57**(3): 343–55.  
[PubMed Abstract](#) | [Publisher Full Text](#)
6. Pauling L, Itano HA, Singer SJ, *et al.*: **Sickle Cell Anemia, a Molecular Disease.** *Science.* 1949; **110**(2865): 543–8.  
[PubMed Abstract](#) | [Publisher Full Text](#)
7. Ingram VM: **Gene mutations in human haemoglobin: the chemical difference between normal and sickle cell haemoglobin.** *Nature.* 1957; **180**(4581): 326–8.  
[PubMed Abstract](#) | [Publisher Full Text](#)
8. Sanger F, Nicklen S, Coulson AR: **DNA sequencing with chain-terminating inhibitors.** *Proc Natl Acad Sci U S A.* 1977; **74**(12): 5463–7.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
9. Pinkel D, Gray JW, Trask B, *et al.*: **Cytogenetic analysis by in situ hybridization with fluorescently labeled nucleic acid probes.** *Cold Spring Harb Symp Quant Biol.* 1986; **51 Pt 1**: 151–7.  
[PubMed Abstract](#) | [Publisher Full Text](#)
10. Lichter P, Cremer T, Borden J, *et al.*: **Delineation of individual human chromosomes in metaphase and interphase cells by in situ suppression hybridization using recombinant DNA libraries.** *Hum Genet.* 1988; **80**(3): 224–34.  
[PubMed Abstract](#) | [Publisher Full Text](#)
11. Le Beau MM: **One FISH, two FISH, red FISH, blue FISH.** *Nat Genet.* 1996; **12**(4): 341–4.  
[PubMed Abstract](#) | [Publisher Full Text](#)
12. Ferguson-Smith MA: **Putting the genetics back into cytogenetics.** *Am J Hum Genet.* 1991; **48**(2): 179–82.  
[PubMed Abstract](#) | [Free Full Text](#)
13. Beroukhi R, Mermel CH, Porter D, *et al.*: **The landscape of somatic copy-number alteration across human cancers.** *Nature.* 2010; **463**(7283): 899–905.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
14. Baudis M: **Genomic imbalances in 5918 malignant epithelial tumors: an explorative meta-analysis of chromosomal CGH data.** *BMC Cancer.* 2007; **7**: 226.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
15. Zarrei M, MacDonald JR, Merico D, *et al.*: **A copy number variation map of the human genome.** *Nat Rev Genet.* 2015; **16**(3): 172–83.  
[PubMed Abstract](#) | [Publisher Full Text](#)
16. Srebniak MI, Joosten M, Knäpen MFCM, *et al.*: **Frequency of submicroscopic chromosomal aberrations in pregnancies without increased risk for structural chromosomal aberrations: systematic review and meta-analysis.** *Ultrasound Obstet Gynecol.* 2018; **51**(4): 445–52.  
[PubMed Abstract](#) | [Publisher Full Text](#)
17. Tuffery-Giraud S, Bérout C, Leturcq F, *et al.*: **Genotype-phenotype analysis in 2,405 patients with a dystrophinopathy using the UMD-DMD database: a model of nationwide knowledgebase.** *Hum Mutat.* 2009; **30**(6): 934–45.  
[PubMed Abstract](#) | [Publisher Full Text](#)
18. Ryland GL, Doyle MA, Goode D, *et al.*: **Loss of heterozygosity: what is it good for?** *BMC Med Genomics.* 2015; **8**: 45.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
19. Wee Y, Wang T, Liu Y, *et al.*: **A pan-cancer study of copy number gain and up-regulation in human oncogenes.** *Life Sci.* 2018; **211**: 206–14.  
[PubMed Abstract](#) | [Publisher Full Text](#)
20. Kallioniemi A, Kallioniemi OP, Sudar D, *et al.*: **Comparative genomic hybridization for molecular cytogenetic analysis of solid tumors.** *Science.* 1992; **258**(5083): 818–21.  
[PubMed Abstract](#) | [Publisher Full Text](#)
21. Joos S, Scherthan H, Speicher MR, *et al.*: **Detection of amplified DNA sequences by reverse chromosome painting using genomic tumor DNA as probe.** *Hum Genet.* 1993; **90**(6): 584–9.  
[PubMed Abstract](#) | [Publisher Full Text](#)
22. Solinas-Toldo S, Lampel S, Stigenbauer S, *et al.*: **Matrix-based comparative genomic hybridization: Biochips to screen for genomic imbalances.** *Genes Chromosomes Cancer.* 1997; **20**(4): 399–407.  
[PubMed Abstract](#) | [Publisher Full Text](#)
23. Pinkel D, Seagraves R, Sudar D, *et al.*: **High resolution analysis of DNA copy number variation using comparative genomic hybridization to microarrays.** *Nat Genet.* 1998; **20**(2): 207.  
[PubMed Abstract](#) | [Publisher Full Text](#)
24. Wang DG, Fan JB, Siao CJ, *et al.*: **Large-Scale Identification, Mapping, and Genotyping of Single-Nucleotide Polymorphisms in the Human Genome.** *Science.* 1998; **280**(5366): 1077–82.  
[PubMed Abstract](#) | [Publisher Full Text](#)
25. Zhao X, Li C, Paez JG, *et al.*: **An integrated view of copy number and allelic alterations in the cancer genome using single nucleotide polymorphism arrays.** *Cancer Res.* 2004; **64**(9): 3060–71.  
[PubMed Abstract](#) | [Publisher Full Text](#)
26. Haraksingh RR, Abyzov A, Urban AE: **Comprehensive performance comparison of high-resolution array platforms for genome-wide Copy Number Variation (CNV) analysis in humans.** *BMC Genomics.* 2017; **18**(1): 321.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
27. Carter NP: **Methods and strategies for analyzing copy number variation using DNA microarrays.** *Nat Genet.* 2007; **39**(7 Suppl): S16–21.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
28. Zhao M, Wang Q, Wang Q, *et al.*: **Computational tools for copy number variation (CNV) detection using next-generation sequencing data: features and perspectives.** *BMC Bioinformatics.* 2013; **14**(Suppl 11): S1.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
29. Zare F, Dow M, Monteleone N, *et al.*: **An evaluation of copy number variation detection tools for cancer using whole exome sequencing data.** *BMC Bioinformatics.* 2017; **18**: 286.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
30. Yao R, Zhang C, Yu T, *et al.*: **Evaluation of three read-depth based CNV detection tools using whole-exome sequencing data.** *Mol Cytogenet.* 2017; **10**: 30.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
31. Zook JM, McDaniel J, Olson ND, *et al.*: **An open resource for accurately benchmarking small variant and reference calls.** *Nat Biotechnol.* 2019; **37**(5): 561–566.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
32. Krusche P, Trigg L, Boutros PC, *et al.*: **Best practices for benchmarking germline small-variant calls in human genomes.** *Nat Biotechnol.* 2019; **37**(5): 555–560.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
33. Zook JM, Hansen NF, Olson ND, *et al.*: **A robust benchmark for germline structural variant detection.** *bioRxiv.* 2019; 664623.  
[Publisher Full Text](#)
34. Raisaro JL, Tramèr F, Ji Z, *et al.*: **Addressing Beacon re-identification attacks: quantification and mitigation of privacy risks.** *J Am Med Inform Assoc.* 2017; **24**(4): 799–805.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
35. Köhler S, Vasilevsky NA, Engelstad M, *et al.*: **The Human Phenotype Ontology in 2017.** *Nucleic Acids Res.* 2017; **45**(D1): D865–76.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
36. Rath A, Olry A, Dhombres F, *et al.*: **Representation of rare diseases in health information systems: The orphanet approach to serve a wide range of end users.** *Hum Mutat.* 2012; **33**(5): 803–8.  
[PubMed Abstract](#) | [Publisher Full Text](#)
37. Holub P, Kohlmayer F, Prasser F, *et al.*: **Enhancing Reuse of Data and Biological Material in Medical Research: From FAIR to FAIR-Health.** *Biopreserv Biobank.* 2018; **16**(2): 97–105.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
38. Wilkinson MD, Dumontier M, Aalbersberg IJJ, *et al.*: **The FAIR Guiding Principles for scientific data management and stewardship.** *Sci Data.* 2016; **3**: 160018.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
39. Cai H, Kumar N, Baudis M: **arrayMap: A Reference Resource for Genomic Copy Number Imbalances in Human Malignancies.** *PLoS One.* 2012; **7**(5): e36944.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)
40. Ison J, Ménager H, Brancotte B, *et al.*: **Community curation of bioinformatics software and data resources.** *Brief Bioinform.* 2019; bbz075.  
[PubMed Abstract](#) | [Publisher Full Text](#)
41. Doppelt-Azeroual O, Mareuil F, Deveaud E, *et al.*: **ReGaTE: Registration of Galaxy Tools in Elixir.** *GigaScience.* 2017; **6**(6): 1–4.  
[PubMed Abstract](#) | [Publisher Full Text](#) | [Free Full Text](#)

# Open Peer Review

Current Peer Review Status:  

---

Version 1

Reviewer Report 20 July 2021

<https://doi.org/10.5256/f1000research.27459.r88724>

© 2021 Lonie A. This is an open access peer review report distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.



**Andrew Lonie** 

University of Melbourne, Melbourne, Vic, Australia

Overall this is an excellent proposal and I only have minor grammatical suggestions. The science case is strong and is described well; the approach is well thought through and well articulated. This would be a very worthwhile ELIXIR community.

### Minor suggestions:

*Meeting: "The Elixir Human Cnv Community"*

CNV should be properly capitalised here, as should 'ELIXIR'. And in the previous paragraph, "The Elixir Human Cnv Community" is already introduced and acronymed as 'hCNV Community'.

Throughout the document, sometimes 'ELIXIR hCNV Community' is used, sometimes 'hCNV Community', sometimes hCNV. Would be best to standardise.

*Objective #1:* It would be good to discuss how pipelines will be made available for the entire community. It's a complex problem, in practice.

*Objective #2:* It would be good to discuss how the reference datasets will be made available in a FAIR way to the global community.

*Objective #3:* "Task #3.2 will develop recommendations to use a standardized format to report CNVs. If a few alternative formats are frequently used, it will provide bioinformatics resources to convert data into the common data exchange format." - this sentence doesn't make sense.

*Objective #5:* "The hCNV Community will develop innovative tools to: annotate CNV; facilitate their interpretation through a combinatorial approach; and help to pinpoint key genes in regions of interest. The following tasks have been identified and will most likely evolve as more data become available and as technologies evolve:"

It should be.

"The hCNV Community will develop innovative tools to annotate CNVs, facilitate their interpretation through a combinatorial approach, and help to pinpoint key genes in regions of interest.

The following tasks have been identified and will most likely evolve as more data become available and as technologies evolve:"

"*Task #5.1* will define CNV annotations including: type; genotype; genes and transcripts; expression level; exons; regulatory elements; breakpoints/ fusion fragments for WGS only" - remove the space after "breakpoints/".

"*Task #5.3* will develop specific bioinformatics tools to select candidate genes localized in the CNV region by combining genes' annotations and patients' phenotype." - this reads a bit strangely. Candidate genes for what? I assume specific rare diseases?

*Objective #6*: "This will respect databases' ownerships and national regulations' compliance" - there should be no trailing apostrophe after regulations; the compliance does not belong to the regulations.

Nothing much said about FAIRness of all the other artefacts that will be produced (workflows, standards)...

"*Alignment with other ELIXIR Communities*  
CNVs are genetic mutations..."

Maybe this is better:  
"*Alignment with other ELIXIR Communities*  
CNVs are genetic variations..."

"*Conclusions*": Again, would be good to standardise on a particular nomenclature of hCNV / hCNV Community / ELIXIR hCNV Community / human Copy number Variation Community and stick with it from the start.

**In summary, this is a very worthwhile community and my comments are generally minor and by way of expression clarifications.**

**Is the topic of the opinion article discussed accurately in the context of the current literature?**

Yes

**Are all factual statements correct and adequately supported by citations?**

Yes

**Are arguments sufficiently supported by evidence from the published literature?**

Yes

**Are the conclusions drawn balanced and justified on the basis of the presented arguments?**

Yes

**Competing Interests:** No competing interests were disclosed.

**Reviewer Expertise:** Bioinformatics, bioinformatics infrastructure, genomics, genetics

**I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.**

Reviewer Report 22 March 2021

<https://doi.org/10.5256/f1000research.27459.r74635>

© 2021 Rausell A. This is an open access peer review report distributed under the terms of the [Creative Commons Attribution License](#), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.



**Antonio Rausell** 

<sup>1</sup> Université de Paris, INSERM UMR1163, Imagine Institute, Clinical Bioinformatics Laboratory, Paris, F-75006, France

<sup>2</sup> Molecular genetics service, AP-HP, Necker Hospital for Sick Children, F-75015, Paris, France

In the white paper "The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research", Salgado and co-authors present the working plan of the ELIXIR human CNV community. The manuscript summarises the strategy adopted in order to address current challenges in CNV detection and clinical interpretation. First, the introduction reviews the clinical relevance of structural variants in the human genome as well as the evolution of the technologies used for their identification. Second, a total of 7 main objectives are described, which are further detailed into specific tasks. Here, authors propose the development of enhanced CNV detection protocols, reference datasets, computational methods and analyses pipelines, standards for CNV reporting and data exchange and dissemination actions. The manuscript is clearly written and provides a complete and fair overview of the state-of-the-art in the field and of the challenges ahead. Thus, it not only represents a sound and ambitious action plan but, importantly, an insightful reference for current research in human genetics. I congratulate the authors for such effort. I provide below minor comments and suggestions:

1. For non-familiar readers, I would suggest to add a short paragraph introducing ELIXIR and their missions, and to place the human CNV community in such a broader context.
2. The manuscript would benefit from a table summarising the database and software resources previously developed or adopted by the hCNV community that served as a reference or starting baseline for the proposed actions.
3. I missed some mention to recent long-read sequencing technologies. A discussion about the benefits that they may bring to the human CNV field and whether the hCNV community would consider future actions in this direction would be welcome.
4. Also, additional discussion would be welcome as for how the hCNV community effort may

indeed boost machine-learning developments oriented to the clinical assessment of CNVs detected from short-read sequencing data. In this direction, the establishment of federated learning strategies across Elixir nodes and associated partners would represent a big step forward. While the manuscript mentions the interaction with the "Federated Human Data" and "Rare Diseases" ELIXIR Communities, the importance of those aspects would deserve more attention.

5. The use of the term "cytogenetic" as opposed to "genomic" alterations can lead to confusion. I would suggest to rather use structural variants versus single-nucleotide variants and indels.
6. I would suggest rephrasing of the following two sentences: "beyond a limited number of cancer-associated gene loci." [...] "It is thus possible to use the technology for genome-scale analysis through to region specific analysis".

**Is the topic of the opinion article discussed accurately in the context of the current literature?**

Yes

**Are all factual statements correct and adequately supported by citations?**

Yes

**Are arguments sufficiently supported by evidence from the published literature?**

Yes

**Are the conclusions drawn balanced and justified on the basis of the presented arguments?**

Yes

**Competing Interests:** No competing interests were disclosed.

**Reviewer Expertise:** Clinical bioinformatics

**I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.**

---

The benefits of publishing with F1000Research:

- Your article is published within days, with no editorial bias
- You can publish traditional articles, null/negative results, case reports, data notes and more
- The peer review process is transparent and collaborative
- Your article is indexed in PubMed after passing peer review
- Dedicated customer support at every stage

For pre-submission enquiries, contact [research@f1000.com](mailto:research@f1000.com)

**F1000Research**