

Workshop on Education in Bioinformatics 2021



# **Making training materials FAIR experiences, challenges, solutions**

Flash talks from: Saskia Hiltemann, Anna Swan, Verena Ras, Maria Doyle, Melissa Burke, Patricia M. Palagi and Celia van Gelder

# Flash talks

- Experiences from the Galaxy Training Network - Saskia Hiltemann
- Experiences from the EMBL-European Bioinformatics Institute - Anna Swan
- Experiences from the H3ABioNet - Verena Ras
- Experiences from an Individual Trainer - Maria Doyle
- Experiences from the Australian BioCommons - Melissa Burke
- Experiences from the SIB Swiss Institute of Bioinformatics - Patricia M. Palagi
- Experiences from the OpenAire CoP for Training Coordinators - Celia van Gelder



# Galaxy Training Network

Saskia Hiltemann



# Galaxy Training Network (GTN): Who we are

- Data Analysis Training using [Galaxy platform](#)
- Community-driven!
- Self-contained materials
  - For self-study by learners
  - For teaching by educators
- Everything Open (from the start)
  - Materials, data, tools, workflows, servers, ..
  - Development, discussions, feedback, usages stats, ..
- Regular Global Training events
- Accessibility for all
  - Alt text for all images, captions on all videos
  - Automated Slide Decks -> Video slides
  - [WAVE Web accessibility tool](#)



## Welcome to Galaxy Training!

Collection of tutorials developed and maintained by the worldwide Galaxy community

### Galaxy for Scientists

Topic	Tutorials
<a href="#">Introduction to Galaxy Analyses</a>	10

### Galaxy Tips & Tricks

Topic	Tutorials
<a href="#">Using Galaxy and Managing your Data</a>	19

A screenshot of the GTN Statistics dashboard. It features a header with the "Galaxy Training!" logo and navigation links. Below the header, there are three large boxes showing "21 Topics", "213 Tutorials", and "187 Contributors". The main content area is divided into two sections: "16 Scientific Topics" and "Growing Community".  
**16 Scientific Topics**  
A horizontal bar chart showing the number of tutorials per topic. The data is as follows:

Topic	Tutorials
Assembly	9
Climate	5
Computational chemistry	6
Ecology	6
Epigenetics	8
Genome Annotation	7
Imaging	4
Introduction to Galaxy Analyses	11
Metabolomics	5
Metagenomics	6
Proteomics	32
Sequence analysis	2
Statistics and machine learning	14
Transcriptomics	31
Variant Analysis	9
Visualisation	9

  
**Growing Community**  
A line graph showing the number of contributors over time from 2012 to 2020. The number of contributors shows a steady increase from approximately 60 in 2012 to over 180 in 2020. A profile for Maria Doyle is highlighted, showing her contributions to various topics and a donut chart representing her contribution distribution.

<https://training.galaxyproject.org>

# How we implement FAIR for training materials

R1	Plan to share online	Webpage, no login required. (via GitHub pages)
R2	Properly describing	BioSchemas markup, EDAM
R3	Unique identity	Internal system for keeping URLs persistent, but no official DOIs
R4	Register online	Automatically scraped by TeSS
R5	Access Rules	No access restrictions, open licences
R6	Interoperable format	Markdown format (converted to HTML by Jekyll framework, PDF export options)
R7	(Re)usable for trainers	MIT/CC-BY licence, speaker notes, instructor tutorials, FAQs, feedback forms, community calls, Gitter, training infrastructure & dashboard.
R8	Usable for trainees	Metadata at top of every tutorial (objectives, time, level, resources, prerequisites, ..), tutorial search, FAQs, Gitter support
R9	Contribution friendly	GitHub, "Edit me" button, Tutorials for contributors, regular contribution fests, Gitter support, citable materials, acknowledgement of contributions.
R10	Keeping up-to-date	Automated testing, regular contribution fests, topic maintainers, open development on GitHub



# Big challenges and wished for solutions

## Challenges

Balance between ease of contribution and feature-richness of framework

Sustainability; keeping materials up to date with a volunteer community

## Wished-for solutions

Obtaining DOIs for training materials (automatable and updateable)

FAIR in practice: more practical, concrete solutions (guides, checklists, tools, badges, .. )



# EMBL-EBI

Anna Swan

# Who we are



## EMBL-EBI Training

Delivering world-class training in data-driven life sciences.

# Who our materials are for

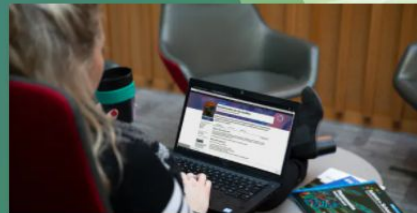
Scientists, from all around the world, at all career stages who would like to make the most of biological data.

Scientists who would like to use the wealth of public biodata available, whilst also learning to be more confident users and guardians of their own data.



### [Live training](#) →

View opportunities to join us, either virtually or in person, to learn with other scientists from around the world.



### [On-demand training](#) →

Dive straight into learning through our online tutorials and library of recorded webinars anytime, anywhere.



### [Support for trainers](#) →

Looking for training inspiration? Find out how we support trainers and educators in Bioinformatics.



# How we implement FAIR for training materials

The image is a collage of screenshots from the EMBL-EBI Training website, illustrating the implementation of FAIR (Findable, Accessible, Interoperable, Reusable) principles for training materials. The screenshots are arranged in a layered, overlapping fashion.

- Top Left:** A screenshot of the EMBL-EBI Training homepage with the header "EMBL-EBI Training" and the tagline "Delivering world-class training in data-driven life sciences." A search bar is visible.
- Top Center:** A screenshot of a course page titled "A guide to multiomics pathway analysis" under the "Recorded webinar" category. It includes an "Overview" section and a "How to attend" section.
- Top Right:** A screenshot of the "Cancer genomics" course materials page, showing a list of topics such as "Introduction to cancer genomics", "Introduction to high throughput sequencing and its application in cancer", and "Cancer epigenetics and whole-genome haplotyping".
- Middle Left:** A screenshot of the "Featured courses" section, highlighting a webinar "A guide to analysing binding sites in protein structure" and a virtual course "From specimens to genomics".
- Middle Center:** A screenshot of the "Course materials" page for "Cancer genomics", listing various topics like "Structural and single nucleotide variation", "Copy number variation analysis", and "CRISPR-Cas9 genome editing".
- Middle Right:** A screenshot of the "Introduction to high throughput sequencing and its application in cancer" page, detailing learning outcomes and materials.
- Bottom Left:** A screenshot of the "Live trainin" section, showing an opportunity for scientists to view content virtually.
- Bottom Center:** A screenshot of the "EBI Resources" section, featuring the "Reactome pathways database" as a manually curated, peer-reviewed database of biological pathways.
- Bottom Right:** A screenshot of a video player showing "Introduction to Next Generation sequencing" by Mathieu Bourgey, Ph.D., from the Canadian Centre for Computational Genomics.

Key elements across the screenshots include:

- Searchability:** A prominent search bar on the homepage.
- Accessibility:** Clear navigation menus and structured content.
- Interoperability:** Links to external resources like the Reactome database.
- Reusability:** Open Access (OA) icons and Creative Commons Attribution-ShareAlike 4.0 International licenses for the materials.

# Big challenges and wished for solutions

- Naming conventions for different types of training and materials that everyone can easily understand
  - Regular user testing to check terminology is understandable
- Keeping materials up to date is time consuming (but very worthwhile)
  - Making our trainers aware of updating requirements when creating materials
- Interoperable can be a challenge for practical materials
  - Virtual machines, the same set up as used in live courses, made available on AWS



# H3ABioNet

Verena Ras



## Who we are

- [Pan African Bioinformatics Network](#) as part of the [Human Hereditary and Health in Africa Consortium \(H3Africa\)](#)
- “H3ABioNet was established to develop bioinformatics capacity in Africa and specifically to enable genomics data analysis by H3Africa researchers across the continent. H3ABioNet is developing human capacity through training and support for data analysis, and facilitating access to informatics infrastructure by developing or providing access to pipelines and tools for human, microbiome and pathogen genomic data analysis.”
- Major goal is to increase the number of qualified bioinformatics graduates on the continent while creating research opportunities and providing financial support for promising newly-graduated bioinformatics students in Africa, as well as attracting Africans studying abroad back to the continent.
- H3ABioNet delivers high quality training in a variety of formats (see image below).
- Increasing presence across Africa and now globally

✍ Face to face workshops +

💬 Live online training +

🎮 Hackathons and jamborees +

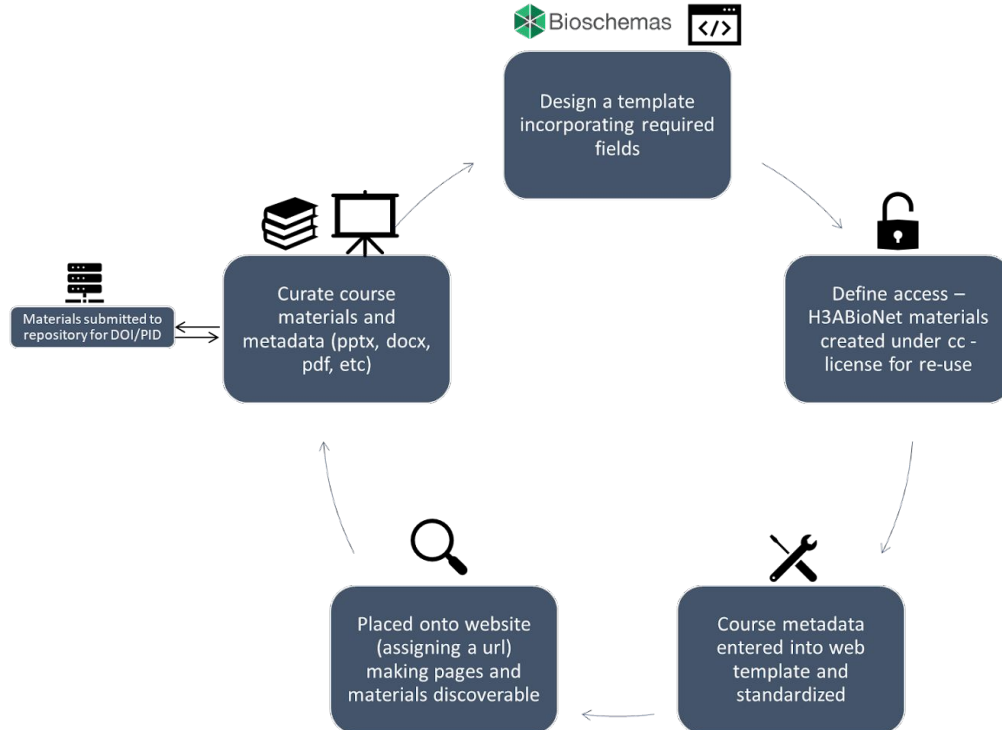
📁 Access to training materials +

👨‍🎓 Train the Trainer +

The screenshot displays the H3ABioNet website interface. At the top, the logo and name 'H3ABioNet Pan African Bioinformatics Network for H3Africa' are visible. Below the navigation bar, a banner image shows a hand holding a tablet displaying a DNA double helix, with the text 'H3ABioNet delivers high quality training covering various aspects of bioinformatics'. The main content area is divided into two sections: 'Training' and 'Upcoming and Current Training'. The 'Training' section lists 'H3ABioNet Courses and Events', 'Internships', 'Bioinformatics Education', and 'Online Training'. The 'Upcoming and Current Training' section features a prominent announcement for the 'Next Generation Sequencing Bioinformatics Course 2021', stating that the course will equip participants with the essential informatics skills required to best.



## How we implement FAIR for training materials




- Developed a repeatable process
- Aligning data to bioschemas
- Submitting data to internal repository (local instance of Figshare) for PIDs
- Adding licensing information to all slides
- Early stages - in the process of implementing bioschemas and creating web page templates



# How we implement FAIR for training materials

- Example template for collecting metadata and placing onto website:



**H3ABioNet**  
Pan African Bioinformatics Network for H3Africa  
H3ABioNet Workshop Call Template

**Workshop Title/name:**

**Course Overview/description:**

**Keywords:** Please provide at least 2 – 5 keywords for your training. These should ideally be EDAM terms but general keywords are fine.

**Skill level of training:** Please specify whether the training is aimed at a "beginner", "intermediate" or "advanced" level

**Language:** in what language/s is the course and materials offered

**Credential awarded:** "None", "letter of completion", "accredited certificate", "workshop certificate", etc.

**Has this course been run before?** Provide links to previous course pages/content if available

**Type of training:** "online", "face-to-face", "blended", "other"

**Venue of workshop:**

**Dates for the workshop (duration if run as a MOOC):**

**Workshop organisers:**

**Registration opens:**

**Registration closes:**

**Notification date:**


**Link to application form:**

**Workshop Sponsors:** H3ABioNet and xx

**Intended Audience:**

**Syllabus and Tools:**

**Licensing for course materials:** The default licensing attached to any workshop and materials will be a creative commons license. Please do specify if a different license is required or whether materials will not be available publicly. If materials cannot be linked to our website, please specify a contact person in order to gain access to materials in future.



**H3ABioNet**  
Pan African Bioinformatics Network for H3Africa  
H3ABioNet Workshop Call Template

**Workshop limitations:** This workshop will only provide a foundation for continued learning in

**Workshop Programme:**

Time	Topic	Trainer
	27 <sup>th</sup> July 2018	
	Registration and introductions	
10:30	Tea Break	
11:00		
1:00	Lunch	
2:00		
3:30	Tea Break	
6:00	Workshop End	

**\*\* Please note that by completing this template you agree to deposit any training materials used throughout the course in a location specified by the Training Material duration team.**

**This template was completed by:** <Name of person who completed/submitted the form>

**This template was checked by:** Name of training taskforce member who checked document before uploading to H3ABioNet website



# H3ABioNet

## Pan African Bioinformatics Network for H3Africa

# Big challenges and wished for solutions

- Manual process - needs automation, especially for sustainability
- Many don't understand FAIR and the benefits so not always easy onboarding people
- Bioschemas not as intuitive to implement when you already have your own framework in place - need for a simple reproducible method for implementation



Search on University of Cape T... Log in

h3abionet

need help?

Follow this search

13 results found

sort by: Relevance

include figshare content

Select date ▼

Licence

CC BY 4.0 (12)

MIT (1)

Item Type

presentation (9)

educational resource (2)

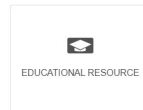
software (1)



**H3ABioNet TEWP Training Guide**  
Educational resource posted on 30.03.2021  
Verena Ras ▼



**H3ABioNet reproducible workflows project**  
\_SciDataCon\_Nov\_2...  
Presentation posted on 04.12.2018  
Sumir Panji ▼



**H3ABioNet Training Support Pack**  
Educational resource posted on 30.03.2021  
Verena Ras ▼



**Genomic Data Access in the Era of Personal Privacy - challenges...**  
Presentation posted on 18.03.2020  
Sumir Panji ▼

BioNet\_schema\_mappings - Copy

File Edit View Insert Format Data Tools Help Last edit was on December 11, 2020

Fields we collect and may want to add to this template

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	
1																				
2																				
3		schema	field	Description	Revisions description	Multiplicity	Cardinality	Example markup	BiNET Training template	H3ABioNet Grants Management	H3ABioNet Technical Training Course	H3ABioNet NABDA Node Training Course	H3ABioNet NABDA Node University of Botswana	H3ABioNet Postgraduate Bioinformatics	H3ABioNet Management Workshop 2021	NABDA Management	H3ABioNet Management	Computational Genomics	H3ABioNet Advanced Systems	Introlab Genom
4			about	The subject matter of the resource	Recommended	Many	"about": { "type": "about" } This schema will take you to Course Overview	EDM Ontology	http://edamontology.org/topic_01	http://edamontology.org/topic_02	http://edamontology.org/topic_03	http://edamontology.org/topic_04	http://edamontology.org/topic_05	http://edamontology.org/topic_06	http://edamontology.org/topic_07	http://edamontology.org/topic_08	http://edamontology.org/topic_09	http://edamontology.org/topic_10	http://edamontology.org/topic_11	http://edamontology.org/topic_12
5			abstract	The subject of this resource	optional	One	"abstract": { "type": "text" } This schema will take you to Course Overview		http://edamontology.org/topic_01	http://edamontology.org/topic_02	http://edamontology.org/topic_03	http://edamontology.org/topic_04	http://edamontology.org/topic_05	http://edamontology.org/topic_06	http://edamontology.org/topic_07	http://edamontology.org/topic_08	http://edamontology.org/topic_09	http://edamontology.org/topic_10	http://edamontology.org/topic_11	http://edamontology.org/topic_12
6			description	The subject of this resource	Recommended	Many	"description": { "type": "text" } This schema will take you to Course Overview		http://edamontology.org/topic_01	http://edamontology.org/topic_02	http://edamontology.org/topic_03	http://edamontology.org/topic_04	http://edamontology.org/topic_05	http://edamontology.org/topic_06	http://edamontology.org/topic_07	http://edamontology.org/topic_08	http://edamontology.org/topic_09	http://edamontology.org/topic_10	http://edamontology.org/topic_11	http://edamontology.org/topic_12
7			coursePrereq	Prerequisite specifies the course/subject/creator/credential description	Recommended	Many	"coursePrereq": { "type": "text" } This schema will take you to Course Overview		not specified	Each course component will	Each course component will	Each course component will	Each course component will	Each course component will	Each course component will	Each course component will	Each course component will	Each course component will	Each course component will	Each course component will
8			creator	The creator/author	optional	Many	"creator": { "type": "text" } This schema will take you to Course Overview		not mentioned	H3ABioNet	H3ABioNet	H3ABioNet	H3ABioNet	H3ABioNet	H3ABioNet	H3ABioNet	H3ABioNet	H3ABioNet	H3ABioNet	H3ABioNet
9			credential	A credential description	Recommended	Many	"credential": { "type": "text" } This schema will take you to Course Overview													
10			hasCredential	A course may be ran on a training material	Recommended	Many	"hasCredential": { "type": "text" } This schema will take you to Course Overview													
11			hasCredential	A course may be ran on a training material	Recommended	Many	"hasCredential": { "type": "text" } This schema will take you to Course Overview		Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
12			hasCredential	A course may be ran on a training material	Recommended	Many	"hasCredential": { "type": "text" } This schema will take you to Course Overview		Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
13			keywords	Keywords or tags used to describe the content	optional	One	"keywords": { "type": "text" } This schema will take you to Course Overview													
14			statements	Statements or key words	optional	Many	"statements": { "type": "text" } This schema will take you to Course Overview													
15			license	A license document indicates that the	Recommended	One	"license": { "type": "text" } This schema will take you to Course Overview													
16			mentions	If you have an open Data, you should mention that the	Recommended	Many	"mentions": { "type": "text" } This schema will take you to Course Overview													

Schema\_all Course mappings Course\_Instance Explore



# Individual Trainer

Maria Doyle



# Who I am

- Application and Training Specialist for Research Computing at Peter MacCallum Cancer Centre, Melbourne, Australia
- Provide both internal and external training
- External training collaborations
  - Melbourne Bioinformatics  
[https://mblue9.github.io/r-intro-biologists/intro\\_r\\_biologists.html](https://mblue9.github.io/r-intro-biologists/intro_r_biologists.html)
  - Galaxy Training Network  
<https://training.galaxyproject.org/training-material/hall-of-fame/mblue9/>
  - **TidyTranscriptomics**  
<https://github.com/stemangiola/tidytranscriptomics#workshops>



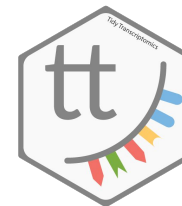
# How I implemented FAIR for training materials\*

R1	<a href="#">GitHub Pages website</a>
R2	<a href="#">Bioconductor Biocviews</a>
R3	<a href="#">GitHub release -&gt; Zenodo DOI</a>
R4	<a href="#">TeSS manual registration</a> (for some)
R5	<a href="#">Open access website</a>
R6	<a href="#">R markdown</a>
R7	<a href="#">CC-BY-4.0 GitHub Licence</a>
R8	<a href="#">Prerequisites and Learning Outcomes on website</a>
R9	<a href="#">Contributing.md file in website</a>
R10	Provide frozen version of past workshops through <a href="#">GitHub website for workshop and Docker</a> , newer workshops use <a href="#">updated material</a>

\*Started thinking how to do as saw [FAIR Rules](#) & using Bioc [template](#) (now used by [>50 workshops](#)).

Green: part of Bioc template. White: manual steps.

# Big challenges and wished-for solutions



Challenges	Solutions wished
How exactly to make material FAIR?	Checklist and how-tos e.g how to get DOI from Zenodo, <a href="#">what should go in metadata?</a> , <a href="#">contributing file?</a> ... What I did is <a href="#">here</a>
What does FAIR training material look like?	Examples of training material that is FAIR so can see specifics, describing how they meet FAIR rules
How to make FAIR easily doable?	<b>Automated way to be FAIR. IDEALLY: included in Bioconductor workshop GitHub Actions template <a href="#">here</a></b>
How to know that material is FAIR?	Badge to add to material. Could then add similar to other badges <a href="#">here</a>

\*White is what I've also heard from others, Grey is personal wishes that I think might make FAIR easier for others



# Australian BioCommons

Melissa Burke

# Who we are

Australian BioCommons is building digital capability for the life science communities



Support volunteer trainers to deliver events nationally

[tinyurl.com/hybridworkshops](https://tinyurl.com/hybridworkshops)

# How we FAIRify materials

Review

Assess

Develop

Do

## Catalogue materials

- What
- Where
- How
- Who

## How FAIR are we?

ARDC FAIR  
assessment tool

10 Simple Rules

Quick wins  
→ Improve findability  
→ Improve metadata

## Inspiration

ARDC Metadata  
checklist

CINECA hackathon

Other training  
providers

**Who are we  
FAIRifying for?**

## Our plan

Zenodo

- Event metadata
- Materials
- Link to materials shared elsewhere
- Crosslink to TeSS etc

Keep learning and adapting!

<https://zenodo.org/communities/australianbiocommons-training>

# Big challenges and wished for solutions

Challenge	Solution/wish list
Translating the principles into practical steps	<ul style="list-style-type: none"><li>● Checklists to help make sure everything is done</li><li>● Tools/method for checking FAIRness and finding areas for improvement</li><li>● How to guides/ Case studies</li></ul>
Materials are owned by others	Incentives - make it easy, citable DOI, give credit
Materials shared elsewhere	Crosslink via Zenodo
Time	<ul style="list-style-type: none"><li>● Make it part of the process</li><li>● Templates</li><li>● Automated way of copying info between registries</li></ul>

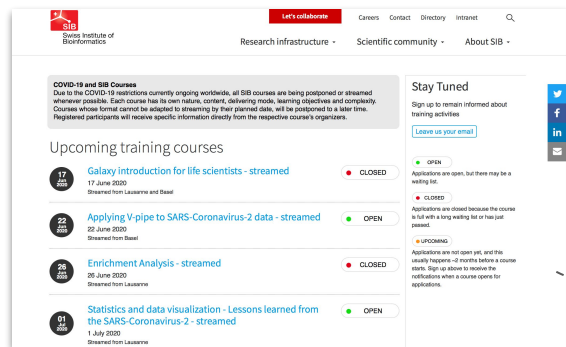


# SIB Swiss Institute of Bioinformatics

Patricia M. Palagi



# Who we are - SIB Training



<https://www.sib.swiss/training>



## Data Management Plan

Date ↓	Location	Slides	Exercises	Scripts / Dataset	Video
10 June 2020	Fribourg	✓	✓	✓	<a href="#">Link</a>
15 March 2020	Streamed	✓	✓	✓	✓ <a href="#">Link</a>
25 December 2019	Lausanne	✓	✓	✓	<a href="#">Link</a>
15 October 2019	Streamed	✓	✓	✓	✓ <a href="#">Link</a>
15 August 2019	Bâle	✓	✓	✓	<a href="#">Link</a>

FAIR

FAIRness today - a sample:  
<https://sib-swiss.github.io/NGS-introduction-training/>



### Next dates:

- XX Month 2020  Streamed
- XX Month 2021  Lausanne
- XX Month 2021  Streamed

# How we implement FAIR for training materials\*

R1	Not yet systematically, should be automated (or at least partially) with new SIB website
R2	Bioschemas, EDAM. Internal terminology for terms as materials, levels, etc
R3	GitHub, DOI with Zenodo, ORCID for trainers and managers
R4	TeSS scrapper, (GOBLET)
R5	Moving towards Open... work in progress
R6	MD, PPT, PDF, Jupyter Notebooks
R7	CC-BY-4.0, copyright guide, Bioschemas metadata, but more data needed to support trainers and trainees (eg lesson time duration)
R8	
R9	GitHub - contribution rules can be improved
R10	GitHub-Zenodo version control stamp, SIB Training Zenodo Community



# Big challenges and solutions wished

Challenges	Solutions wished
Change in mindset: from authorship to contributorship	Need to continue raising awareness of the benefits - Recognition of trainers is one of them
Collating all pieces of the puzzle together - technically not simple	Checklists and guidelines - no one solution fits all
Common agreement & standardization	Training terminology
It is time consuming	Automation, FAIR training materials checker Learning with and from the community

Life/Success is a journey, not a destination

- Open and FAIR is a journey and a destination



# Open Aire Community of Practice for Training Coordinators

Celia van Gelder

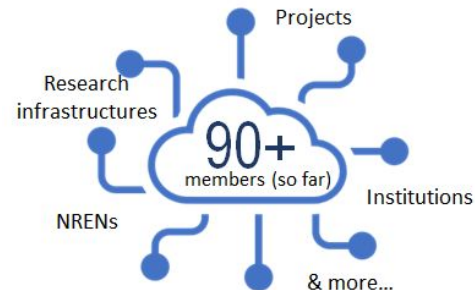


Open Aire Community of Practice for training coordinators

# CoP: Who we are and our training resources

## CoP for training coordinators

- Started in 2018; monthly meetings and a Slack channel
- For training coordinators in communities, projects and research infrastructures
- A discipline transcending community of trainers and training organisers
- Owned and driven by members... sharing, collaborating, contributing, coordinating
- Strong link with themes Open Science, Research Data Management (RDM) and Data Stewardship
- Examples of activities:
  - Organizing workshops
  - [Webinar/writing sprint](#) about GDPR and training
  - Several CoP members were part of the EOSC Working Group Skills & Training (2020), [Digital Skills for FAIR and Open Science report](#)



[Slack channel](#)

## CoP Training resources

- Individual trainings/courses and their materials
- Course Catalogues/Registries
  - ELIXIR TeSS, ENVRI-FAIR Training Catalogue, SSHOC training toolkit, etc, etc
- EOSC-Catalogue (*under development*)
  - Catalogue of catalogues



[www.openaire.eu/cop-training](http://www.openaire.eu/cop-training)



# Activities related to FAIR training resources by CoP & CoP members

[www.openaire.eu/cop-training](http://www.openaire.eu/cop-training)

- Working on findability and interoperability for training resources & catalogues
  - **RDA ETHRD-IG Task force** minimal metadata for Training resources
  - **Catalogues Task force** in the EOSC Skills & Training Working Group (2020)
  - **FAIRsFAIR D6.3**: checklist (built on/added on the 10SR paper)
  - **ELIXIR Training**: bioschemas to annotate Training resources in [ELIXIR Training Portal TeSS](#)
  - **Terms4fairskills**: a terminology for the skills necessary to make data FAIR and to keep it FAIR
- Metadata & Training Catalogues related workshops by/with CoP members
  - [Workshop Training in the EOSC](#) (Feb 2020, the Hague)
  - [Training Resource Catalogue Interoperability Workshop](#) (October 2020, virtual)
  - Workshop on [Harmonising Training Resource Metadata for EOSC Communities](#) (April 2021, virtual)
  - Have informed EOSC Training Catalogue efforts

[Workshop report & recommendations](#)

The screenshot shows a Zenodo record for a workshop report. The title is "Workshop report 'Training in the EOSC'". The date is April 3, 2020. The report is available for open access. The authors listed are: Marjan Grootveld, Ellen Leenaris, Iona von Stein, Cees Hof, Giuseppe La Rocca, Iryna Kuchina, Pedro Principe, Alexei Belotserkovsky, Rene Belse, Thibaud Cayla, Helen Clare, Gerard Coers, Ingrid Dilic, Iaria Fava, Vincent Favre-Nicolin, Sonja Filiposka, Owen Franco, Celia van Gelder, Felix van Gelderen, Lowri Harris, Maggie Hellström, Frans Huijgen, Vaaso Kalatzis, Mateusz Kuzak, Frances Maddern, Ivan Martin Hernandez, Irina Mikhailova, Marcin Plociennik, Päivi Rauste, Floy Rodrigues, Hugh Shanahan, Efraïm Tóth-Czifra, Irena Vávrová, Brvar, Angus Whyte, Tatsiana Yankelevich, and Katerina Zourou. The abstract states: "This document 'TrainingInTheEOSC\_WorkshopReport\_L01\_00.pdf' is the output of a three-day workshop on Training in the EOSC, 26-28 February 2020, The Hague, The Netherlands. The workshop was organised by DANS in collaboration with EUDAT, EGI and OpenAIRE. It provides recommendations regarding Rules of Participation for training as well as recommendations regarding practical guidance for training service providers. As an additional workshop output the file..."



# Our challenges & wish list related to FAIR training resources

[www.openaire.eu/cop-training](http://www.openaire.eu/cop-training)

- Main challenges:
  - Findability of training resources
  - Interoperability of training catalogues/registries
  - Sustainability
- CoP wants to bundle expertise and provide guidance to training coordinators, and to the EOSC Board/Governance
- July 2021 CoP started a Task Force about Making training materials FAIR
  - Aims:
    - Review of current relevant projects and activities and to what extent they implemented FAIR for their training materials
    - Identify implementation studies/examples
    - Outputs by Jan 2022 - Best practice guidance, article, possible assessment tool
- Join us for the next round of discussions at the Open Science Fair on September 20 - 23, 2021: <https://www.opensciencefair.eu> - Fostering local and global open science communities