



## Welcome: Building your own Computational Pipeline for Social Scientists

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### Introduction

Computational social science (CSS) brings computational approaches to social science questions.

This student-led training explores a practical introduction to building computational workflows with [Nextflow](#).

[Nextflow](#) is a workflow management software which enables the writing of scalable and reproducible scientific workflows. It can integrate various software package and environment management systems such as Docker, Singularity, and Conda. It allows for existing pipelines written in common scripting languages, such as R and Python, to be seamlessly coupled together. It simplifies the implementation and running of workflows on cloud or high-performance computing (HPC) infrastructure.

The guided practical component of the training is implemented in the code spaces environment developed and maintained by [Seqera](#) and released under an open-source license ([CC BY-NC-ND](#)) for the benefit of the community. You are welcome to reuse any of these materials according to the terms of the license.

The training is based off [carpentries incubator](#) and [The Turing Way](#). The course material page was designed using the [workbench](#).

### Objectives

- Understand the role of auxiliary tools in supporting best practice within the Open Research framework.
- Design/adapt a research project directory to own research.
- Understand the fundamental components of a workflow implemented in Nextflow, including channels, processes and operators.

- Launch a computational workflow using remote workspace, GitHub Codespaces.
- Curate own configurations and settings on a practice workflow to ensure portability, scalability, automatic resource management and re-entrancy.
- Discuss ways to implement own research directory.
- Explore links to the wider network for computational researchers across Scotland.

## Intended learning outcomes

- Connecting with researchers in your field
- Ability to design and implement research projects from data to report
- Navigate reproducible, efficient, and communicable code via GitHub

## Pre-requisites

- Bring own device to follow practical component
- Set up an account with GitHub, follow link to: [GitHub page](#)
- Optionally, upgrade to a GitHub Education account. For more information follow link: [GitHub Education](#)

## Synthetic Data

The data involves low fidelity synthetic data. This means that the data is generated using functions, and only resembles real-world data in a very basic way. This type of synthetic data can be useful for teaching and learning, or helping develop code. Generative AI was used to construct the data generating functions for this synthetic data. Please ensure any further use of this data includes this statement. The code used to generate data can be shared upon request, drop a line to [\(PGR\) Eleni Omiridou](#).

## Course materials

The guided practical material for the half day course can be found in the [sgsss-workflow](#) scripts repository. The teaching and learning material lives in the [course training](#) page. Material was prepared by [\(PGR\) Eleni Omiridou](#), University of Glasgow. The course was first run in July 2025.

## Materials

This workshop makes use of an online teaching and learning space. This online environment involves using the GitHub Codespaces training environment:



[Open in GitHub Codespaces](#)

The material and supporting resources can be found in the following folders:

- [set-up](#) - Instructions to set up the material for the workshop.
- [code](#) - Files for the guided practical material on building a workflow.
- [template](#) - Template folder to adapt to your own workflow.
- [workflow](#) - Full demo - ready-set-workflow !

## Guided Practical Resources (Asynchronous)

Link to Pre-recorded Material:

[Building your own Computational Pipeline for Social Scientists](#)

Follow along with the companion practical material:

- [Workflow 00: Setup](#)
- [Workflow 01: Intro](#)
- [Workflow 02: Hello Nextflow](#)
- [Workflow 03: Parameters](#)
- [Workflow 04: Channels](#)
- [Workflow 05: Modules + Optional Topics](#)

## Schedule

Section	Time	Topics Covered
<b>1. Introduction</b>	00h 25m	What are the FAIR research principles? How do FAIR principles apply to software? How does folder organisation help me?
<b>2. Hello Nextflow</b>	00h 50m	What is Nextflow? Why should I use a workflow management system? What are the features of Nextflow? What are the main components of a Nextflow script? How do I run a Nextflow script?
<b>Break</b>	10m	
<b>3. Parameters</b>	01h 00m	How can I change the data a workflow uses? How can I parameterise a workflow? How can I add my parameters to a file?
<b>4. Channels</b>	01h 40m	How do I move data around in Nextflow? How do I handle different types of input, e.g. files and parameters? How can I use pattern matching to select input files?
<b>Break</b>	10m	
<b>5. Modules</b>	02h 00m	How do I run tasks/modules in Nextflow? How do I get data, files and values, into a module?
<b>Finish Introductory Material</b>	02h 20m	
<b>6. Modules Part 2</b>	optional	How do I get data, files, and values, out of processes? How do I handle grouped input and output? How can I control when a process is implemented? How do I control resources, such as number of CPUs and memory, available to processes? How do I save output/results from a process?

Section	Time	Topics Covered
<b>7. Workflow</b>	optional	How do I connect channels and processes to create a workflow? How do I invoke a process inside a workflow?
<b>8. Operators</b>	optional	How do I perform operations, such as filtering, on channels? What are the different kinds of operations I can perform on channels? How do I combine operations? How can I use a CSV file to process data into a Channel?
<b>9. Reporting</b>	optional	How do I get information about my pipeline run? How can I see what commands I ran? How can I create a report from my run?
<b>10. Nextflow configuration</b>	optional	How do I configure a Nextflow workflow? How do I assign different resources to different processes? How do I separate and provide configuration for different computational systems?
<b>11. Auxiliary Tools</b>	optional	When should I use a pre-built container? How can I customise a container? What is a remote codespace?
<b>12. Resuming a Workflow</b>	optional	How can I restart a Nextflow workflow after an error? How can I add new data to a workflow without starting from the beginning? Where can I find intermediate data and results?
<b>13. Portability of Workflow</b>	optional	How can I move my analysis to a computer cluster?

## Acknowledgements

I am grateful to the Scottish Graduate School of Social Sciences (SGSSS) for funding and organising this course.

This lesson is a template lesson that uses [The Carpentries Workbench](#). Built with [sandpaper \(0.16.12\)](#), [pegboard \(0.7.9\)](#), and [varnish \(1.0.5\)](#).

## Further information

Please do not hesitate to get in contact if you have queries, suggestions or corrections regarding the material:  
[\(PGR\) Eleni Omiridou](#)

Any errors, omissions or inaccuracies are my own.

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## AI Disclosure

This document was created with assistance from AI tools. The content has been reviewed and edited by the author. For more information on the extent and nature of AI usage, please contact the author.

## Citations

Graeme R. Grimes, Evan Floden, Paolo Di Tommaso, Phil Ewels and Maxime Garcia Introduction to Workflows with Nextflow and nf-core. <https://github.com/carpentries-incubator/workflows-nextflow> 2021.

Ruth M. Ripley, Tom A. B. Snijders, Zsofia Boda, Andras Voros, and Paulina Preciado (2024). Manual for Siena version 4.0. R package version 1.4.13. <https://www.cran.r-project.org/web/packages/RSiena/>.

The Turing Way Community. (2022). The Turing Way: A handbook for reproducible, ethical and collaborative research (1.0.2). Zenodo. DOI 10.5281/zenodo.3233853.

The Turing Way Community, & Scriberia. (2020, March 3). Illustrations from the Turing Way book dashes. Zenodo. <http://doi.org/10.5281/zenodo.3332807>.

The lesson material was adapted with permission from seqera labs [nextflow-tutorial](#)