



## Practical information

**Location:** Google office Amsterdam  
**Directions:** <https://maps.app.goo.gl/HXeZtjQhid1xxrn19>.  
**Registration:** Please tell the reception that you're visiting a **Google event** and take the elevator to the 8th floor. You will receive your badge for the day at the entrance kiosk.  
**Time:** 12:00 - 18:30  
**Code of conduct:** <https://opensource.creativecommons.org/community/code-of-conduct/>

## Workshop schedule

Time	Session	Topics	Facilitators
12:00 - 13:00	Registration and lunch	<ul style="list-style-type: none"> <li>Registration of participants, lunch and networking opportunity</li> </ul>	Joep
13:00 - 13:30	Welcome and introductions	<ul style="list-style-type: none"> <li>General introduction Hartwig Medical Foundation tools &amp; how we run on Google</li> <li>Overview of relevant GCP services we will be using</li> </ul>	Joep + Daphne
13:30 - 13:50	Oncoanalyser	<ul style="list-style-type: none"> <li>Introduction to Oncoanalyser and nf-core</li> <li><a href="https://nf-co.re/oncoanalyser/dev/docs/usage/">https://nf-co.re/oncoanalyser/dev/docs/usage/</a></li> </ul>	Stephen
13:50 - 14:00	<b>Workshop part 1</b> set up environment	<ul style="list-style-type: none"> <li>Divide into groups for the workshop</li> <li>Access workshop documentation</li> <li>Access the GCP environment</li> </ul>	Daphne + Rayan + Stephen + Joep + helpers
14:00 - 16:00	<b>Workshop part 2</b> configuration and starting OncoAnalyser	<ul style="list-style-type: none"> <li>Set up networking, storage, service accounts</li> <li>Prepare data and samplesheet</li> <li>Create NextFlow configuration</li> <li>Spin up a VM for NextFlow overhead</li> <li>Monitor progress</li> </ul>	Parallel session using MySQL or BigQuery
16:00 - 16:25	<b>Workshop wrap-up</b>	<ul style="list-style-type: none"> <li>Troubleshooting</li> <li>Evaluate the results from the pipeline</li> </ul>	
16:25 - 17:25	DeepSomatic	TBD	Andrew Carroll
17:25 - 17:30	Closing remarks and thanks		Joep
17:30 - 18:30	Drinks & snacks		All