

<b>Event title</b>	bio.tools - making it easier to find, understand and cite biological tools and software
<b>Event type</b>	Webinar
<b>Date of event</b>	21/06/2022
<b>Time of event</b>	3pm AEST
<b>Topic description</b>	<p><a href="#">bio.tools</a> provides easy access to essential scientific and technical information about software, command-line tools, databases and services. It's backed by ELIXIR, the European Infrastructure for Biological Information, and is being used in Australia to register software (e.g. <a href="#">Galaxy Australia</a>, <a href="#">prokka</a>). It underpins the information provided in the Australian BioCommons discovery service <a href="#">ToolFinder</a>.</p> <p>Hans Ienasescu and Matúš Kalaš join us to explain how bio.tools uses a community driven, open science model to create this collection of resources and how it makes it easier to find, understand, utilise and cite them. They'll delve into how bio.tools is using standard semantics (e.g. the EDAM ontology) and syntax (e.g. biotoolsSchema) to enrich the annotation and description of tools and resources. Finally, we'll see how the community can contribute to bio.tools and take advantage of its key features to share and promote their own research software.</p>
<b>Format description</b>	Webinar presentation followed by a brief question and answer session
<b>Identifier(s)/URL</b>	<a href="https://www.biocommons.org.au/events/biotools">https://www.biocommons.org.au/events/biotools</a>
<b>Licence</b>	Materials are shared under a Creative Commons Attribution 4.0 International agreement unless otherwise stated on the materials

<b>Keywords</b>	<p>Research software Tools Workflows <a href="http://edamontology.org/topic_0769">http://edamontology.org/topic_0769</a> Bioinformatics <a href="http://edamontology.org/topic_0091">http://edamontology.org/topic_0091</a></p>
<b>Contact</b>	<p>Melissa Burke (<a href="mailto:melissa@biocommons.org.au">melissa@biocommons.org.au</a>)</p>
<b>Audience</b>	<p>Life scientists, bioinformaticians and those seeking to use, develop and share research software, tools, databases and services as well as those interested in supporting the visibility of research software.</p>
<b>Prerequisites</b>	<p>None</p>
<b>Technical requirements</b>	<p>None</p>
<b>Learning outcomes</b>	<ul style="list-style-type: none"> <li>● Outline the categories used by the EDAM ontology</li> <li>● Describe how bio.tools uses EDAM to make it easier to find, use and cite tools</li> <li>● Describe how to find, use and cite tools with bio.tools</li> </ul>
<b>Speaker</b>	<p>Hans Ienasescu, Scientific Programmer / Data Administrator / Lead Curator Technical University of Denmark</p> <p>Matus Kalas, Researcher, Computational Biology Unit, University of Bergen</p>
<b>Related material</b>	<p>None</p>