

## TEMPLATE FOR COMMENTS

Contact information		
<b>Surname:</b>	Jamieson	
<b>Given Name:</b>	Alice	
<b>Government (if applicable):</b>		
<b>Organization:</b>	Wellcome Trust	
<b>E-mail:</b>	a.jamieson@wellcome.ac.uk	
<b>Title of document reviewed:</b>	The Emergence and Growth of Digital Sequence Information in Research and Development: Implications for the Conservation and Sustainable Use of Biodiversity, and Fair and Equitable Benefit-Sharing – A Fact-Finding and Scoping Study Undertaken for the Secretariat of the Convention on Biological Diversity	
Comments on the draft fact-finding and scoping study		
Page #	Para #	Comment
0	0	Overall we found the study authoritative, balanced and a good summary of the opportunities and challenges posed by use of digital sequence information in the context of the CBD. The following comments reflect Wellcome’s perspective and experience as a funder of health research and development.
23-29	0	Section 3- This section could reference how important the use of DSI is to the surveillance of emerging public health threats, such as antimicrobial resistance and infectious diseases. Currently the only health example mentioned is healthcare biotech, which presents a product focused view of healthcare R&D. This could be broadened out.
46	5	7.2.3- This section should mention the importance of DSI to disease surveillance and preparedness efforts, in addition to responding to health emergencies.
50	30-32	<p>“Clearly in cases of virus and pathogen data, biosecurity concerns would dictate the need to not only identify contributors and users, but to track use, with the added benefit of allowing researchers to acknowledge and potentially collaborate with genetic sequence data providers.”</p> <p>This comment does not recognise the technological developments that have changed how pathogen genome data is sequenced, shared and used, which is noted elsewhere in the study. As a result of these changes, pathogen sequences are not subject to the restrictions and controls that were in place years ago, for example, on synthesising pathogens in laboratories. Further, many existing public access databases do contain pathogen sequences (for example for Ebola, herpes, plague) which are routinely shared alongside journal publication. The above statement should be altered to reflect that for <i>certain pathogens you may want to identify contributors and users and track use</i>, as GISAID does, but this shouldn’t be mandated in all cases. If it was, it would impact the timely sharing of pathogen DSI for epidemic risk assessment, or for the development of diagnostics, vaccines and pharmaceuticals.</p>

Please submit your comments to [secretariat@cbd.int](mailto:secretariat@cbd.int) or by fax at +1 514 288 6588.