## TEMPLATE FOR COMMENTS

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Title of document reviewed:		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
		"Differences in terminology in scientific circles reflect differences in the material referred to, as well as the speed and transformative nature of technological change today, which make it difficult to harmonize terminology". (p.8).  While there are difficulties it is important to recognise that different actors are (at least in some cases) using the terms with specific meanings that do not extend across the entire range of meanings of 'Digital sequence information'. The analysis in section 2.1. is very helpful, but the distinctions drawn there are not followed in the rest of the text. This imprecision leads to difficulties in assessing the significance of parts of the text.
21	Table 1	The table suggests that 'full taxonomic analysis of the samples' requires annotation of putative gene functions. This is incorrect – a full taxonomic analysis does not rely on gene functions.
84	Note 36	'20116' in the final line should read '2016'
		Additional rows can be added to this table by selecting "Table" followed by "insert" and "rows below"

Please submit your comments to secretariat@cbd.int or by fax at +1 514 288 6588.