

Departamento de Ciencias de la Computación  
(DCCO) Ingeniería en Tecnologías de la  
Información Metodología de Desarrollo de Software  
NRC 10522

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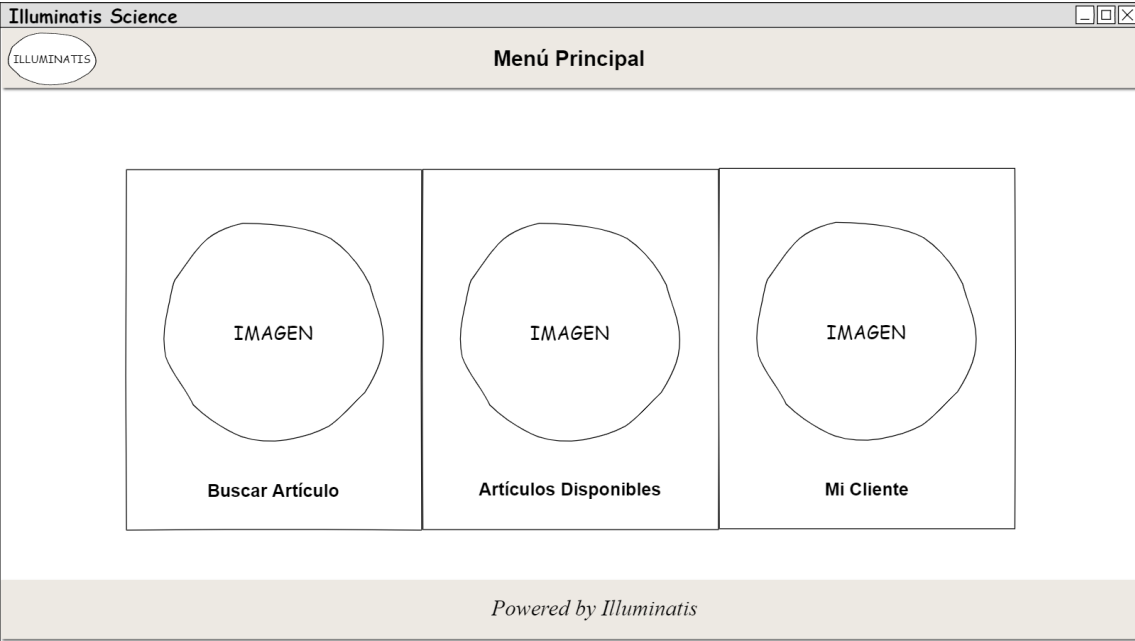
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**Ciudad:** Quito.

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Resumen

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Abstract

In recent years, the explosion of genomic data and bioinformatic tools has been accompanied by a growing conversation around reproducibility of results and usability of software. However, the actual state of the body of bioinformatics software remains largely unknown. The purpose of this paper is to investigate the state of source code in the bioinformatics community, specifically looking at relationships between code properties, development activity, developer communities, and software impact. To investigate these issues, we curated a list of 1,720 bioinformatics repositories on GitHub through their mention in peer-reviewed bioinformatics articles. Additionally, we included 23 high-profile repositories identified by their popularity in an online bioinformatics forum. We analyzed repository metadata, source code, development activity, and team dynamics using data made available publicly through the GitHub API, as well as article metadata. We found key relationships within our dataset, including: certain scientific topics are associated with more active code development and higher community interest in the repository; most of the code in the main dataset is written in dynamically typed languages, while most of the code in the high-profile set is statically typed; developer team

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