Binette: Una herramienta rápida y sencilla para la construcción de genomas ensamblados

*Binette: a fast and accurate bin refinement tool to construct high quality Metagenome Assembled Genomes.*

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| **Repositorio / Repository** | <https://github.com/gastonbecerra/scraping-casa-rosada> |
| **Archivo / Archive** | <https://github.com/gastonbecerra/scraping-casa-rosada> |
| **Documentación / Docs / Vignette** | <https://github.com/gastonbecerra/scraping-casa-rosada> |
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Justificación / Statement of need

In a metagenomic analysis, sequence reads are first assembled into longer sequences called contigs. These contigs are then grouped into bins based on common characteristics in a process called binning to obtain MAGs. There are several tools that can be used to bin contigs into MAGs. These tools are based on various statistical and machine learning methods and use contig characteristics such as tetranucleotide frequencies, GC content and (Cadenas, 2012; Giordano, 2016; Yocelevszky, 1997) similar abundances across samples (Alneberg et al., 2014; Kang et al., 2019; Nissen et al., 2021).

Consideraciones Metodológicas y Teóricas / Methodological and Theoretical Considerations

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Herramientas alternativas / Comparison with Alternative Tools

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