

MUA Flash presentation:

# Towards better genome assemblies with riboSeed

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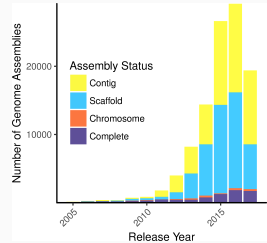
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National University of Ireland, Galway, Ireland  
The James Hutton Institute, Dundee, Scotland

# The Problem



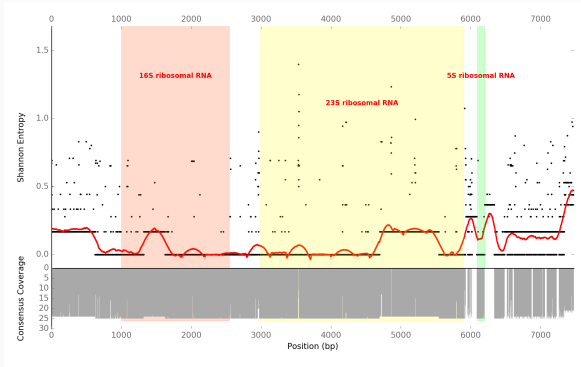
- most assemblies remain unfinished
- Repeated regions complicate genome assembly
- rDNAs are most common repeats (1-15x)



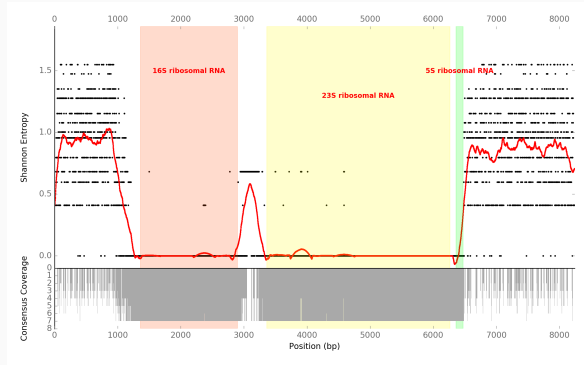
# rDNA context



conserved between strains



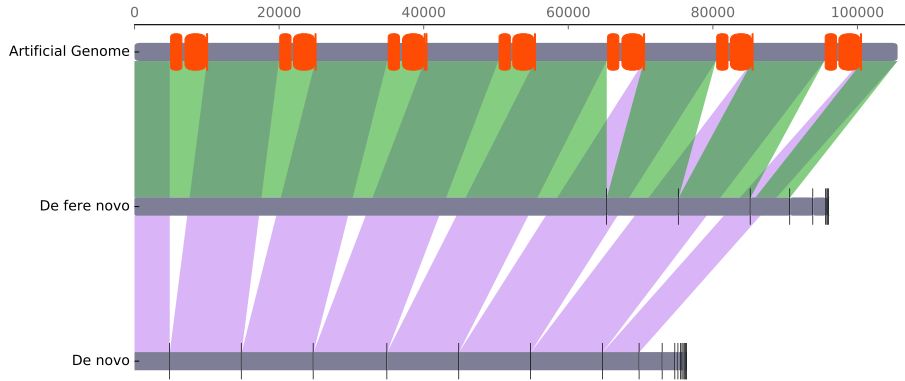
... but not within a genome



# riboSeed's *de fere novo* assembly



🎯 riboSeed  $\approx$  hybrid  $>$  reference-base



Come visit poster #12 to claim a free riboSeed assembly!