

# Virtual Workshop: RAD-seq

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January 13-15, 2026  
10:00 am - 2:00 pm EST

Learn the complete RAD-seq analysis workflow from quality control to variant calling and population structure. This virtual workshop covers Linux basics, RAD-seq data processing, de novo and reference-based variant calling using Stacks and Freebayes, and filtering and formatting variant datasets for downstream analyses. Designed for beginners—no prior bioinformatics experience required.

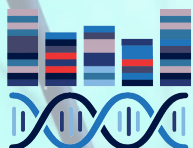
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**Cost:** \$500 (\$400 for UConn affiliates)

**Where:** Live Sessions via MS Teams | Recordings distributed

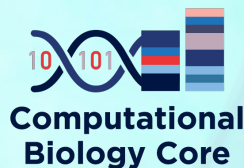
**Register now:** <https://bioinformatics.uconn.edu/cbc-workshops/>

**Questions?** Email [cbcsupport@helpspotmail.com](mailto:cbcsupport@helpspotmail.com)



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