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Modeling ecological drivers in marine viral communities using comparative metagenomics and network analyses

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Protocol Information

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Summary: Long-standing questions in marine viral ecology are centered on understanding how viral assemblages change along gradients in space and time. However, investigating these fundamental ecological questions has been challenging due to incomplete representation of naturally occurring viral diversity in single gene- or morphology-based studies and an inability to identify up to 90% of reads in viral metagenomes (viromes). In this protocol, I describe how to use an annotation- and assembly-free strategy for comparative metagenomics that combines shared k-mer and social network analyses (regression modeling). This robust statistical framework enables visualization of complex sample networks and determination of ecological factors driving community structure. This tutorial describes a protocol to reproduce work from the Pacific Ocean virome comprised of 32 viromes from diverse sites in the Pacific Ocean. "Modeling ecological drivers in marine viral communities using comparative metagenomics and network analyses" (July 7, 2014, doi: 10.1073/pnas.1319778111, PNAS July 22, 2014 vol. 111 no. 29 10714-10719) Code is freely available at Github.

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