example, misleading covariation can result from an incorrect alignment of sequences, or from alignments of sequences that do not function as structured RNAs. Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to

analyze the full alignment. To disable this warning,

run r2r with --disable-usage-warning"

WARNING: R2R is not intended to evaluate evidence

question. It is not appropriate to use R2R's covariation

structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg

"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For

for covariation or RNA structure where this is in

markings to declare that there is evidence of

and Breaker, 2011 wrote:

IMES-3.cons