markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg and Breaker, 2011 wrote:
"This automated R2R annotation [of covariation] does

not reflect the extent or confidence of covariation.

confidence that entirely eliminates the need to analyze the full alignment. To disable this warning,

WARNING: R2R is not intended to evaluate evidence

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

for covariation or RNA structure where this is in

While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For 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

run r2r with --disable-usage-warning"

SAH-P2 cons subfam\_weight=0.632009

63%

63%

SAH.cons showPlace=1

C-G O C-G A U G-C C-G Y-R

0-0

4-72 nt

SAH.cons

