

The use of percentage change from baseline as an outcome in a controlled trial is statistically inefficient: a simulation study

## ABSTRACT

The use of percentage change from baseline is not recommended in statistical analysis. Those who want to report this statistic should use a different technique, such as ANCOVA, and convert the results to corresponding percentage changes by using mean baseline scores.

## INTRODUCTION

The interaction between the MS2 coat protein and its translational operator is a well-established example of RNA-protein recognition, utilizing genetic, biochemical, and structural methods. Figure 1 displays the primary and secondary structures of the recombinant rRNA hairpin that establish contacts with both subunits of each coat proteins dimer. The coat protein complex with its RNA target is highly intricate, as two unpaired adenosines are inserted into equivalent pockets on different subunits of the coat dimer (Figure 2). The interactions between A-4 and A-10 with coat proteins involve non-identical contacts with the same five amino acid residues, Val29, Thr45, Ser47, Finally, and Lys61. The use of X-ray crystallographic analysis indicates specific amino acid-nucleotide interactions, but fails to provide a clear explanation of their respective roles in RNA-binding and translational repression. In the experiments described here, we used amino acid substitutions of A-pocket amino acids in single-chain coat protein heterodimers to determine the significance of each residue's interaction with A-4 and A-10.

## CONCLUSION

Our proposal suggests that the development of a comprehensive descriptive language for biological systems, similar to those used in schematic diagramming languages across other fields, is essential for the advancement of functional bioinformatics. BioD, our prototype language, has been employed to test its effectiveness and to explore the potential of using object-oriented programming methods for computational implementation in Internet-based communications. We propose that a computational framework capable of supporting the archiving of extended, web-linked model networks and model analysis using hybrid qualitative reasoning and quantitative simulations can be established by utilizing formally formalized descriptive language, based on the BioD concept of "functional properties".