

APPENDIX A: RESULTS FOR EV SIMULATIONS

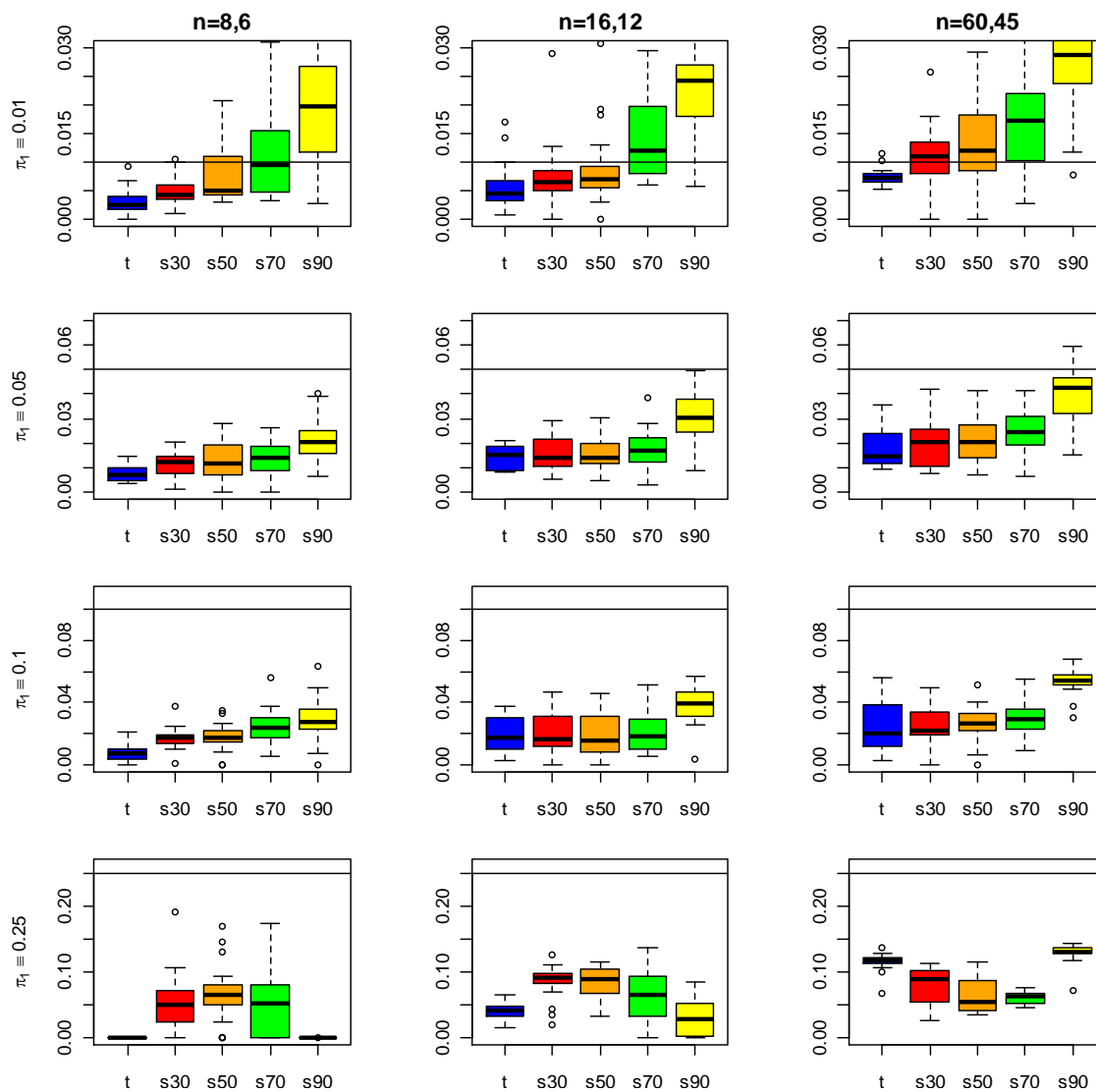


Figure 7. 'fdrtool' estimates of π_1 for the t-statistic and four s-statistics in a type EV simulation with the IQR rescaling factor and t-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

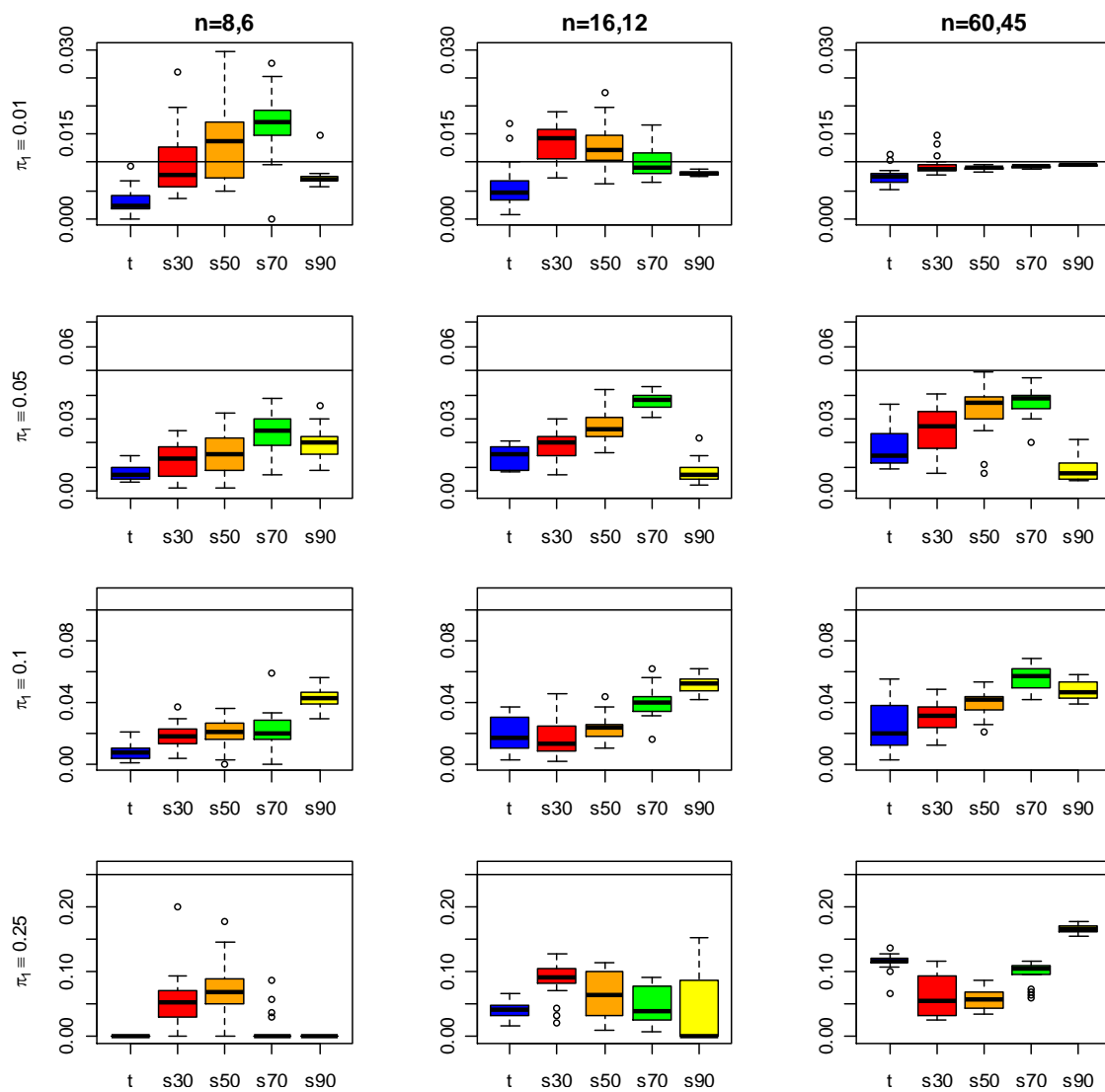


Figure 8. 'fdrtool' estimates of π_1 for the t-statistic and four s-statistics in a type EV simulation with the SD rescaling factor and t-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

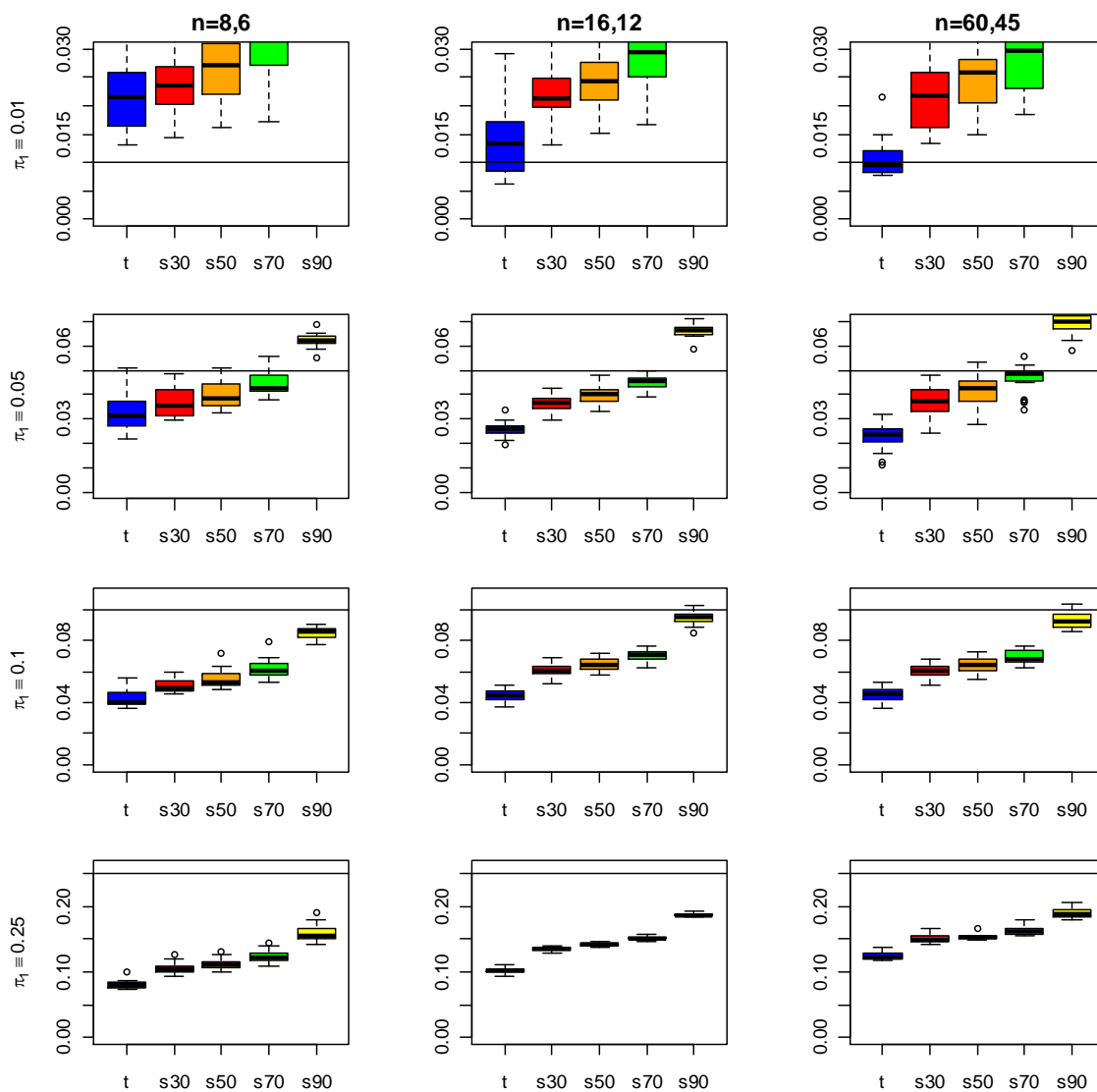


Figure 9. ‘fdrtool’ estimates of π_1 for the t-statistic and four s-statistics in a type EV simulation with the IQR rescaling factor and z-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

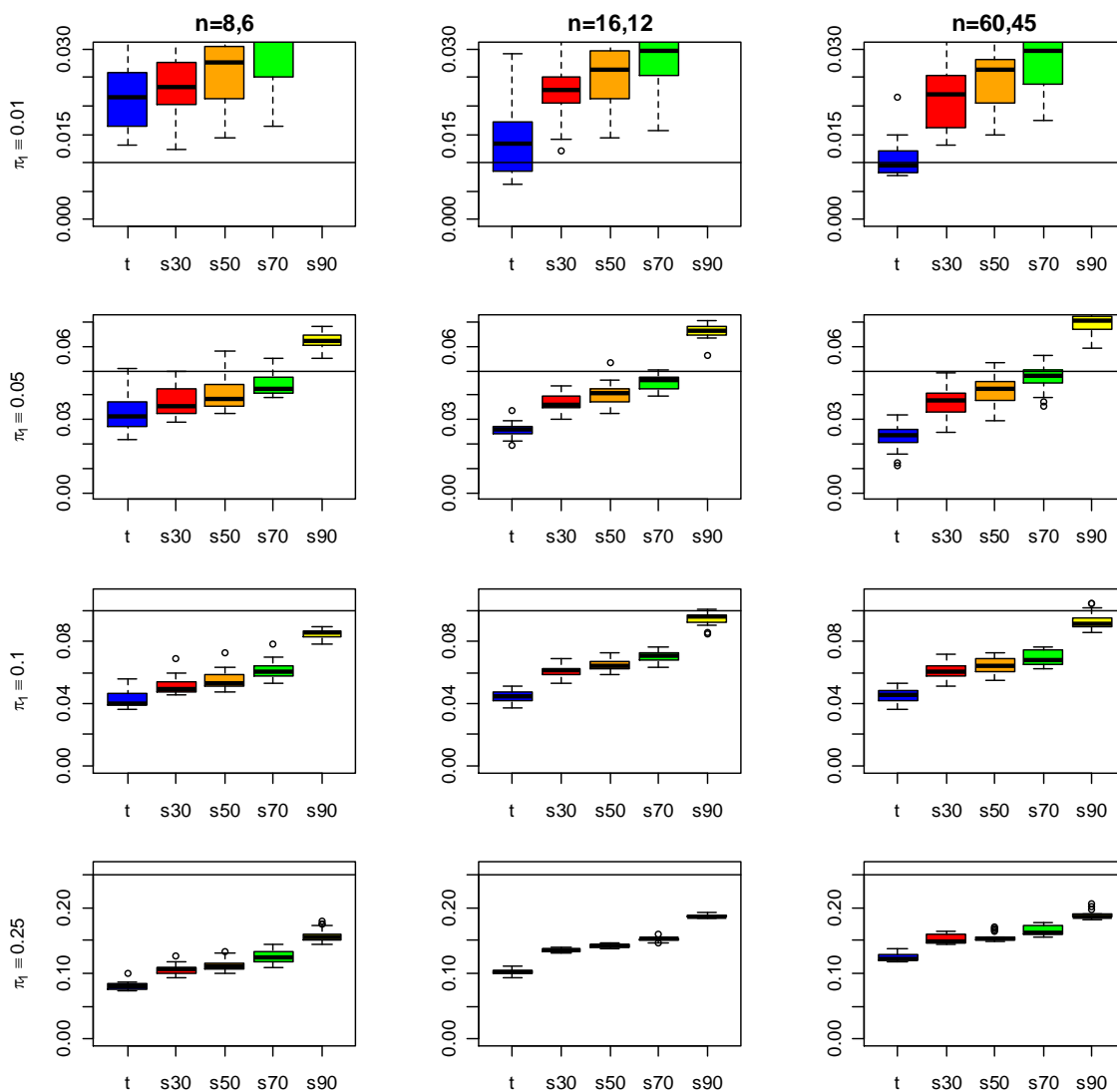


Figure 10. 'fdrtool' estimates of π_1 for the t-statistic and four s-statistics in a type EV simulation with the SD rescaling factor and z-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

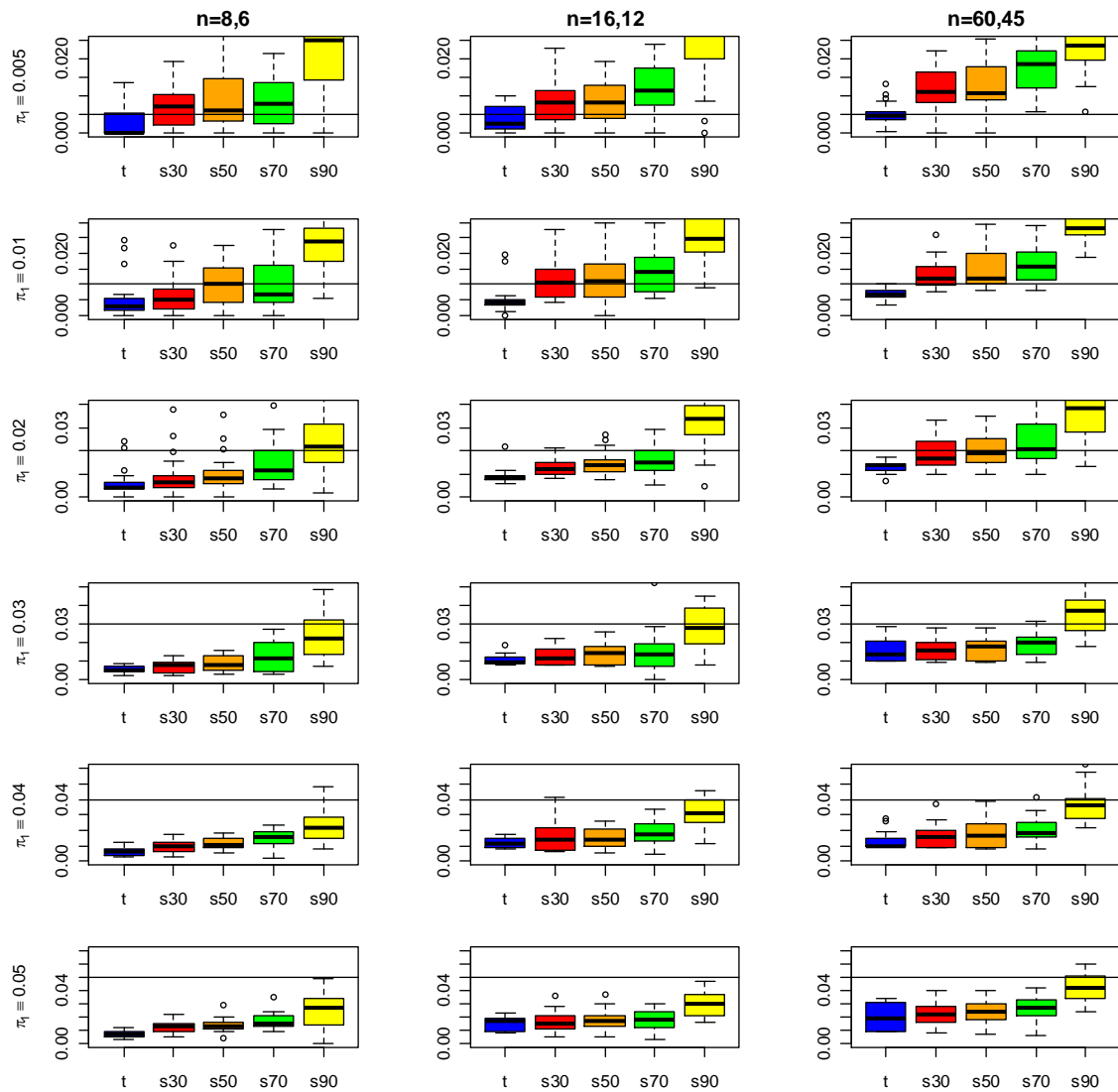


Figure 11. 'fdrtool' estimates of π_1 for the t-statistic and four s-statistics in a type EV simulation with the IQR rescaling factor and t-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

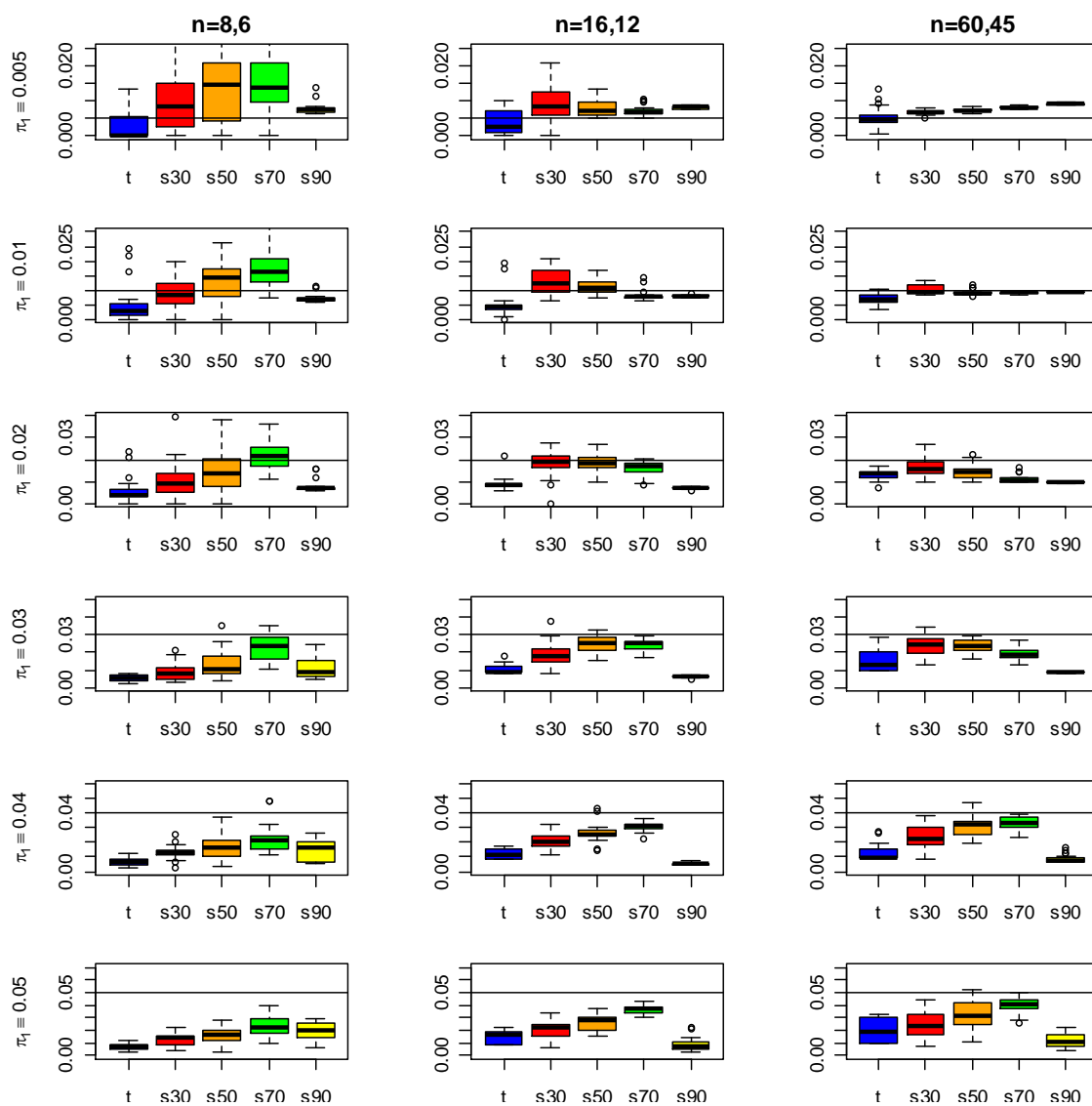


Figure 12. 'fdrtool' estimates of π_1 for the t-statistic and four s-statistics in a type EV simulation with the SD rescaling factor and t-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

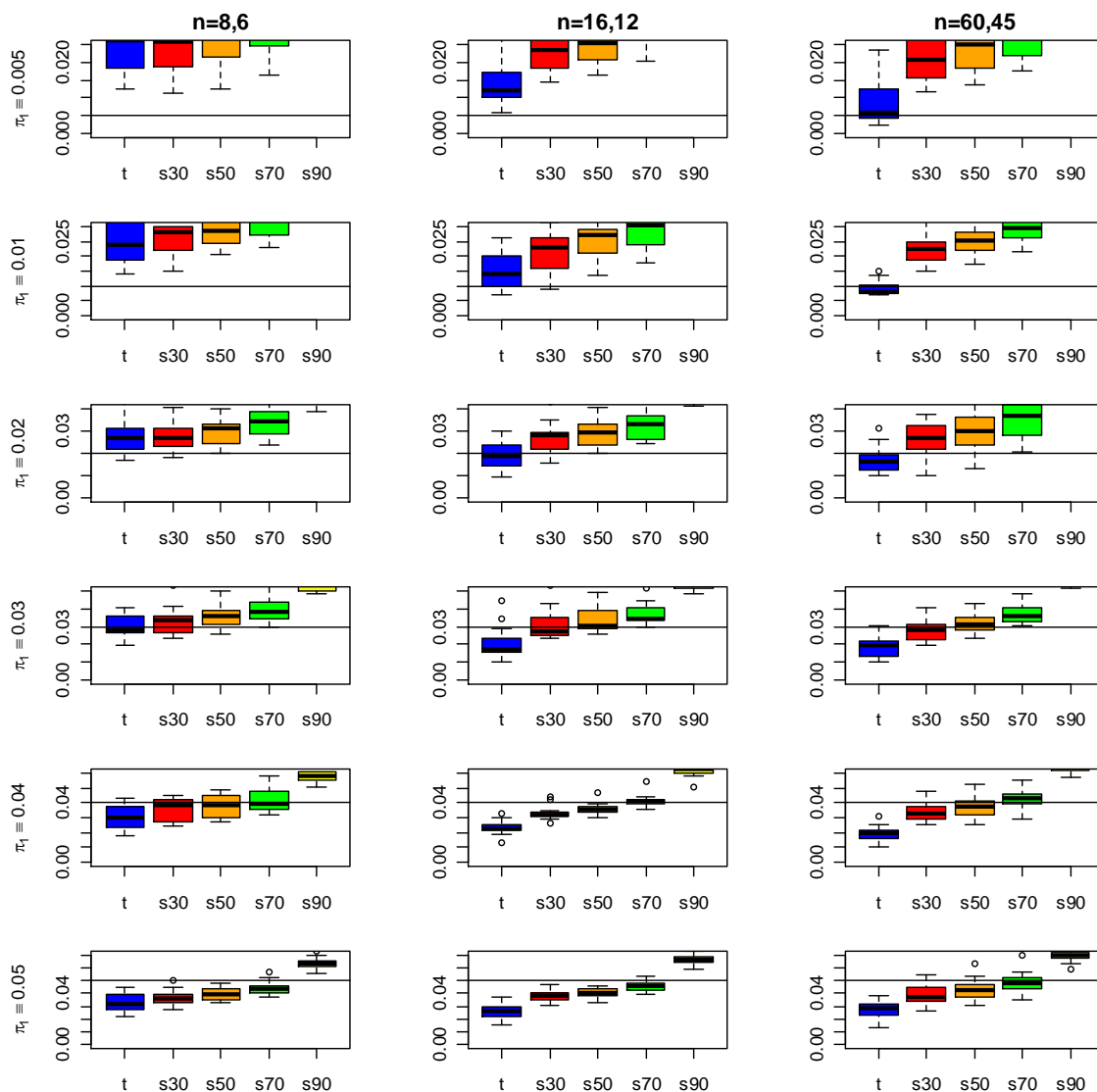


Figure 13. 'fdrtool' estimates of π_1 for the t-statistic and four s-statistics in a type EV simulation with the IQR rescaling factor and z-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

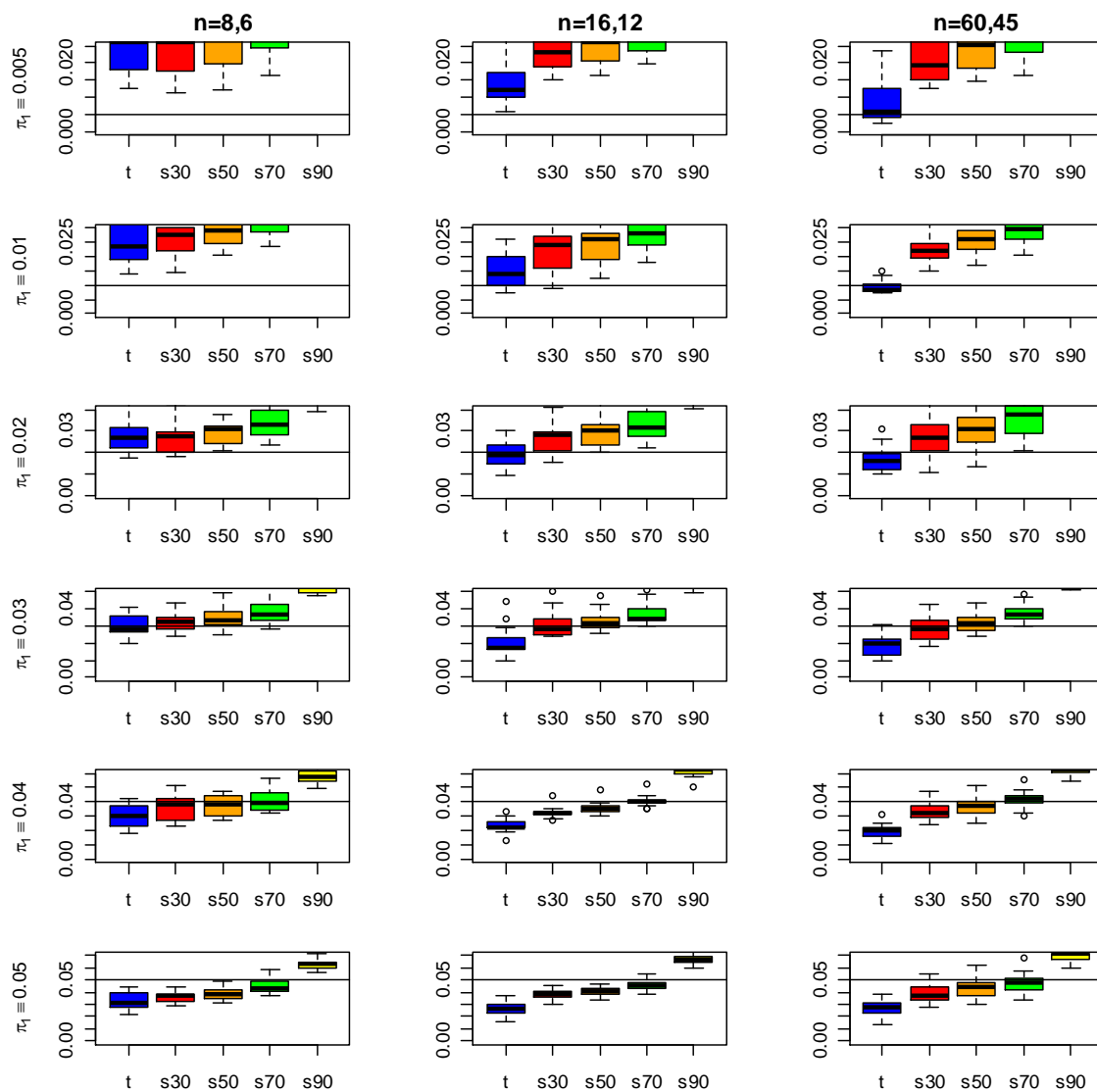


Figure 14. ‘fdrtool’ estimates of π_1 for the t-statistic and four s-statistics in a type EV simulation with the SD rescaling factor and z-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

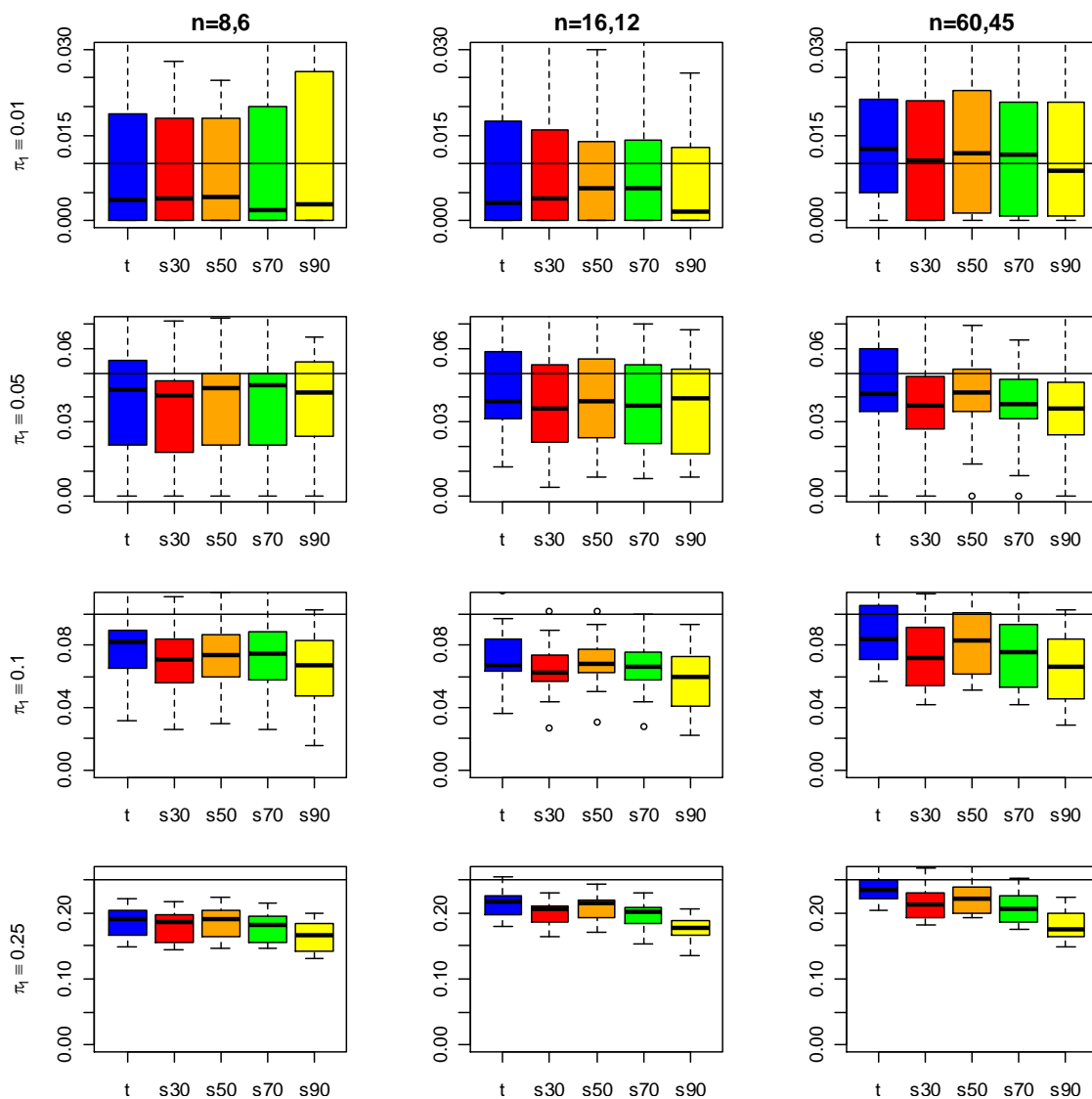


Figure 15. 'qvalue' estimates of π_1 for the t-statistic and four s-statistics in a type EV simulation. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

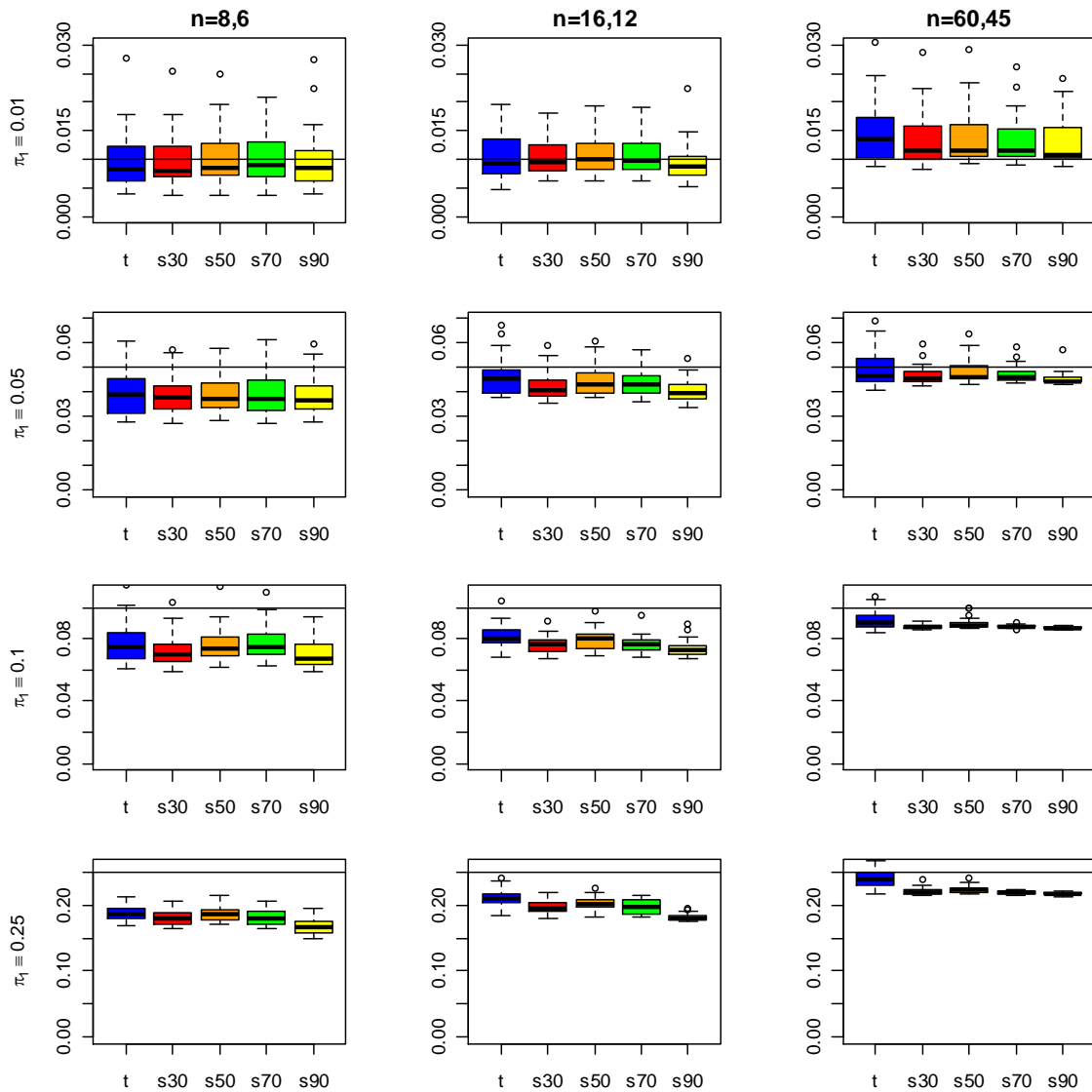


Figure 16. 'convest' estimates of π_1 for the t-statistic and four s-statistics in a type EV simulation. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

APPENDIX B: RESULTS FOR UV1 SIMULATIONS

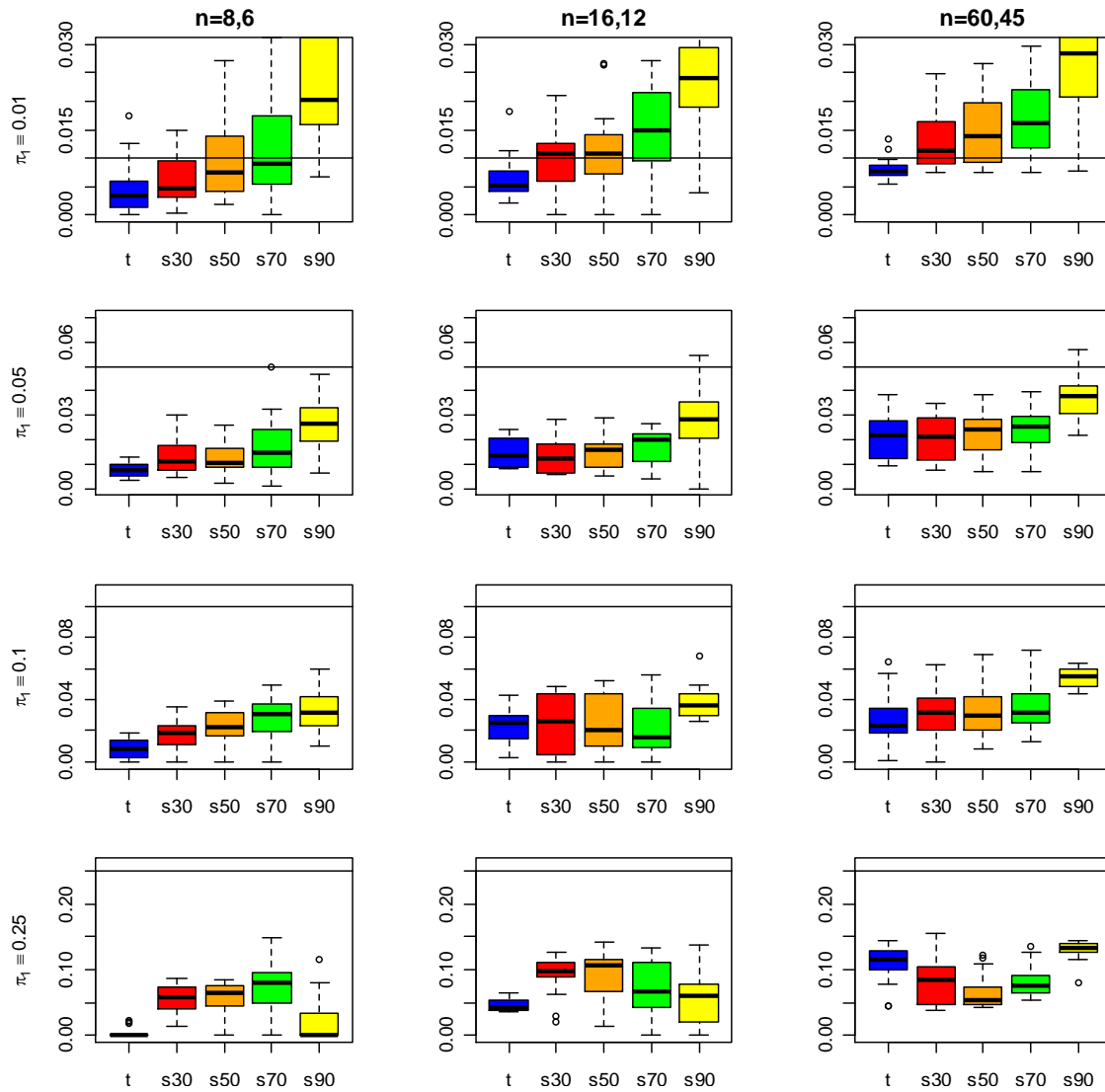


Figure 17. 'fdrtool' estimates of π_1 for the t-statistic and four s-statistics in a type UV1 simulation with the IQR rescaling factor and t-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

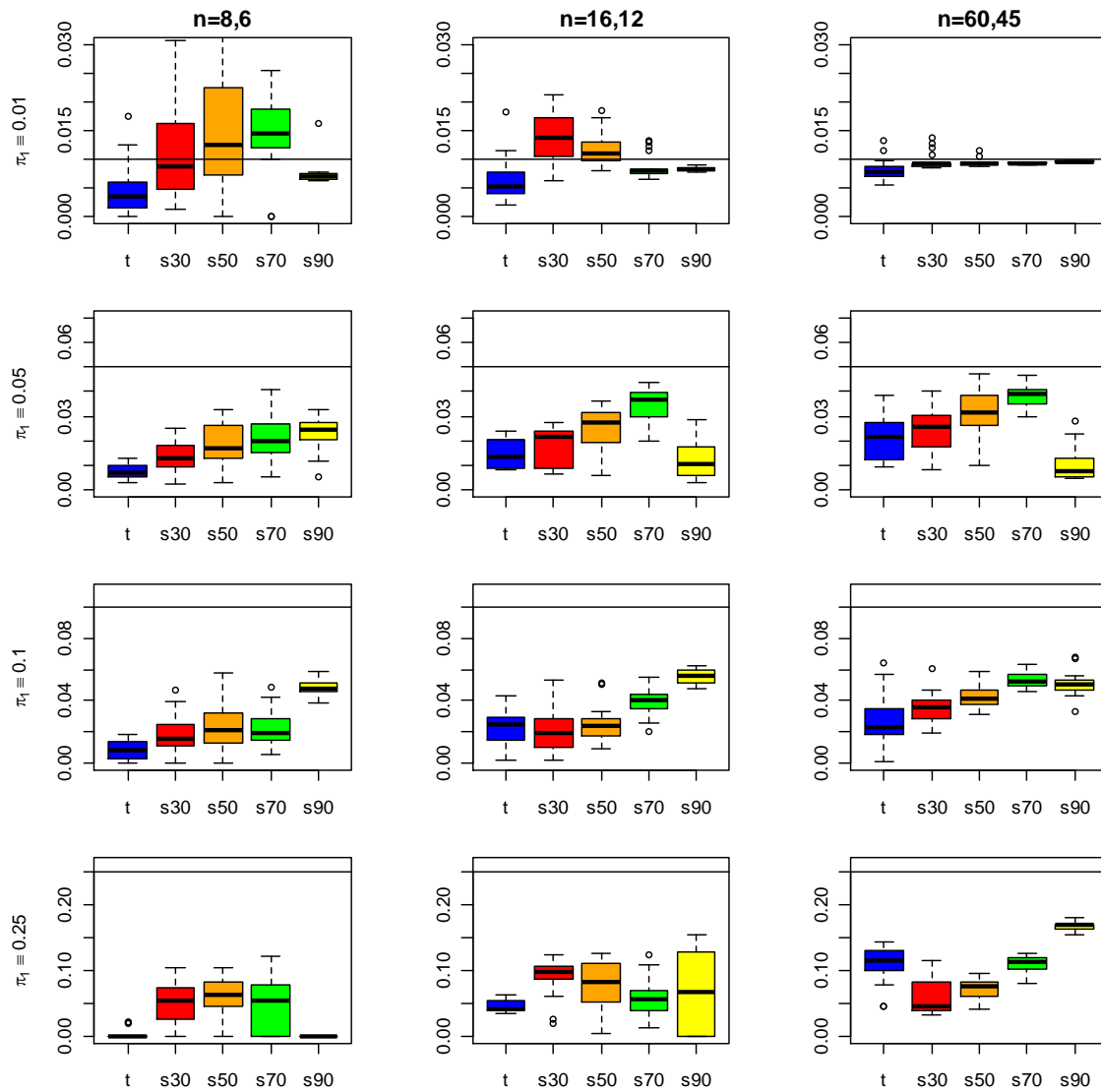


Figure 18. 'fdrtool' estimates of π_1 for the t-statistic and four s-statistics in a type UV1 simulation with the SD rescaling factor and t-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

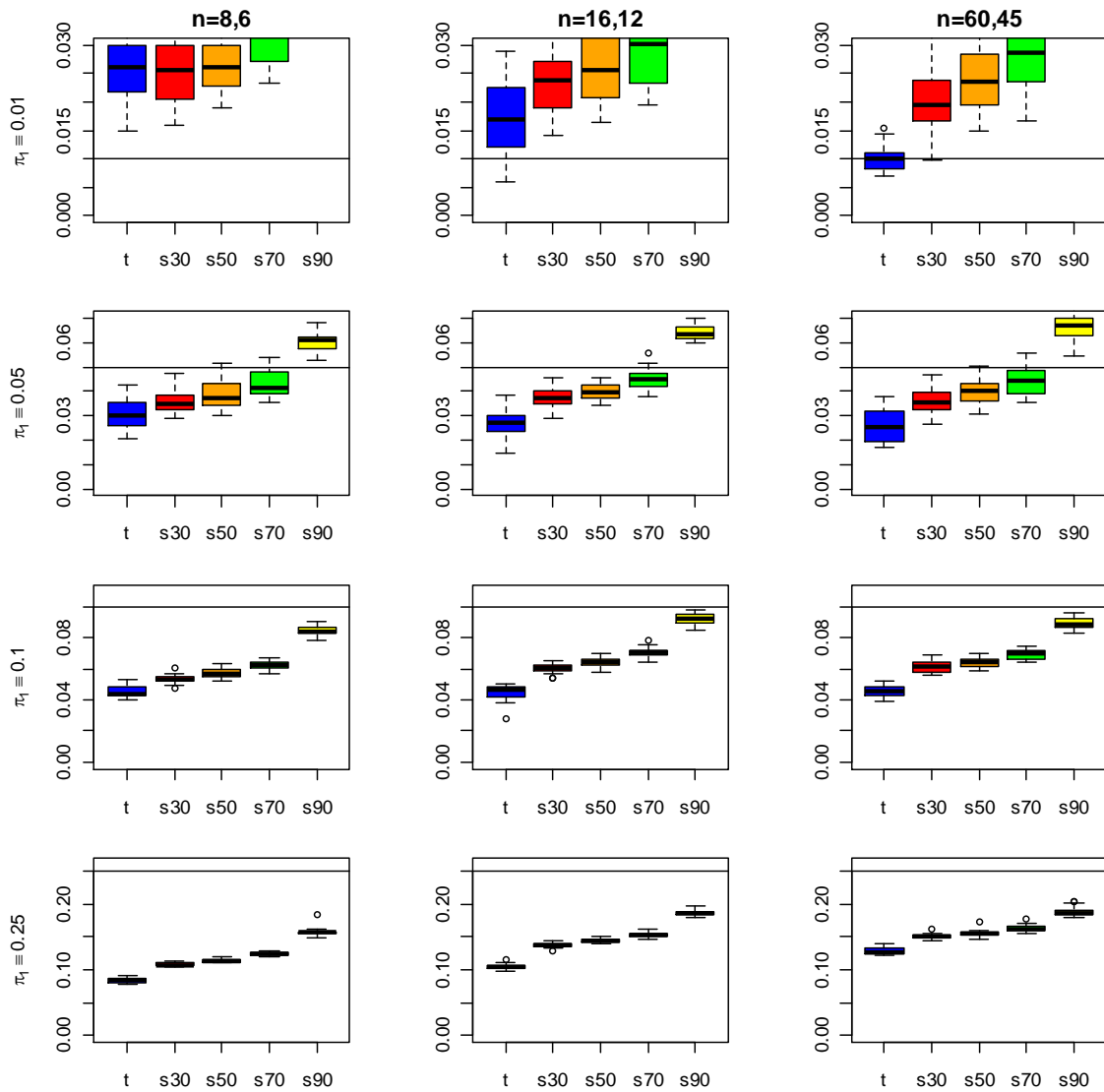


Figure 19. 'fdrtool' estimates of π_1 for the t-statistic and four s-statistics in a type UV1 simulation with the IQR rescaling factor and z-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

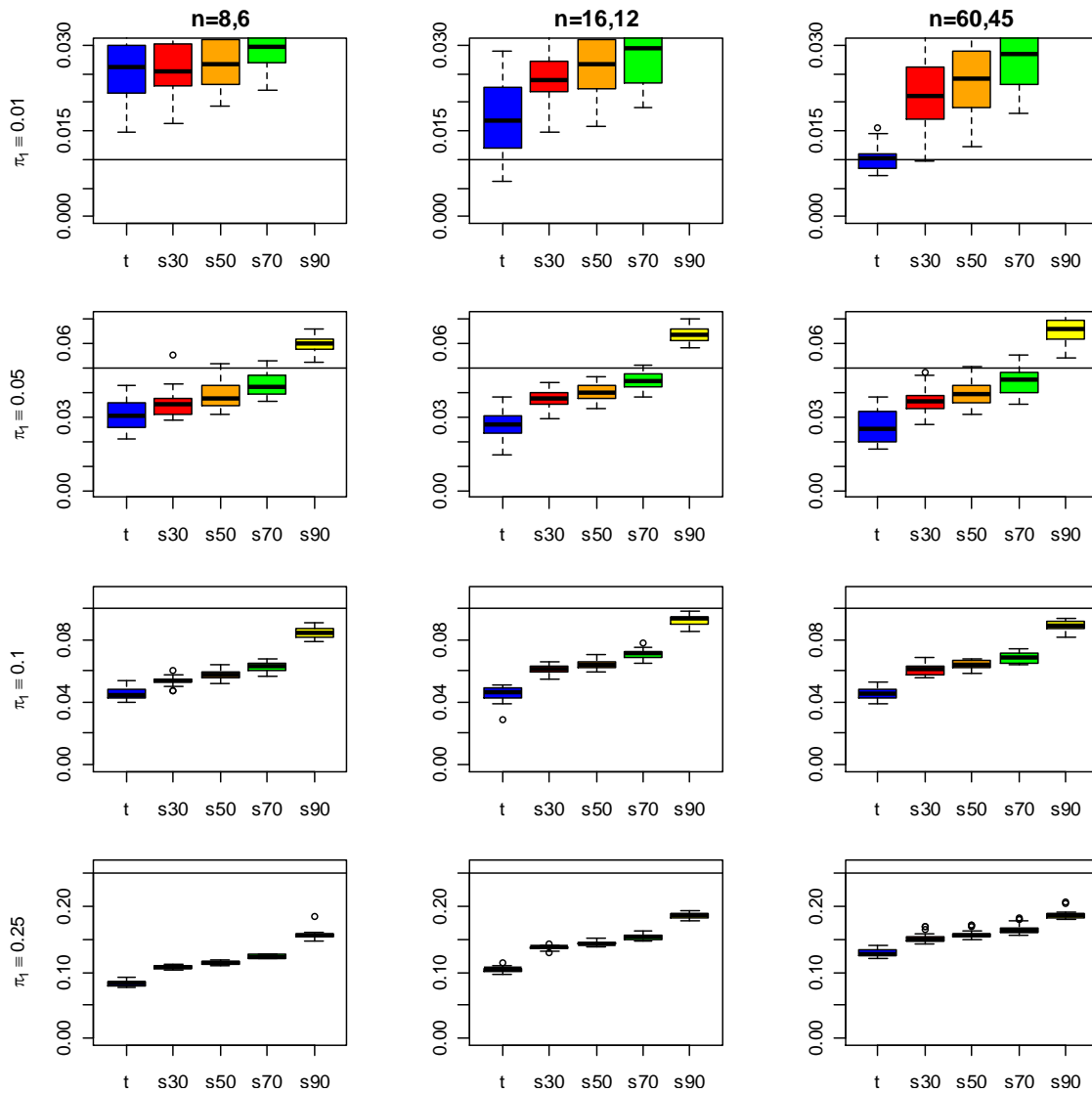


Figure 20. 'fdrtool' estimates of π_1 for the t-statistic and four s-statistics in a type UV1 simulation with the SD rescaling factor and z-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

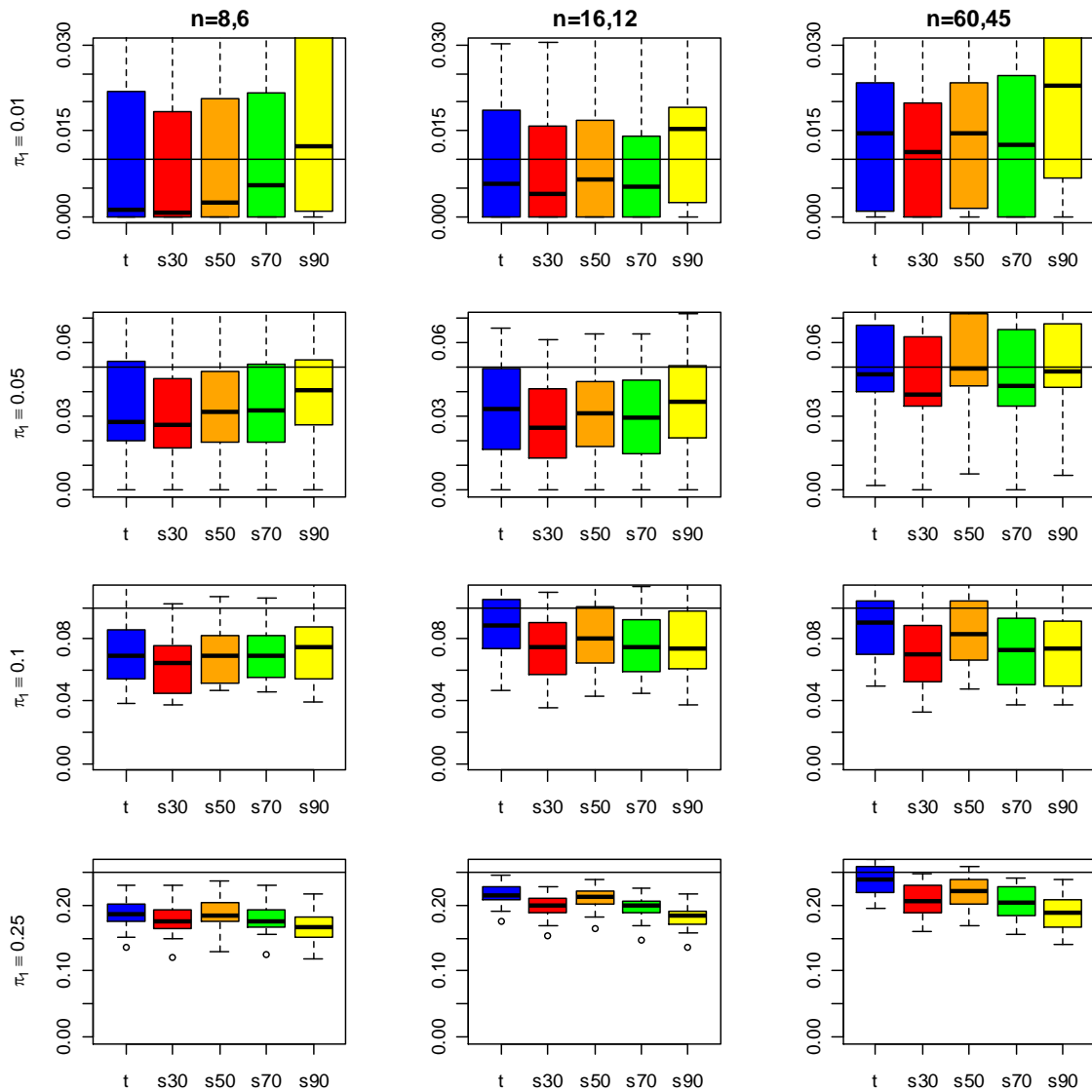


Figure 21. 'qvalue' estimates of π_1 for the t-statistic and four s-statistics in a type UV1 simulation. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

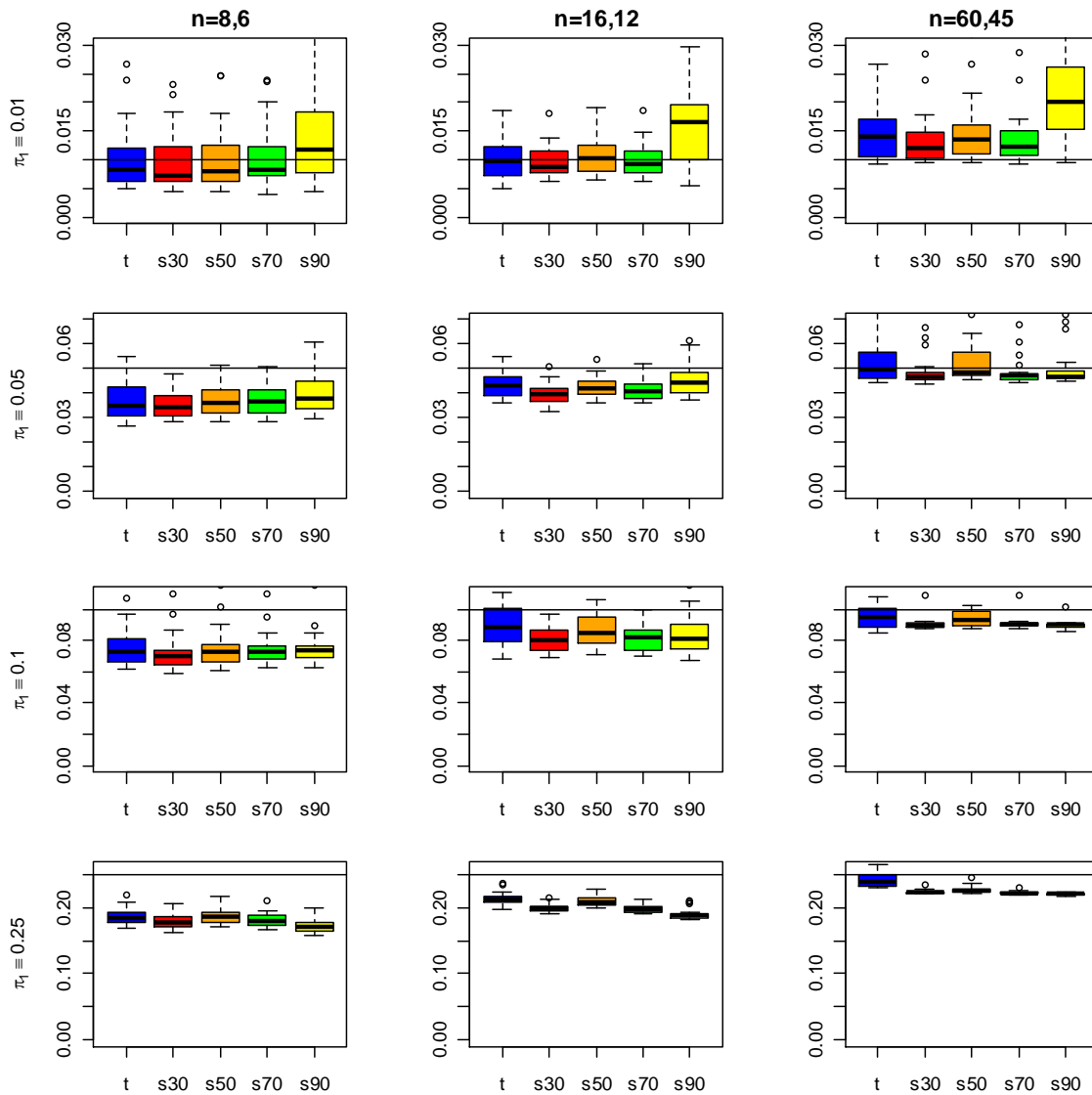


Figure 22. 'convest' estimates of π_1 for the t-statistic and four s-statistics in a type UV1 simulation. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

APPENDIX C: RESULTS FOR UV2 SIMULATIONS

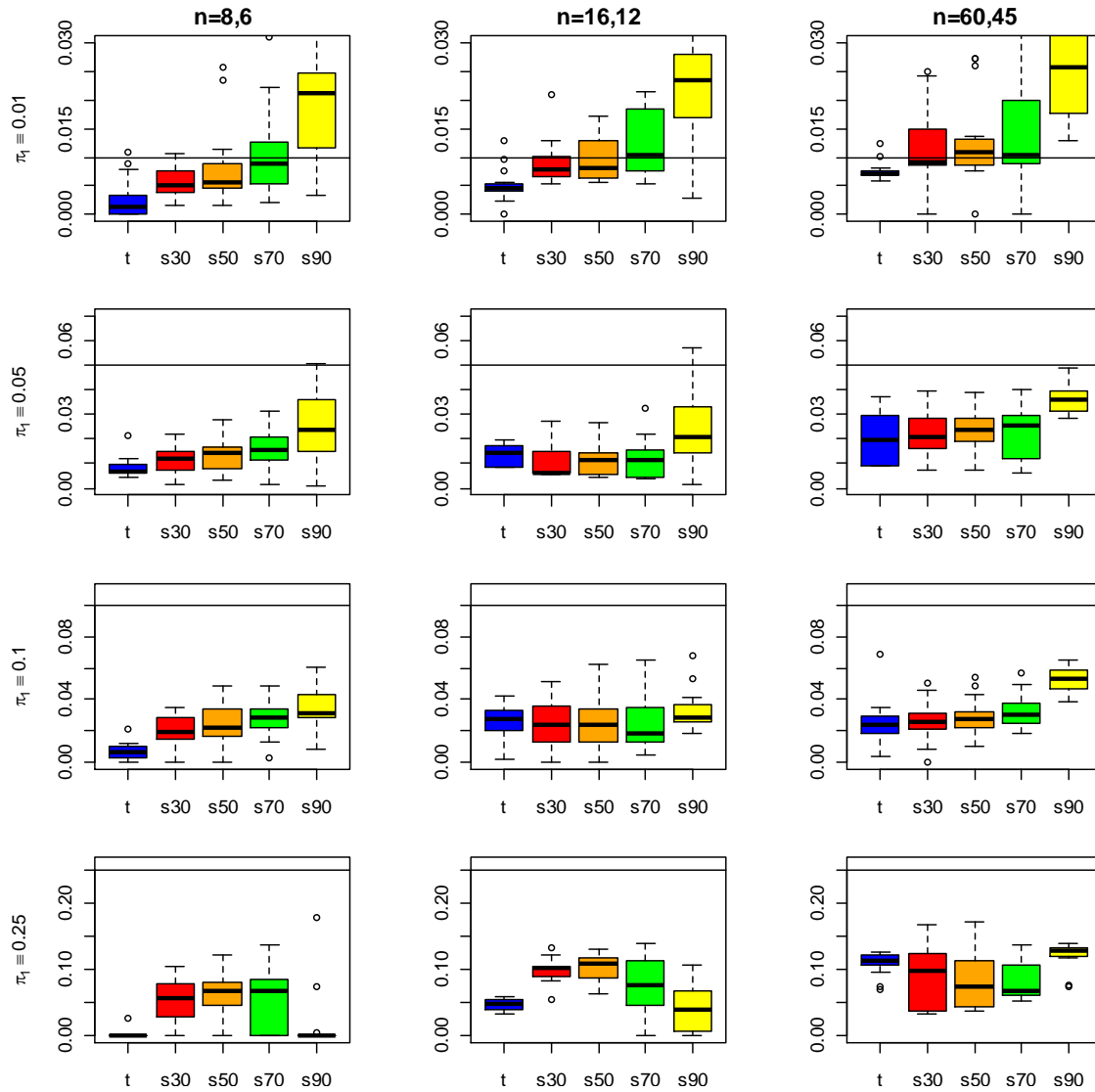


Figure 23. 'fdrtool' estimates of π_1 for the t-statistic and four s-statistics in a type UV2 simulation with the IQR rescaling factor and t-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

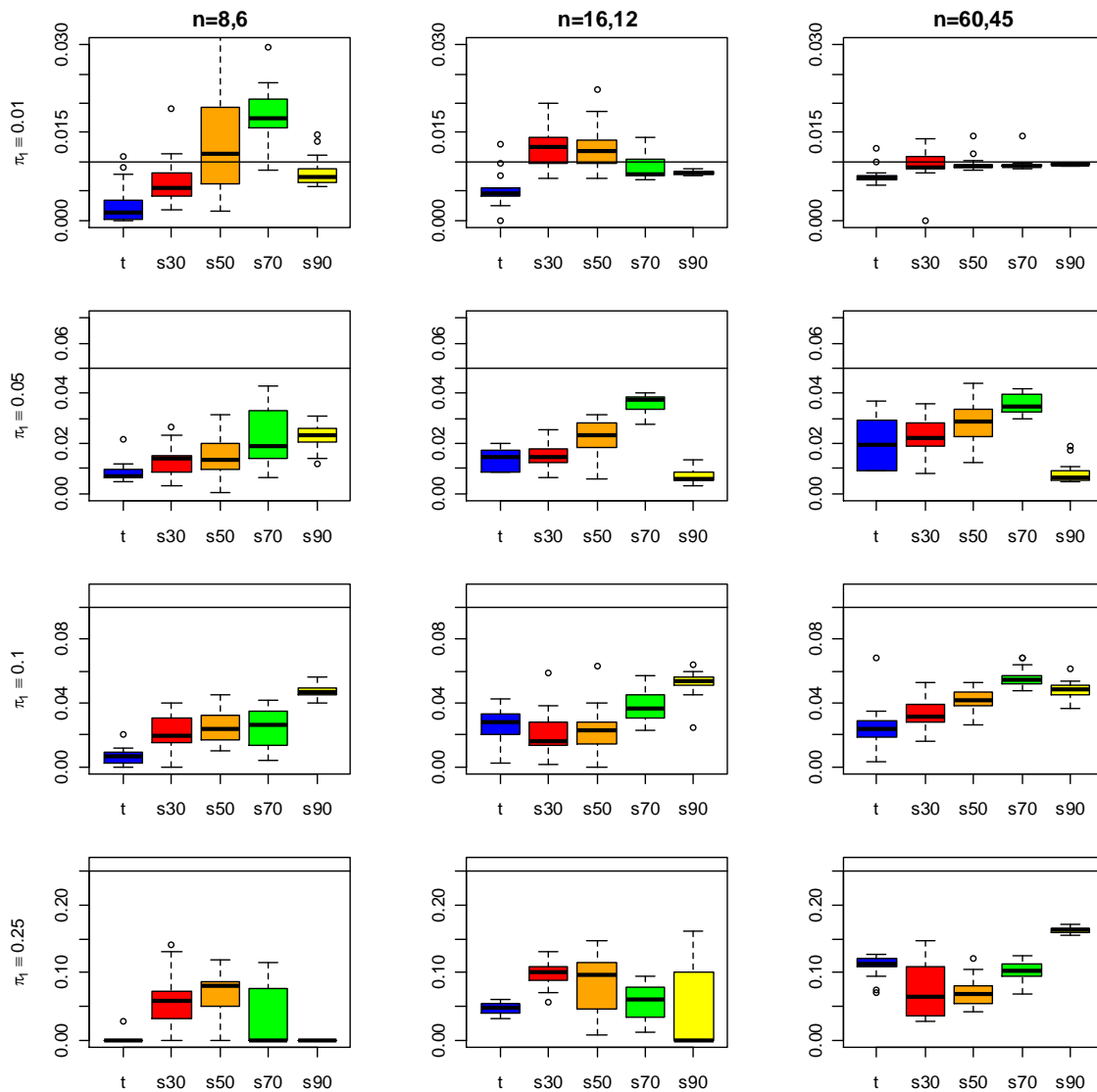


Figure 24. 'fdrtool' estimates of π_1 for the t-statistic and four s-statistics in a type UV2 simulation with the SD rescaling factor and t-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

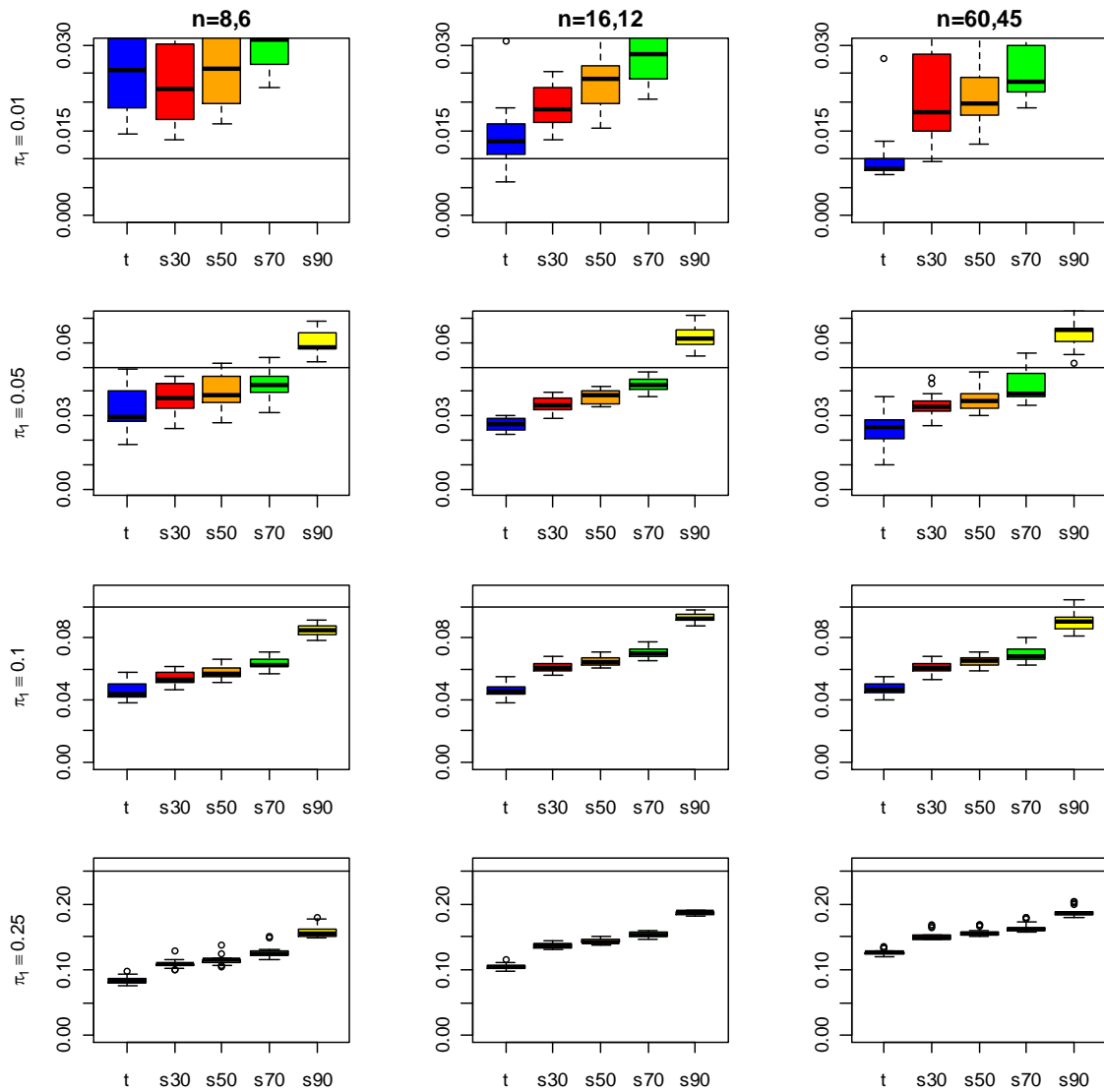


Figure 25. 'fdrtool' estimates of π_1 for the t-statistic and four s-statistics in a type UV2 simulation with the IQR rescaling factor and z-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

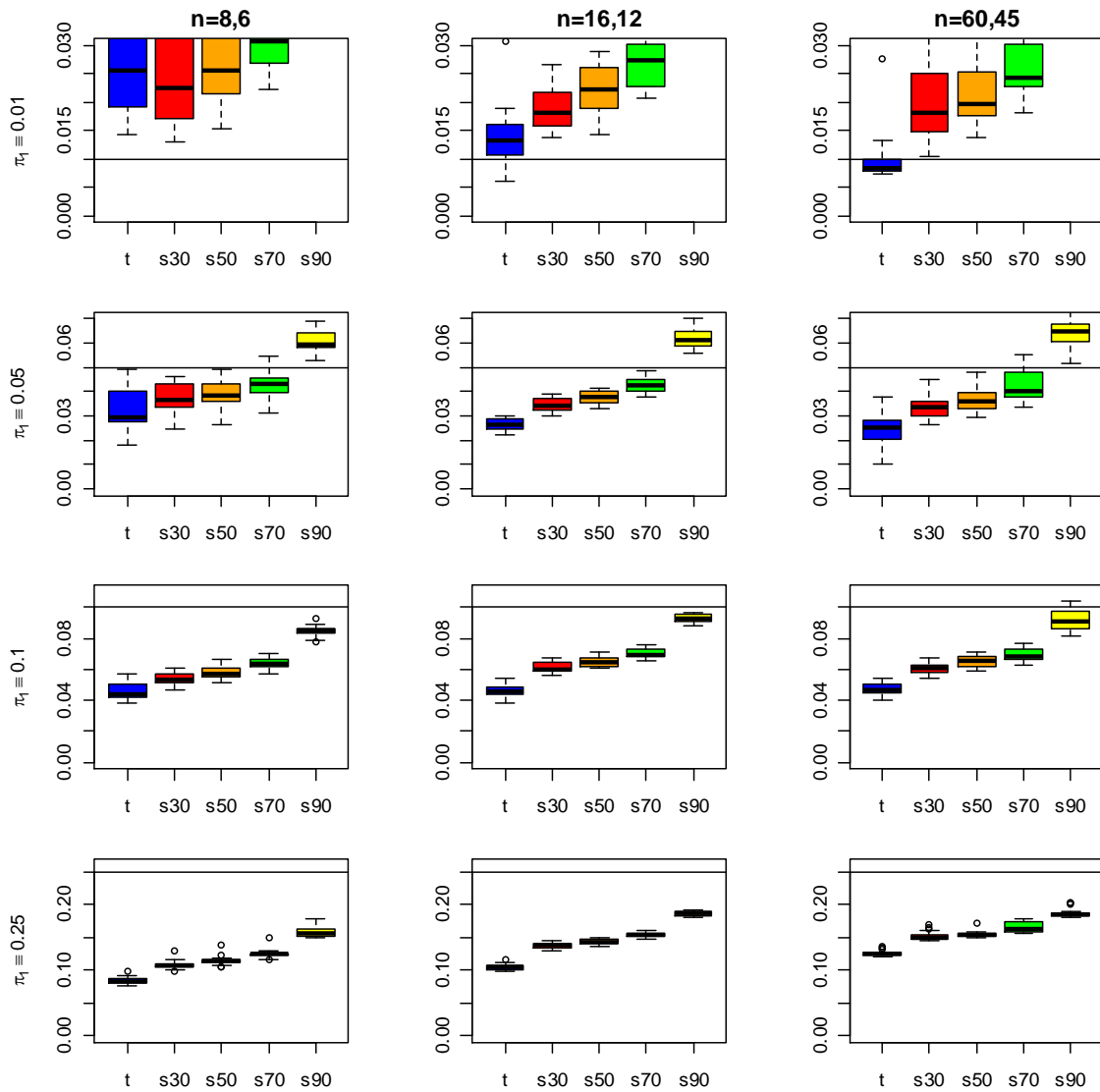


Figure 26. 'fdrtool' estimates of π_1 for the t-statistic and four s-statistics in a type UV2 simulation with the SD rescaling factor and z-statistic input specification. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

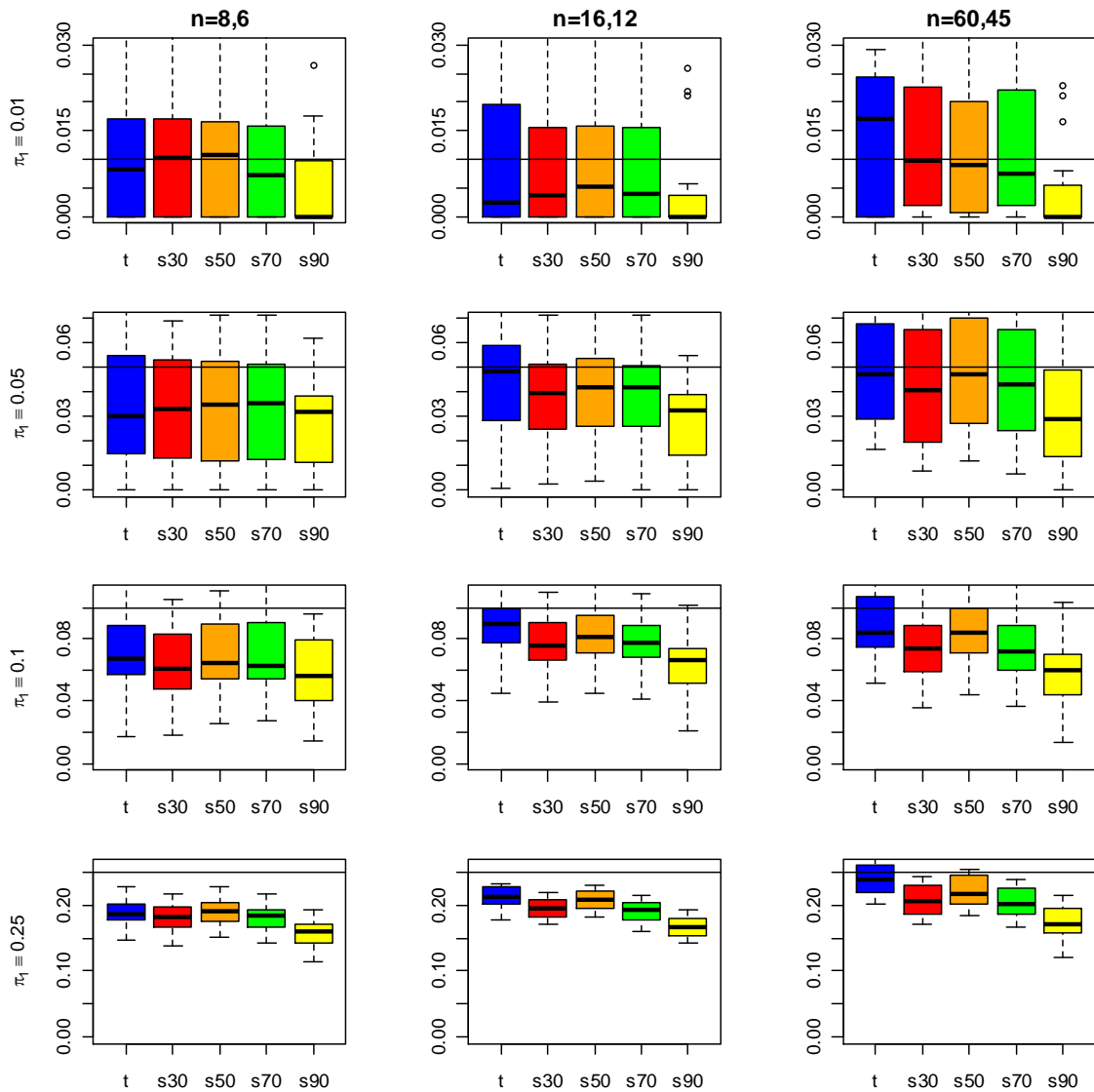


Figure 27. 'qvalue' estimates of π_1 for the t-statistic and four s-statistics in a type UV2 simulation. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.

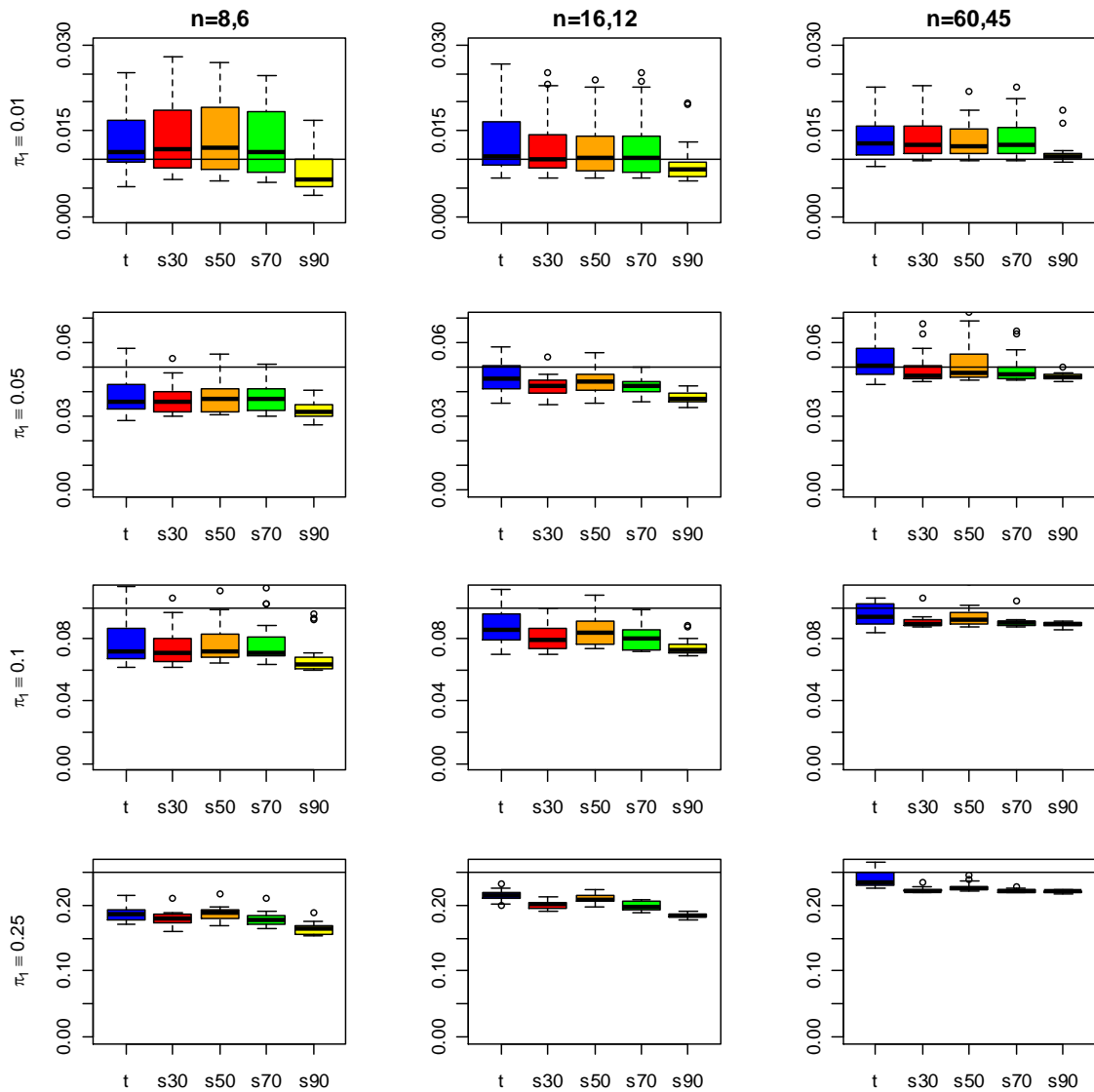


Figure 28. 'convest' estimates of π_1 for the t-statistic and four s-statistics in a type UV2 simulation. A reference line is drawn at π_1 , the true proportion of differentially expressed genes.