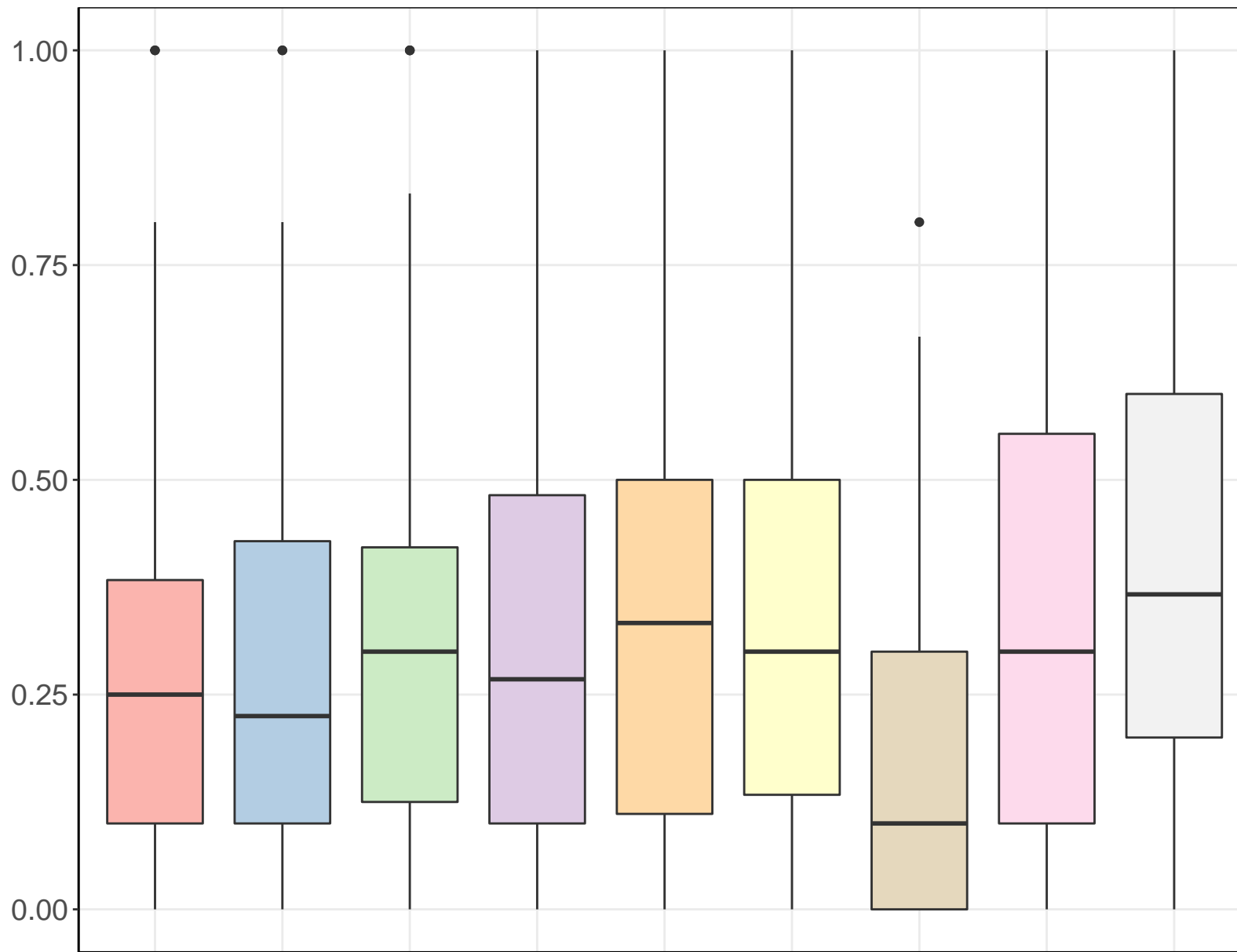


Number of binding positions in top 10 predicted – peptide

hits fraction in top predicted



measurment

method

- aa\_ref\_overlap\_individuals\_change\_ratio
- instances\_individuals\_change\_ratio
- jsd\_100way\_aa\_not\_used\_ratio
- jsd\_100way\_instances\_major\_ratio
- jsd\_mul\_aa\_ref\_SE
- jsd\_SE\_diff\_ratio
- jsds\_ratio
- jsds\_subtraction
- SE\_jsd\_diff\_ratio