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Data: Data frame input by user
Result: Interactive litre plot
/* Declare Shiny server
server \leftarrow function(input, output, session){
   /* User input options
   observeEvent(inputsoButton, valuesx \leftarrow valuesx + 1)
   observeEvent(input$selPair, values$x \leftarrow 0)
   observeEvent(input$selMetric, values$x \leftarrow 0)
   observeEvent(input$selOrder, values$x \leftarrow 0)
   observeEvent(input$binSize, values$x \leftarrow 0)
    /* Create reactive expression of plotly background litre plot
   gP \leftarrow reactive(p \leftarrow ggplot(data); gP \leftarrow ggplotly(p))
    /* Declare shiny output litre plot
   output$hexPlot \leftarrow renderPlotly({
        /* Create reactive expression of plotly background litre plot
       plotlyHex \leftarrow reactive(gP())
       /* Tailor interactivity of the plotly litre plot object using custom
       plotlyHex() %>% onRender("function(el, x, data){
           /* Read handle called 'points' to obtain variables sent from R into
           Shiny.addCustomMessageHandler('points', function(drawPoints){
               /* Delete any old superimposed plotly geoms (dots)
               if (x.data.length > 0){Plotly.deleteTraces(el.id)}
               /* Create traces for selected gene IDs as points that state gene
                names upon hovering
               {\bf trace} = {\bf x} {:} \; {\bf drawPoints.geneX}, \, {\bf y} {:} \; {\bf drawPoints.geneY}, \, {\bf mode} {:}
                'markers', color: drawPoints.pointColor, size:
                drawPoints.pointSize, text: drawPoints.geneID, hoverinfo:
                'text'
               /* Superimpose traces onto the plotly litre plot object
               Plotly.addTraces(el.id, trace)
           })
       }")
    })
   /* If the user changes the superimposed gene
   observe({
    /* Save information about superimposed gene selected by user with a
     handle called 'point'. These values can then be sent from R to JavaScript
   session$sendCustomMessage(type = "points",
     message=list(geneX=geneX, geneY=geneY, pointSize = pointSize,
     geneID=geneID, pointColor=pointColor))
   /* Declare Shiny output boxplot
   output$boxPlot \leftarrow renderPlotly({
```

/* Create reactive errorssion of plotly background bornlot RP \leftarrow