

Data: Data frame input by user

Result: Interactive parallel coordinate plot

/ Declare Shiny server*

```
server ← function(input, output, session){
```

```
  /* Create an empty ggplotly object with same dimensions as data
```

```
  p ← ggplot(); gp ← ggplotly(p)
```

```
  /* Send user-defined line color into onRender() function
```

```
  session$sendCustomMessage(type = "lines", message = list(lineColor = lineColor))
```

```
  /* Declare Shiny output parallel coordinate plot
```

```
  output$pcpPlot ← renderPlotly({
```

```
    /* Tailor interactivity of plotly parallel coordinate plot using custom JavaScript
```

```
    gp %>% onRender("function(el, x, data){
```

```
      /* Define rects array object to hold IDs of remaining lines
```

```
      var rects = []
```

```
      /* Draw lines for the original dataset
```

```
      var pcpLine = {x: xArr, y: yArr, mode: 'lines', color: data.lineColor}
```

```
      Traces.push(pcpLine)
```

```
      Plotly.addTraces(el.id, Traces)
```

```
      /* If the user draws a rectangle
```

```
      el.on('plotly_selected', function(e){
```

```
        /* Delete lines outside the user-defined rectangle
```

```
        Traces.push(delLine)
```

```
        Plotly.addTraces(el.id, Traces)
```

```
        /* Create new object called pcpDat that only contains genes within rectangle
```

```
        /* Push IDs of remaining lines to rects array object
```

```
        for (a=0; a<pcpDat.length; a++){rects.push(pcpDat[a]['ID'])}
```

```
        /* Save remaining gene IDs in an object called rects with handle called 'rects' so it can be read outside  
        current JavaScript function back in Shiny
```

```
        Shiny.onInputChange('rects', rects)
```

```
      })
```

```
    })
```

```
    /* Pass R objects into the JavaScript function
```

```
    ", data = list(pcpDat = pcpDat, lineColor = lineColor)
```

```
  })
```

```
  /* Read into Shiny the gene IDs that remain within rectangle drawn by user
```

```
  inputRectDf ← reactive(input$rects)
```

```
  /* Print the selected gene IDs in interactive data table
```

```
  output$rectdf = renderDataTable(pcpDat %>% filter(ID %in% inputRectDf()))
```

```
}
```

S4 Pseudocode: Pseudocode for interactive parallel coordinate plot