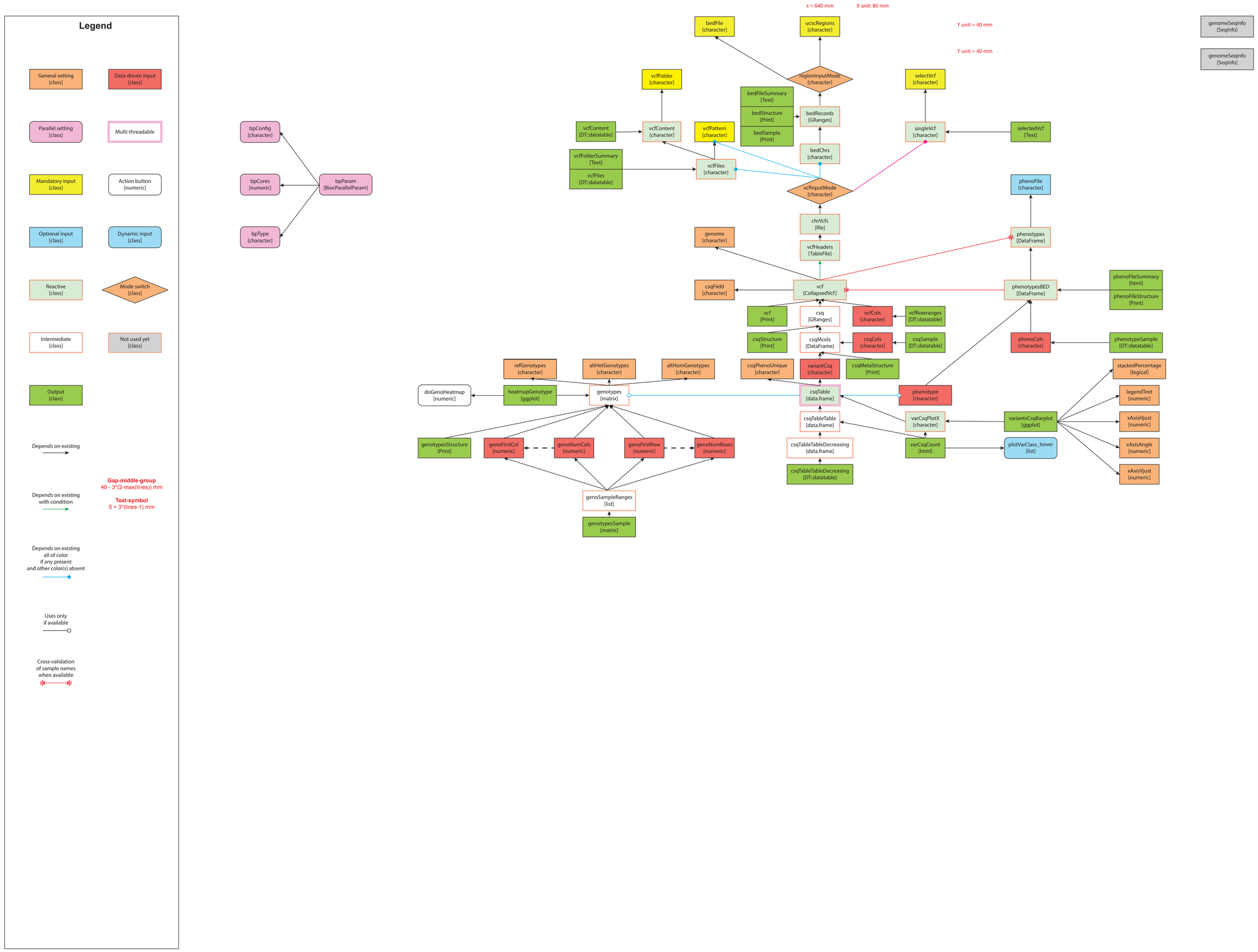
Legend
General setting [class]
Data-driven input [class]
Parallel setting [class]
Multi-threadable
Mandatory input [class]
Action button [numeric]
Optional input [class]
Dynamic input [class]
Reactive [class]
Mode switch [class]
Intermediate [class]
Not used yet [class]
Output [class]
Depends on existing
Depends on existing with condition
Gap-middle-group
40 - 3*(2-max(lines)) mm
Text-symbol
5 + 3*(lines-1) mm
Depends on existing all of color if any present and other color(s) absent
Uses only if available
Cross-validation of sample names when available
x = 640 mm
X unit: 80 mm
Y unit = 40 mm
Y unit = 40 mm
bpConfig [character]
bpCores [numeric]
bpType [character]
bpParam [BiocParallelParam]
bedFile [character]
ucscRegions [character]
genomeSeqinfo [Seqinfo]
genomeSeqinfo [Seqinfo]
regionInputMode [character]
vcfFolder [character]
selectVcf [character]
bedFileSummary [Text]
bedStructure [Print]
bedSample [Print]
bedRecords [GRanges]
vcfContent [DT::datatable]
vcfContent [character]
vcfPattern [character]
singleVcf [character]
selectedVcf [Text]
bedChrs [character]
vcfFolderSummary [Text]
vcfFiles [DT::datatable]
vcfFiles [character]
vcfInputMode [character]
phenoFile [character]
chrVcfs [Rle]
genome [character]
vcfHeaders [TabixFile]
phenotypes [DataFrame]
csqField [character]
vcf [CollapsedVcf]
phenotypesBED [DataFrame]
phenoFileSummary [html]
phenoFileStructure [Print]
vcf [Print]
csq [GRanges]
vcfCols [character]
vcfRowranges [DT::datatable]
csqStructure [Print]
csqMcols [DataFrame]
csqCols [character]
csqSample [DT::datatable]
phenoCols [character]
phenotypeSample [DT::datatable]
refGenotypes [character]
altHetGenotypes [character]
altHomGenotypes [character]
csqPhenoUnique [character]
variantCsq [character]
csqMetaStructure [Print]
stackedPercentage [logical]
doGenoHeatmap [numeric]
heatmapGenotype [ggplot]
genotypes [matrix]
csqTable [data.frame]
phenotype [character]
legendText [numeric]
csqTableTable [data.frame]
varCsqPlotX [character]
variantsCsqBarplot [ggplot]
xAxisHjust [numeric]
genotypesStructure [Print]
genoFirstCol [numeric]
genoNumCols [numeric]
genoFirstRow [numeric]
genoNumRows [numeric]
csqTableTableDecreasing [data.frame]
varCsqCount [html]
plotVarClass_hover [list]
xAxisAngle [numeric]
csqTableTableDecreasing [DT::datatable]
xAxisVjust [numeric]
genoSampleRanges [list]
genotypesSample [matrix]