## ggbio: extending the grammar of graphics for genomic data Tengfei Yin<sup>1</sup>, Dianne Cook<sup>1</sup>, Michael Lawrence<sup>2</sup> 1. Iowa state university 2. Genentech Research and Early Development, Inc. Geometric object: We introduce ggbio, a new methodology to geonm arch: arches visualize and explore genomics annotations geom chevron: chevron and high-throughput data. The plots provide geom\_alignment: rectangle with chevron detailed views of genomic regions, summary geom arrow: small arrow geom\_arrowrect: rectangle with arrow views of sequence alignments and splicing geom\_bar: barchart patterns, and genome-wide overviews with geom\_segment: segment geom karyogram, circular and grand linear layouts. Statistical transformation: stat\_mismatch: mismatch summary stat reduce: single gene structure stat\_coverage: coverage stat table: tabulate intervals Subset of the data.: stat\_aggregate: summary over bins facet\_gr: facet by ranges, stat\_stepping: avoid overlapping stat facet\_seqnames: facet by stat\_slice: peak finding seqnames stat identity: do nothing facet data Core bioconductor data objects. tx\_id exon\_id strand ranges seqnames 132624 [48242968, 48243005]35775 [48243475, 48243563]132625chrXGrammar of graphics 35775132626chrX[48244003, 48244117] 132627chrX[48244794, 48244889] chrX35775132628[48246753, 48246802][48270193, 48270307] 35778132637chrXchrX[48269421, 48269516] 35778132636chrX[48267508, 48267557] 3577813263535778132633 chrX[48262894, 48262998] [48261524, 48262111]35778132632 Example of GRanges object coord scale chrX kb bp Mb Scale: chrY chrX scale x unit: Mb, kb or bp scale\_fill\_fold\_change: low Coordinate system: for blue, hight for red and linear: default, facet by chromosome genome: show as linear genome truncate\_gaps: remove gaps between intervals Specialized plots Layout and tracks Annotation geometric object: chevron scale: strands are mapped to color

