About annots.xml

Use annots.xml to specify track color, annotation style, and more

An **annots.xml** file resides in an IGB QuickLoad genome directory. It lists all data files available for that genome.

The file contains one or more **file** tags, enclosed in a **files** element. The file tag has attributes that control how the data looks when loaded as new track into IGB. Many options correspond to options you can configure using the **Annotation** or **Graph** tabbed panels in IGB**.**

attribute	optional	Description
name	**Required**	The path to the file on the Quickload site itself *or* an absolute URL. The URL can point to any file, anywhere, provided it's accessible via the internet.
		You can specify the location of the file using an absolute URL or the path to the file **relative to the genome version directory** where the annots.xml file resides.
		ex) file path
		filename="bamfiles/treatment.bam" - a directory "bamfiles" must reside in the genome version directory, alongside annots.xml for that genome version
		ex)
		name="http://www.example.com/bamfiles/treatment.bam" (absolute)
		If the file is a reference file, such as 2bit, the reference option must be set to "true".
index	Optional	If the file is a BAM, CRAM, or tabix indexed file, then IGB assumes the index file has the same name as the target file with a standard extension appended. BAM file indexes have extension ".bai", CRAM file indexes have extension ".crai", and tabix indexes have extension ".tbi."
		However, if the index is in a different location or has a non-standard name, you can specify its location and file name using the index attribute.
		ex) file path
		index="indexes/myindex.tbi"
		ex) absolute URL
		index="http://www.example.com/indexfile.bai"
title	**Required**	User-friendly text IGB will show in the **Data Access Panel** as the title of the data set.
		If you would like IGB to display data set titles in nested folders in the **Available Data Sets** section of the Data Access panel, insert the folder separator character "/" used under the Unix operating system (a forward slash) into the title.
		For example, if a file title is RNA-Seq/Treatment/Sample1, then IGB displays the data set named Sample1 inside a named Treatment inside another folder named RNA-Seq.
description	Optional	IGB displays this text in the tooltip that appears when the mouse hovers over the data set title in the **Data Access** tab.
		If this value is present, then IGB displays an "info" icon next to the file name.
url	Optional	Use this tag to specify the location of an external Web page describing the data set. If provided, IGB will display an "info" icon next to the data set title.
		When users click the icon, their Web browser will open showing the contents of the URL you provide.
		You can specify the location of the file using an **absolute** URL or a **relative** URL.
		An absolute URL looks like this: "http://www.example.com"
		Relative in this case means: **relative to the Quickload root directory**. (Note that this is different from how the file attribute works!)
		For example, to show "About.html" residing inside a genome version directory named E_unicornis_Jun_2009, use relative url "E_unicornis_Jun_2009/About.html"

load_hint	Optional	If used, its value should be "Whole Sequence". Using this tag will force IGB to load the entire file when users select the genome version, which is usually appropriate only for reference gene model annotations or other equally small data sets. **Note**: IGB stores local copies of files with load_hint "Whole Sequence" for faster access. See **Cache** tab under **Settings**.
label_field	Optional	Use this field to indicate the annotation property (e.g., "score" or "id") used to label individual annotations within a track. To show no label, insert **none**. To find out what annotation properties are available, view the **Selection Info** for an annotation loaded from the file. To view annotation properties: - Open the file and load some data. - Click an annotation to select it. - View **Selection Info** by clicking the "i" button (top left) or opening the **Selection Info** tab. - Alternatively, choose the **Selection Info** tab to view another tabular view of properties. Annotation properties are listed in the first column.
reference	Optional	Set to "true" if the file is a 2bit reference file.
background	Optional	Use this field to set a track's background color. Set colors using [six-digit, hexadecimal triplets]. For example, to set a white background, use background="FFFFFF".
foreground	Optional	Use this field to define annotation or graph colors (e.g. foreground="00FFFF"). See above.
max_depth	Optional	Use this field to define the default maximum stack height for an annotations track. This is the number of annotations shown individually in a stack. Any annotations exceeding this number will be drawn on top of each in a single row at the top of the track. This is called the "slop" row. If the track is configured to show plus and minus strand features separately, then the "slop row" for minus strand features appears in the bottom row. To allow IGB to show all available annotations use max_depth="0" for unlimited.
name_size	Optional	Use this field to define the default track label name font size (e.g. name_size="12")
connected	Optional	Use this field to define the default boolean value for the connected field (e.g. connected="true" or connected="false"). The default is "true". This tells IGB to draw lines linking the blocks belonging to compound features assembled from smaller ones.
show2tracks	Optional	Use this field to define the default boolean value for the show2Tracks field (e.g. show2tracks="true" or show2tracks="false"). If you would like minus and plus strand features to be displayed in the same track, set this to "false." The default is "true."
direction_type	Optional	Use this field to dictate whether annotations or alignments will be shown using arrows and/or color to indicate direction. (e.g. direction_type="arrow", direction_type="color", direction_type="both", direction_type="none"). The default is "none."
positive_strand_color	Optional	Use this field to define the default positive strand color (e.g. positive_strand_color="CCFFFF") for when the direction_type setting is "color."
negative_strand_color	Optional	Use this field to define the default negative strand color (e.g. negative_strand_color="33FFFF") for when the direction_type setting is "color."