

1. Have you been able to successfully build and display a UCSC Genome Browser data hub?

		Response Percent	Response Count
Yes		72.7%	16
No		13.6%	3
Haven't tried		13.6%	3
answered question			22
skipped question			0

2. How many working data hubs do you have?

	Response Count
	14
answered question	14
skipped question	8

3. For which organism(s) do you have data hub(s)?

		Response Percent	Response Count
Human		64.3%	9
Mouse		64.3%	9
Other (please specify)		50.0%	7
answered question			14
skipped question			8

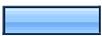
4. What types of data tracks do you have in your data hub(s)?

		Response Percent	Response Count
bigBed		92.9%	13
bigWig		78.6%	11
BAM		57.1%	8
VCF		7.1%	1
answered question			14
skipped question			8

5. How many tracks do you have in your data hub(s)?

	Response Count
	14
answered question	14
skipped question	8

6. What is the average amount of time it took you to build one data hub?

		Response Percent	Response Count
<1 hour		35.7%	5
1-5 hours		42.9%	6
5-10 hours		7.1%	1
>10 hours		14.3%	2
answered question			14
skipped question			8

7. Please explain why you were not able to successfully build and display your data hub.

	Response Count
	1
answered question	1
skipped question	21

8. What can the UCSC group do to make it easier for you to build and display your data hub?

	Response Count
	1
answered question	1
skipped question	21

9. Did you find our instructions for the data hub easy to follow and understand?

		Response Percent	Response Count
Yes		53.3%	8
No		33.3%	5
Couldn't find them		13.3%	2
N/A		0.0%	0
	answered question		15
	skipped question		7

10. How could we improve the data hub instructions?

	Response Count
	5
answered question	5
skipped question	17

11. What features would you like to see added to the data hub functionality?

	Response Count
	4
answered question	4
skipped question	18

Page 2, Q1. How many working data hubs do you have?

1	1	Jan 11, 2012 7:21 AM
2	7	Jan 6, 2012 1:14 PM
3	2	Dec 14, 2011 3:27 PM
4	2	Dec 7, 2011 9:18 AM
5	2	Dec 7, 2011 1:48 AM
6	8	Dec 1, 2011 9:57 AM
7	1	Nov 29, 2011 1:21 PM
8	6	Nov 23, 2011 2:05 PM
9	1	Nov 21, 2011 10:16 AM
10	1	Nov 21, 2011 6:48 AM
11	15	Nov 19, 2011 8:22 AM
12	1	Nov 17, 2011 2:58 PM
13	1	Nov 17, 2011 7:51 AM
14	10	Nov 16, 2011 5:07 AM

Page 2, Q2. For which organism(s) do you have data hub(s)?

1	C. elegans	Dec 7, 2011 9:18 AM
2	dm3	Dec 1, 2011 9:57 AM
3	We built to everything we could, and got most of the organisms you provide.	Nov 29, 2011 1:21 PM
4	Drosophila (dm3)	Nov 21, 2011 10:16 AM
5	Zea mays (local installation)	Nov 19, 2011 8:22 AM
6	Rat, Dog, Fly	Nov 17, 2011 2:58 PM
7	dm3	Nov 16, 2011 5:07 AM

Page 2, Q4. How many tracks do you have in your data hub(s)?

1	2	Jan 11, 2012 7:21 AM
2	4,7,8,36,45,49,52	Jan 6, 2012 1:14 PM
3	20	Dec 14, 2011 3:27 PM
4	about 50	Dec 7, 2011 9:18 AM
5	24	Dec 7, 2011 1:48 AM
6	10-20 in each	Dec 1, 2011 9:57 AM
7	1	Nov 29, 2011 1:21 PM
8	4-10	Nov 23, 2011 2:05 PM
9	16	Nov 21, 2011 10:16 AM
10	10 ish	Nov 21, 2011 6:48 AM
11	~5/hub	Nov 19, 2011 8:22 AM
12	~15	Nov 17, 2011 2:58 PM
13	1	Nov 17, 2011 7:51 AM
14	15	Nov 16, 2011 5:07 AM

Page 3, Q1. Please explain why you were not able to successfully build and display your data hub.

1	The methylation sites worked for hg19 The methylation sites did not match the CpG's in the Hg18 (forthe Sp1 gene)	Nov 16, 2011 10:10 AM
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Page 3, Q2. What can the UCSC group do to make it easier for you to build and display your data hub?

1	I think that the WashU data for CpG methylations look really good I recommend adding the data as regular tracks in the browser At UCSC genome browser, a few tracks are not very useful Maybe these tracks could be removed to make room for better data	Nov 16, 2011 10:10 AM
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Page 5, Q1. How could we improve the data hub instructions?

1	There is not enough information regarding the use of containers in order to build multiwig and multibed tracks.	Dec 7, 2011 1:50 AM
2	Had to dig in kentsrc to find the docs then had to reverse-engineer an ENCODE hub to iron out details. If I remember correctly, the relationships between stanzas and how those relationships translate into elements on the hub config page (e.g., the checkbox matrix, "signal" and "alignment" separation of bigWig/BAM tracks) were most unclear to me.	Dec 1, 2011 10:06 AM
3	Explanation for all possible fields and instructions Instructions about containers	Nov 21, 2011 10:19 AM
4	Provide a download-able example	Nov 17, 2011 7:53 AM
5	Yes. Provide a detailed instructions with examples.	Nov 16, 2011 10:11 AM

Page 5, Q2. What features would you like to see added to the data hub functionality?

1	It would be good to have a refresh button in the genome browser to reload a specific hub.	Dec 7, 2011 1:50 AM
2	custom labeling of tracks, on a per-user basis. my auto-generated hubs tend to have long unwieldy names (even the shortNames, for various reasons specific to the hubs i make), but it would be nice to have biologist be able to edit an adjacent text field to temporarily re-name tracks for their current viewing session. not sure if this would be best as a hub-specific or a browser-wide feature, but the issue definitely becomes apparent when using hubs.	Dec 1, 2011 10:06 AM
3	Combine BigWig and BigBed within one container	Nov 21, 2011 10:19 AM
4	script to convert bed files to wig files (for example), and vice versa	Nov 17, 2011 7:53 AM