

CoGe LoadExp+: A web-based suite that integrates next-gen sequencing data analysis workflows and visualization


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Supplementary Information

The screenshot displays the CoGe LoadExp+ web interface. At the top, there is a search bar and navigation links for 'My Data', 'Tools', and 'Help'. Below the search bar, the 'Notebooks' section is active, showing a list of 20 notebooks. The notebooks are organized into a table with columns for 'Name' and 'Date added'. The notebook 'wierzbicki_bismark_col-0_benchmarking' is highlighted in green. A red arrow points to the 'Groups with access' section of the notebook details on the right, which lists 'Eric Lyons (elyons)', 'Jeffrey Grover (groverj3)', and 'Rebecca Mosher (rmosher)'. The 'Tools' section includes 'Edit' and 'Share' options.

Name	Date added
hsapiens_brain1_maseq_tophat2_ruiz: Benchmarking the maseq pipeline with data from Ruiz-Orera et al. 2015 (Experiment)	Oct 12
hsapiens_brain1_maseq_hisat2_ruiz: Benchmarking the maseq pipeline with data from Ruiz-Orera et al. 2015 (Experiment)	Oct 11
hsapiens_brain1_maseq_bowtie2_ruiz: Benchmarking the maseq pipeline with data from Ruiz-Orera et al. 2015 (Experiment)	Oct 6
b73_maseq_hisat2_walley: Benchmarking the maseq pipeline with data from Walley et al. 2016 (Experiment)	Oct 3
hsapiens_brain1_maseq_gsnap_ruiz: Benchmarking the maseq pipeline with data from Ruiz-Orera et al. 2015 (Experiment)	Oct 1
b73_leaf8_tophat2_walley: Benchmarking the maseq pipeline with data from Walley et al. 2016 (Experiment)	Sep 29
b73_leaf8_bowtie2_walley: Benchmarking the maseq pipeline with data from Walley et al. 2016 (Experiment)	Sep 29
b73_leaf8_gsnap_walley: Benchmarking the maseq pipeline with data from Walley et al. 2016 (Experiment)	Sep 29
col-0_maseq_hisat2_deleris: Benchmarking the maseq pipeline with data from Deleris et al. 2012 (Experiment)	Sep 28
col-0_maseq_tophat2_deleris: Benchmarking the maseq pipeline with data from Deleris et al. 2012 (Experiment)	Sep 28
col-0_maseq_bowtie2_deleris: Benchmarking the maseq pipeline with data from Deleris et al. 2012 (Experiment)	Sep 28
col-0_maseq_gsnap_deleris: Benchmarking the maseq pipeline with data from Deleris et al. 2012 (Experiment)	Sep 28
lister_h1-esc_bwameth_benchmarking: Running the Lister et al. 2009 h1 esc data through the bwameth pipeline for benchmarking (Experiment)	Sep 22
lister_h1-esc_bismark_benchmarking: Running the Lister et al. 2009 h1 esc data through the bismark pipeline for benchmarking (Experiment)	Sep 21
regulski_b73_maize_bwameth_benchmarking: Running the Regulski maize b73 methylation dataset through the bwameth pipeline for benchmarking purposes (Experiment)	Sep 5
Favorites: This notebook contains genomes you have marked as favorites. It is created automatically by CoGe. (Mixed)	Aug 21
regulski_b73_maize_bismark_benchmarking: Running the Regulski maize b73 methylation dataset through the Bismark pipeline for benchmarking purposes. (Experiment)	Aug 20
wierzbicki_bismark_col-0_benchmarking: Running the Wierzbicki 2012 dataset through the bismark pipeline for benchmarking purposes on the new server. Using -N 1 option. (Experiment)	Aug 18
wierzbicki_bwameth_col-0_benchmarking: Running the Wierzbicki 2012 dataset through the bwameth pipeline for benchmarking purposes on the new server. (Experiment)	Aug 18
wierzbicki_bismark_col-0_benchmarking: Benchmarking Bismark workflow with data from Wierzbicki et al. 2012 (Experiment)	Aug 17

Figure S1. Data Can Be Organized Into Notebooks. Individual experiment files may be organized into one notebook. This aids in data management, allowing related datasets from LoadExp+ workflows to be grouped together and privately shared with other users or made fully public. The highlighted notebook has been shared with other users (red arrow).

☆  **wierzbicki_bismark_col-0_benchmarking: Benchmarking Bismark workflow with data from Wierzbicki et al. 2012 (id1616)**

Info

ID: 1616
 Name: wierzbicki_bismark_col-0_benchmarking
 Description: Benchmarking Bismark workflow with data from Wierzbicki et al. 2012-
 Type: Experiment
 Note:
 Restricted: Yes
 Creation: Jeffrey Grover 2016-08-17 15:03:28
 Owner: Jeffrey Grover
 Users with access: Eric Lyons, Jeffrey Grover, Rebecca Mosher

Metadata

There are no additional metadata items for this notebook.

+ Add

Edit Info

Make Public

Delete

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Contents

Type	Name	Date	Remove
Experiments 4:	 wierzbicki_bismark_col-0_benchmarking (BAM alignment): Running (v1.0, id8568): NCBI-SRA	2016-08-17 15:00:50	
	 wierzbicki_bismark_col-0_benchmarking (CHG methylation): Running the Wierzbicki 2012 dataset through the Bismark pipeline for benchmarking purposes on the new server. (v1.0, id8567): NCBI-SRA	2016-08-17 14:58:27	
	 wierzbicki_bismark_col-0_benchmarking (CHH methylation): Running the Wierzbicki 2012 dataset through the Bismark pipeline for benchmarking purposes on the new server. (v1.0, id8569): NCBI-SRA	2016-08-17 15:03:23	
	 wierzbicki_bismark_col-0_benchmarking (CpG methylation): Running the Wierzbicki 2012 dataset through the Bismark pipeline for benchmarking purposes on the new server. (v1.0, id8566): NCBI-SRA	2016-08-17 14:58:24	

+ Add

Send contents to:

Go 

Figure S2. Notebooks Can Contain Many Experiment Files. Output files from LoadExp+ BS-seq workflows are visible inside one notebook. Clicking on the individual experiments will open them in Experiment View (Figure S4). This notebook has been shared with other users (red arrow) but otherwise is private ('Restricted: Yes').



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Name	Date added
hsapiens_brain1_maseq_tophat2_ruiz (read depth): Read depth per position (v1.0, id9001)	Oct 12
hsapiens_brain1_maseq_tophat2_ruiz (FPKM): Transcript expression measurements (v1.0, id9000)	Oct 12
hsapiens_brain1_maseq_tophat2_ruiz (BAM alignment): Benchmarking (v1.0, id8999)	Oct 11
hsapiens_brain1_maseq_hisat2_ruiz (read depth): Read depth per position (v1.0, id8997)	Oct 11
hsapiens_brain1_maseq_hisat2_ruiz (FPKM): Transcript expression measurements (v1.0, id8998)	Oct 11
hsapiens_brain1_maseq_hisat2_ruiz (BAM alignment): Benchmarking (v1.0, id8996)	Oct 11
hsapiens_brain1_maseq_bowtie2_ruiz (FPKM): Transcript expression measurements (v1.0, id8983)	Oct 6
hsapiens_brain1_maseq_bowtie2_ruiz (BAM alignment): Benchmarking (v1.0, id8982)	Oct 6
hsapiens_brain1_maseq_bowtie2_ruiz (read depth): Read depth per position (v1.0, id8981)	Oct 6
b73_maseq_hisat2_walley (FPKM): Transcript expression measurements (v1.0, id8903)	Oct 3
b73_maseq_hisat2_walley (BAM alignment): Benchmarking (v1.0, id8901)	Oct 3
b73_maseq_hisat2_walley (read depth): Read depth per position (v1.0, id8902)	Oct 3
hsapiens_brain1_maseq_bowtie2_ruiz (read depth): Read depth per position (v1.0, id8894)	Oct 2
hsapiens_brain1_maseq_bowtie2_ruiz (FPKM): Transcript expression measurements (v1.0, id8895)	Oct 2
hsapiens_brain1_maseq_bowtie2_ruiz (BAM alignment): Benchmarking (v1.0, id8893)	Oct 2
hsapiens_brain1_maseq_gsnap_ruiz (FPKM): Transcript expression measurements (v1.0, id8892)	Oct 1
hsapiens_brain1_maseq_gsnap_ruiz (read depth): Read depth per position (v1.0, id8891)	Oct 1
hsapiens_brain1_maseq_gsnap_ruiz (BAM alignment): Benchmarking (v1.0, id8890)	Oct 1
b73_maseq_hisat2_walley (read depth): Read depth per position (v1.0, id8889)	Sep 30
b73_maseq_hisat2_walley (BAM alignment): Benchmarking (v1.0, id8887)	Sep 30


3 items selected.

Click an action icon at the top to share, organize, delete, or analyze.

Figure S3. LoadExp+ Output Files Are Seen As Separate Experiments. Once analyses have finished a full listing of output files from any workflows that have run are visible in the user's My Data page. The three highlighted experiments (red arrow) were generated from the same LoadExp+ RNAseq run where each intermediate file of an analysis (BAM, read depth, and transcript quantification) have automatically been integrated.

☆  **wierzbicki_bismark_col-0_benchmarking (CHH methylation): Running the Wierzbicki 2012 dataset through the Bismark pipeline for benchmarking p...**

Info

ID: 8569
Name: wierzbicki_bismark_col-0_benchmarking (CHH methylation)
Description: Running the Wierzbicki 2012 dataset through the Bismark pipeline for benchmarking purposes on the new server.
Data Type: Quantitative
Genome: Arabidopsis thaliana Col-0 (thale cress) (v10.02, id16911): unmasked
Source: NCBI-SRA
Version: 1.0
Tags:
Notebooks: wierzbicki_bismark_col-0_benchmarking
Restricted: Yes
Creation: Jeffrey Grover 2016-08-17 15:03:23
Owner: Jeffrey Grover
Users with access: Eric Lyons, Jeffrey Grover,  Becca Mosher

Statistics

Items: 8,651,576
Data size: 981,506,932 bytes

Tools

Export data to: [Download](#) | [CyVerse Data Store](#) 

[Edit Info](#)
[Add Tag](#)
[Make Public](#)
[Browse](#) 

Metadata

note: [Generated by CoGe's Methylation Analysis Pipeline](#) [Link](#)
 deduplicate_bismark -s
 bismark_methylation_extractor --ignore 0 --ignore_3prime 0
 SRA Accession: SRA054962, SRX156068  
 Source: Wierzbicki et al. 2012 [Link](#)  
 Arabidopsis thaliana, Col-0  

[Add](#)

Figure S4. Experiment View. Detailed information about each output file from LoadExp+ is visible by opening that file in Experiment View. Data can also be exported for direct download or to the CyVerse Data Store (purple arrow). The experiment can be made public by clicking the “Make Public” button. User-defined metadata such as the “Name” and “Description” are visible (black arrow) and may be changed by clicking “Edit Info.” Run-time options are captured in the “Metadata” section (red arrow) and these are immutable by the user, but additional metadata may be added in the form of text, links, and images. The “Browse” button (blue arrow) will open the experiment for viewing in the EPIC-CoGe browser.



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Name	Date added
hsapiens_brain1_maseq_gsnap_ruiz: Benchmarking the maseq pipeline with data from Ruiz-Orera et al. 2015 (Experiment)	Oct 1
b73_leaf8_tophat2_walley: Benchmarking the maseq pipeline with data from Walley et al. 2016 (Experiment)	Sep 29
b73_leaf8_bowtie2_walley: Benchmarking the maseq pipeline with data from Walley et al. 2016 (Experiment)	Sep 29
b73_leaf8_gsnap_walley: Benchmarking the maseq pipeline with data from Walley et al. 2016 (Experiment)	Sep 29
col-0_maseq_hisat2_deleris: Benchmarking the maseq pipeline with data from Deleris et al. 2016 (Experiment)	Sep 28
col-0_maseq_tophat2_deleris: Benchmarking the maseq pipeline with data from Deleris et al. 2016 (Experiment)	Sep 28
col-0_maseq_bowtie2_deleris: Benchmarking the maseq pipeline with data from Deleris et al. 2016 (Experiment)	Sep 28
col-0_maseq_gsnap_deleris: Benchmarking the maseq pipeline with data from Deleris et al. 2016 (Experiment)	Sep 28
lister_h1-esc_bwameth_benchmarking (Experiment)	Sep 22
lister_h1-esc_bismark_benchmarking (Experiment)	Sep 21
regulski_b73_maize_bwameth_pipeline for benchmarking purposes on the new server. (Experiment)	Sep 5
Favorites: This notebook contains...	
regulski_b73_maize_bismark_pipeline for benchmarking purposes on the new server. (Experiment)	Aug 21
wierzbicki_bismark_col-0_benchmarking purposes on the new server. (Experiment)	Aug 20
wierzbicki_bwameth_col-0_benchmarking: Running the Wierzbicki 2012 dataset through the bwameth pipeline for benchmarking purposes on the new server. (Experiment)	Aug 18
wierzbicki_bwameth_col-0_benchmarking: Running the Wierzbicki 2012 dataset through the bwameth pipeline for benchmarking purposes on the new server. (Experiment)	Aug 18
wierzbicki_bismark_col-0_benchmarking: Benchmarking Bismark workflow with data from Wierzbicki et al. 2012 (Experiment)	Aug 17

Share Items

Who Has Access

- Eric Lyons (elyons) - Reader *
- Jeffrey Grover (groverj3) - Owner
- Rebecca Mosher (rmosher) - Reader *

Add Access

Enter user or group names:

Add

Or make available to everyone:

Make Public

Notebook id1616

Name: wierzbicki_bismark_col-0_benchmarking

Description: Benchmarking Bismark workflow with data from Wierzbicki et al. 2012

Contents:

Experiments: 4

Groups with access:

None

Users with access:

Eric Lyons (elyons)
Jeffrey Grover (groverj3)
Rebecca Mosher (rmosher)

Tools:

Edit
Share

Figure S5. Sharing Data Within CoGe. Whole notebooks or individual experiment files can be shared with collaborators by clicking the “share” button on the right side of the My Data page or the button above the listing of notebooks (red arrow). Typing in a user name will allow searching through all of CoGe’s users. Additionally, data can be made public and viewable by all users from this area as well.

Data Size	Aligner	Source Data	Organism (Genome ID)	Run Time	Options
29,752,004 reads 1.66 GB (gzipped)	GSNAP	(Deleris <i>et al.</i> , 2012) (WT Col-0) SRR3709924	<i>Arabidopsis thaliana</i> (16911)	36 minutes, 37.57 seconds	Single-ended, phred33, CutAdapt: -q 25 -m 17 GSNAP: -N 1, -n 5, -Q -gap-mode none -nofails Expression Analysis: enable, -q 20, -frag-bias-correct, -multi-read-correct
29,752,004 reads 1.66 GB (gzipped)	Bowtie2	(Deleris <i>et al.</i> , 2012) (WT Col-0) SRR3709924	<i>Arabidopsis thaliana</i> (16911)	1 hour, 58 minutes, 22.02 seconds	Single-ended, phred33, CutAdapt: -q 25 -m 17 Bowtie2: default options Expression Analysis: enable, -q 20, -frag-bias-correct, -multi-read-correct
29,752,004 reads 1.66 GB (gzipped)	TopHat2	(Deleris <i>et al.</i> , 2012) (WT Col-0) SRR3709924	<i>Arabidopsis thaliana</i> (16911)	1 hour, 6 minutes, 58.08 seconds	Single-ended, phred33, CutAdapt: -q 25 -m 17 TopHat2: -g 1 Expression Analysis: enable, -q 20, -frag-bias-correct, -multi-read-correct
29,752,004 reads 1.66 GB (gzipped)	HiSat2	(Deleris <i>et al.</i> , 2012) (WT Col-0) SRR3709924	<i>Arabidopsis thaliana</i> (16911)	47 minutes, 33.30 seconds	Single-ended, phred33, CutAdapt: -q 25 -m 17 HISAT2: default options Expression Analysis: enable, -q 20, -frag-bias-correct, -multi-read-correct
20,434,594 reads 1.74 GB (gzipped)	GSNAP	(Walley <i>et al.</i> , 2016) (<i>Zea mays</i> b73, leaf 8) SRR957442	<i>Zea mays</i> (25317)	45 minutes, 17.21 seconds	Single-ended, phred33, CutAdapt: -q 25 -m 17 GSNAP: -N 1, -n 5, -Q -gap-mode none -nofails Expression Analysis: enable, -q 20, -frag-bias-correct, -multi-read-correct
20,434,594 reads 1.74 GB (gzipped)	Bowtie2	(Walley <i>et al.</i> , 2016) (<i>Zea mays</i> b73, leaf 8) SRR957442	<i>Zea mays</i> (25317)	1 hour, 29 minutes, 55.87 seconds	Single-ended, phred33, CutAdapt: -q 25 -m 17 Bowtie2: default options Expression Analysis: enable, -q 20, -frag-bias-correct, -multi-read-correct
20,434,594 reads 1.74 GB (gzipped)	TopHat2	(Walley <i>et al.</i> , 2016) (<i>Zea mays</i> b73, leaf 8) SRR957442	<i>Zea mays</i> (25317)	1 hour, 15 minutes, 28.34 seconds	Single-ended, phred33, CutAdapt: -q 25 -m 17 TopHat2: -g 1 Expression Analysis: enable, -q 20, -frag-bias-correct, -multi-read-correct
20,434,594 reads 1.74 GB (gzipped)	HiSat2	(Walley <i>et al.</i> , 2016) (<i>Zea mays</i> b73, leaf 8) SRR957442	<i>Zea mays</i> (25317)	42 minutes, 59.59 seconds	Single-ended, phred33, CutAdapt: -q 25 -m 17 HISAT2: default options Expression Analysis: enable, -q 20
73,730,964 reads 9.91 GB (gzipped)	GSNAP	(Ruiz-Orera <i>et al.</i> , 2015) (brain1) SRR2040575	<i>Homo sapiens</i> (25747)	3 hours, 22 minutes, 12.54 seconds	Paired end, phred33, CutAdapt: -q 25 -m 17 GSNAP: -N 1, -n 5, -Q -gap-mode none -nofails Expression Analysis: enable, -q 20, -frag-bias-correct, -multi-read-correct
73,730,964 reads 9.91 GB (gzipped)	Bowtie2	(Ruiz-Orera <i>et al.</i> , 2015) (brain1) SRR2040575	<i>Homo sapiens</i> (25747)	14 hours, 13 minutes, 59.75 seconds	Paired end, phred33, CutAdapt: -q 25 -m 17 Bowtie2: default options Expression Analysis: enable, -q 20, -frag-bias-correct, -multi-read-correct
73,730,964 reads 9.91 GB (gzipped)	TopHat2	(Ruiz-Orera <i>et al.</i> , 2015) (brain1) SRR2040575	<i>Homo sapiens</i> (25747)	11 hours, 35 minutes, 55.21 seconds	Single-ended, phred33, CutAdapt: -q 25 -m 17 TopHat2: -g 1 Expression Analysis: enable, -q 20, -frag-bias-correct, -multi-read-correct
73,730,964 reads 9.91 GB (gzipped)	HiSat2	(Ruiz-Orera <i>et al.</i> , 2015) (brain1) SRR2040575	<i>Homo sapiens</i> (25747)	6 hours, 25 minutes, 5.96 seconds	Paired end, phred33, CutAdapt: -q 25 -m 17 HISAT2: default options Expression Analysis: enable, -q 20

Table S1. RNAseq Workflow Benchmarking Information. All aligners calculate FPKM with Cufflinks and read depth with SAMtools. All options selected are based on default values at the time of publication. Genome ID is assigned upon upload to CoGe and is searchable. Run times are dependent on server load and may vary.

Data Size	Aligner	Source Data	Organism (Genome ID)	Run Time	Options
93,770,828 reads 13.28 GB (gzipped)	GSNAP	(Sutinen <i>et al.</i> , 2014) Input: SRR923516 Rep 1: SRR1118386 Rep 2: SRR1118387	<i>Homo sapiens</i> (25747)	7 hours, 54 minutes, 43 seconds	Single-ended, phred33, CutAdapt: -q 25 -m 17 GSNAP: -N 1, -n 5, -Q -gap-mode none -nofails ChIP-seq Analysis: -size 250 -gsize 3000000000 -norm 10000000 -fdr 0.01 -F 3
93,770,828 reads 13.28 GB (gzipped)	Bowtie2	(Sutinen <i>et al.</i> , 2014) Input: SRR923516 Rep 1: SRR1118386 Rep 2: SRR1118387	<i>Homo sapiens</i> (25747)	14 hours, 10 minutes, 30 seconds	Single-ended, phred33, CutAdapt: -q 25 -m 17 Bowtie2: default options ChIP-seq Analysis: -size 250 -gsize 3000000000 -norm 10000000 -fdr 0.01 -F 3
93,770,828 reads 13.28 GB (gzipped)	TopHat	(Sutinen <i>et al.</i> , 2014) Input: SRR923516 Rep 1: SRR1118386 Rep 2: SRR1118387	<i>Homo sapiens</i> (25747)	28 hours, 21 minutes, 47 seconds	Single-ended, phred33, CutAdapt: -q 25 -m 17 TopHat2: -g 1 ChIP-seq Analysis: -size 250 -gsize 3000000000 -norm 10000000 -fdr 0.01 -F 3
93,770,828 reads 13.28 GB (gzipped)	HISAT2	(Sutinen <i>et al.</i> , 2014) Input: SRR923516 Rep 1: SRR1118386 Rep 2: SRR1118387	<i>Homo sapiens</i> (25747)	5 hours, 37 minutes, 43 seconds	Single-ended, phred33, CutAdapt: -q 25 -m 17 HISAT2: default options ChIP-seq Analysis: -size 250 -gsize 3000000000 -norm 10000000 -fdr 0.01 -F 3

Table S2. ChIPseq Analysis Benchmarking Information. All options selected are based on default values at the time of publication. Run times are dependent on server load and may vary.

Data Size	Analysis Tool	Source Data	Organism (Genome ID)	Run Time	Options
41,408,716 reads 2.05 GB (gzipped)	Bismark	(Wierzbicki <i>et al.</i> , 2012) (Col-0 ecotype) SRX156068	<i>Arabidopsis thaliana</i> (16911)	1 hour, 54 minutes, 59.73 seconds	Single-ended, phred33, Trim Galore: -q 20 --length 20, Bismark: -N 0 -L 20, Deduplicate, Minimum Coverage: 5
41,408,716 reads 2.05 GB (gzipped)	bwameth	(Wierzbicki <i>et al.</i> , 2012) (Col-0 ecotype) SRX156068	<i>Arabidopsis thaliana</i> (16911)	1 hour, 11 minutes, 0.45 seconds	Single-ended, phred33, Trim Galore: -q 20 --length 20, bwameth: Default options, Deduplicate, Minimum Coverage: 5
303,269,187 reads 24.99 GB (gzipped)	Bismark	(Regulski <i>et al.</i> , 2013) (b73 variety) SRX159573	<i>Zea mays</i> (25317)	30 hours, 59 minutes, 30.63 seconds	Paired end, phred33, Trim Galore: -q 20 --length 20, Bismark: -N 0 -L 20, Deduplicate, Minimum Coverage: 5
303,269,187 reads 24.99 GB (gzipped)	bwameth	(Regulski <i>et al.</i> , 2013) (b73 variety) SRX159573	<i>Zea mays</i> (25317)	53 hours, 56 minutes, 36.16 seconds	Paired end, phred33, Trim Galore: -q 20 --length 20, bwameth: Default options, Deduplicate, Minimum Coverage: 5
570,423,799 reads 43.12 GB (gzipped)	Bismark	(Lister <i>et al.</i> , 2009) (H1 embryonic stem cells) SRX006239	<i>Homo sapiens</i> (25747)	42 hours, 19 minutes, 13.70 seconds	Single-ended, phred33, Trim Galore: -q 20 --length 20, Bismark: -N 0 -L 20, Deduplicate, Minimum Coverage: 5
570,423,799 reads 43.12 GB (gzipped)	bwameth	(Lister <i>et al.</i> , 2009) (H1 embryonic stem cells) SRX006239	<i>Homo sapiens</i> (25747)	22 hours, 15 minutes, 55.87 seconds	Single-ended, phred33, Trim Galore: -q 20 --length 20, bwameth: Default options, Deduplicate, Minimum Coverage: 5

Table S3. Bisulfite Sequencing Workflow Benchmarking Information. Bismark runs in Bowtie2 mode. All options selected are based on default values at the time of publication with the exception of deduplication. Run times are dependent on server load and may vary.

References

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