A journal's experiences of reproducing published data analyses

Peter Li

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The Rice 3000 Genomes Project Data.

Genomic data of the green sea turtle (Chelonia mydas).

Genomic data of the soft shell turtle (Pelodiscus sinensis).

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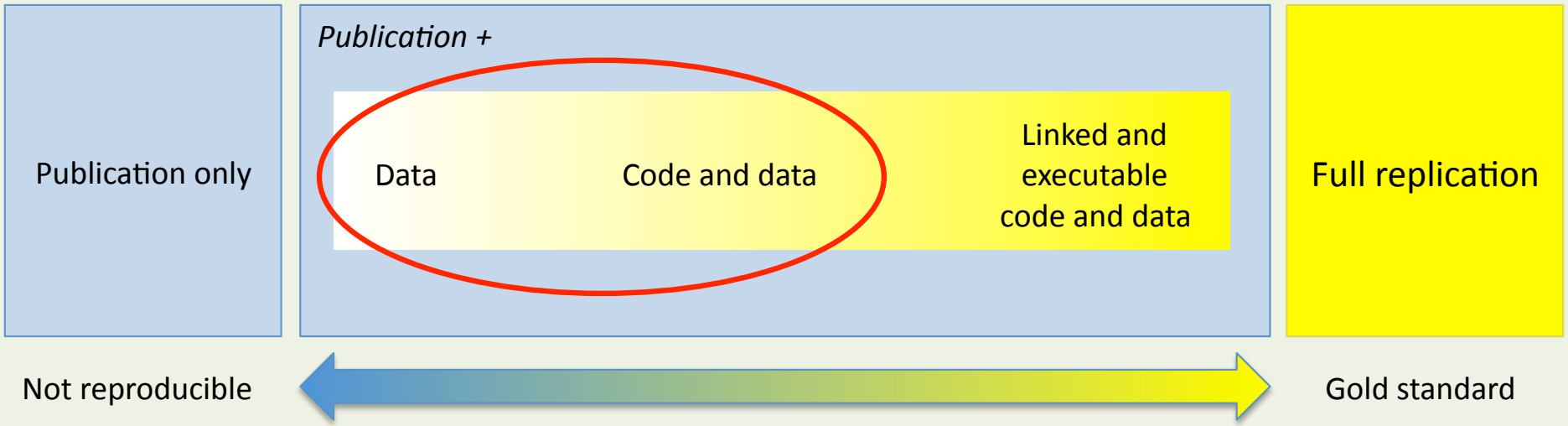

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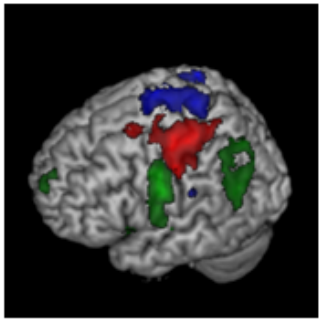

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New dataset added on 2014-05-27: 10.5524/200001 The Rice 3000 Genomes Project Data.

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Oleksyk *et al. GigaScience* 2012, **1**:14
http://www.gigasciencejournal.com/content/1/1/14

DATA NOTE **Open Access**

A locally funded Puerto Rican parrot (*Amazona vittata*) genome sequencing project increases avian data and advances young researcher education

Taras K Oleksyk[1*], Jean-Francois Pombert[2], Daniel Siu[3], Anyimilehidi Mazo-Vargas[1], Brian Ramos[1], Wilfried Guiblet[1], Yashira Afanador[1], Christina T Ruiz-Rodriguez[1,4], Michael L Nickerson[4], David M Logue[1], Michael Dean[4], Luis Figueroa[5], Ricardo Valentin[6] and Juan-Carlos Martinez-Cruzado[1]

Additional file 15: Table S9. Bioinformatics tools and outputs for scaffold and gene annotation.

Additional file 16: Table S10. An example of annotation output produced by a student in the Genome annotation class using *A. vittata* genome.

Competing interests
Oleksyk TK, Pombert JF, Mazo A, Ramos B, Guiblet W, Afanador Y, Ruiz-Rodriguez CT, Nickerson ML, Logue D, Dean M, Figueroa L, Valentin R, and Martinez-Cruzado JC do not have competing interests. Siu D is employed by Axeq Technologies; the company which carried out the DNA Sequencing.

Authors' contributions
TKO, LF, RV, MD, MLN, DL and JCMC came up with the idea, and designed the experiments. TKO, WG, YA, CTRR and JCMC organized public support and raised the funds. TKO, AMV, BR, YA, CTRR and RV collected, extracted and quantified DNA. DS performed sequencing and assembly by SOAPdenovo. JFP performed assembly by Ray. TKO and WG designed the data browser webpage. TKO, JFP, MLN, DL, MD and JCMC wrote the paper. All authors read and approved the final manuscript.

6. Warren WC, Clayton DF, Ellegren H, Arnold AP, Hillier LW, Kunstner A, Searle S, White S, Vilella AJ, Fairley S, *et al*: **The genome of a songbird.** *Nature* 2010, **464**(7289):757–762.
7. Krzywinski MI, Schein JE, Birol I, Connors J, Gascoyne R, Horsman D, Jones SJ, Marra MA: **Circos: An information aesthetic for comparative genomics.** *Genome Res* 2009, **19**(9):1639–45.
8. Koren S, Schatz MC, Walenz BP, Martin J, Howard JT, Ganapathy G, Wang Z, Rasko DA, McCombie WR, Jarvis ED, *et al*: **Hybrid error correction and de novo assembly of single-molecule sequencing reads.** *Nat Biotechnol* 2012, **30**(7):693–700.
9. Oleksyk TK, Guiblet W, Pombert JF, Valentin R, Martinez-Cruzado JC: **Genomic data of the Puerto Rican Parrot (*Amazona vittata*) from a locally funded project.** *GigaScience* 2012. http://dx.doi.org/10.5524/100039.
10. O'Brien SJ: **Genome empowerment for the Puerto Rican parrot – *Amazona vittata*.** *GigaScience* 2012, **1**:13.

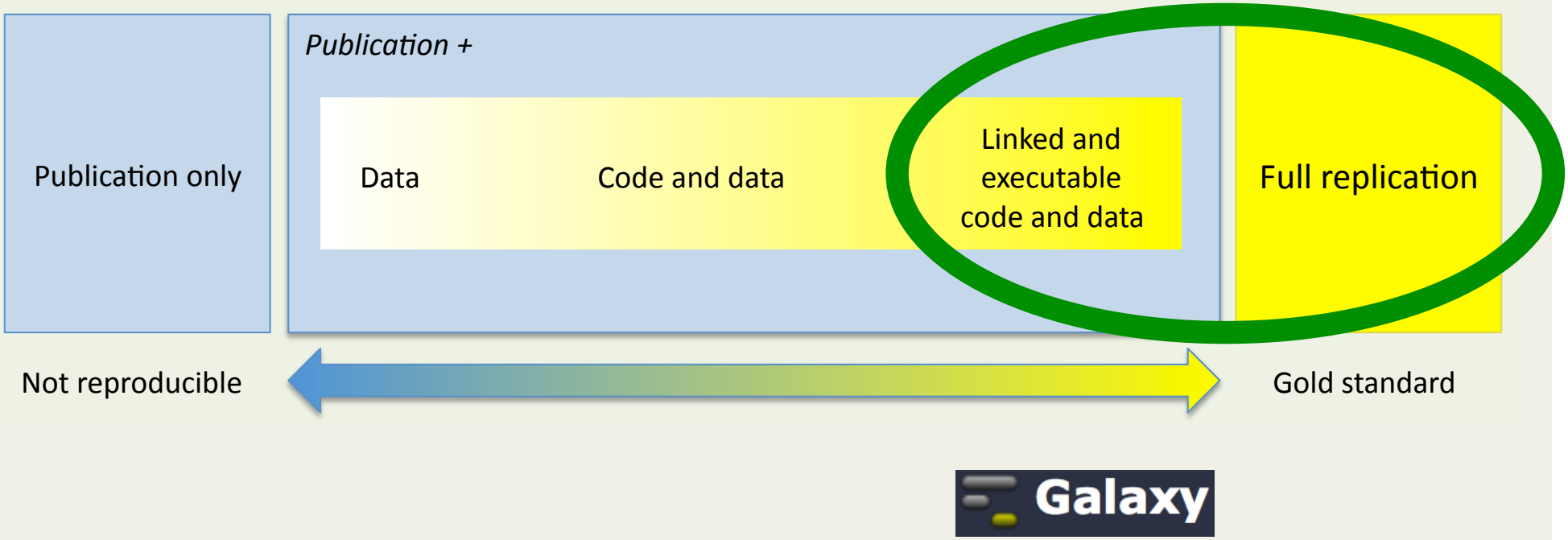
doi:10.1186/2047-217X-1-14
Cite this article as: Oleksyk *et al.*: **A locally funded Puerto Rican parrot (*Amazona vittata*) genome sequencing project increases avian data and advances young researcher education.** *GigaScience* 2012 1:14.

Linking of papers and data by citation of DOIs

Data set DOI

Paper DOI

Reproducibility spectrum



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Pilot project

Luo *et al. GigaScience* 2012, **1**:18
http://www.gigasciencejournal.com/content/1/1/18

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TECHNICAL NOTE **Open Access**

SOAPdenovo2: an empirically improved memory-efficient short-read *de novo* assembler

Ruibang Luo[1,2†], Binghang Liu[1,2†], Yinlong Xie[1,2,3†], Zhenyu Li[1,2†], Weihua Huang[1], Jianying Yuan[1], Guangzhu He[1], Yanxiang Chen[1], Qi Pan[1], Yunjie Liu[1], Jingbo Tang[1], Gengxiong Wu[1], Hao Zhang[1], Yujian Shi[1], Yong Liu[1], Chang Yu[1], Bo Wang[1], Yao Lu[1], Changlei Han[1], David W Cheung[2], Siu-Ming Yiu[2], Shaoliang Peng[4], Zhu Xiaoqian[4], Guangming Liu[4], Xiangke Liao[4], Yingrui Li[1,2], Huanming Yang[1], Jian Wang[1], Tak-Wah Lam[2*] and Jun Wang[1*]

Replicate

Table 2 Assemblies of *S. aureus* and *R. sphaeroides*

Species	Version	Contigs				Scaffolds			
		Number	N50 (kb)	Errors	N50 corrected(kb)	Number	N50 (kb)	Errors	N50 corrected (kb)
S. aureus	SOAPdenovo1	79	148.6	156	23	49	342	0	342
	SOAPdenovo2	80	98.6	25	71.5	38	1,086	2	1,078
	ALLPATHS-LG*	37	149.7	13	117.6	10	1,477	1	1,093
R. sphaeroides	SOAPdenovo1	2,242	3.5	392	2.8	956	105	18	70
	SOAPdenovo2	721	18	106	14.1	333	2,549	4	2,540
	ALLPATHS-LG*	190	41.9	31	36.7	32	3,191	0	3,310

All datasets were downloaded from http://gage.cbcb.umd.edu/data/.
*ALLPATHS-LG was using the latest version 42807.

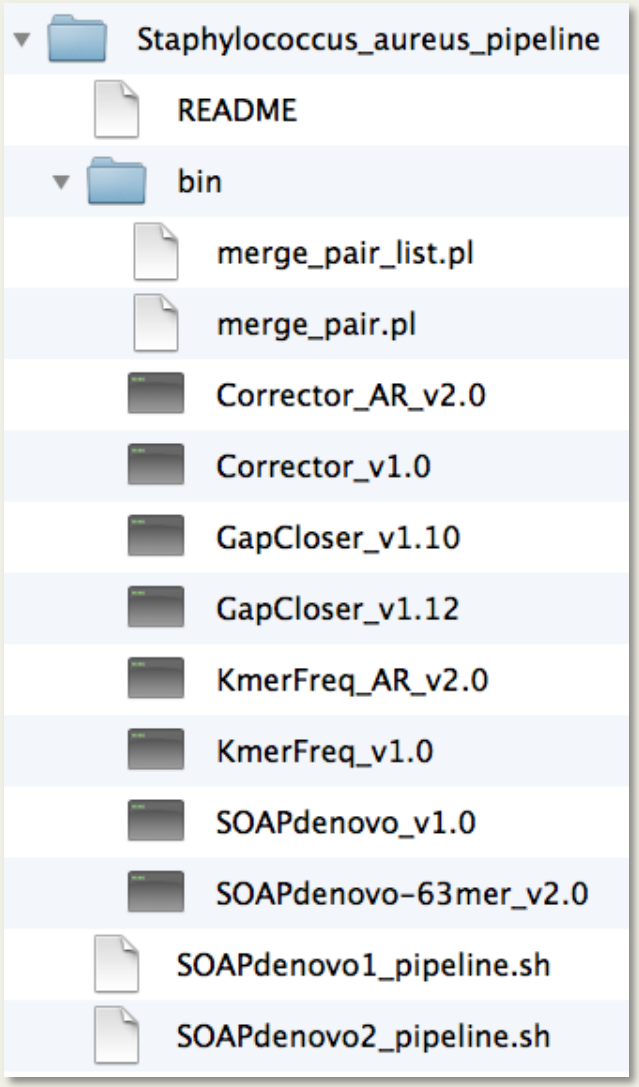
Tools

Files (FTP site) (Aspera): Aspera user name: gigadb , password: gigadb **Table Settings**

File Name	Sample ID	File Type	File Format	Size	Release Date	
README.pdf		Readme	PDF	231.99 KB	2012-12-13	
Assemblathon1_pipeline.tgz		Software	UNKNOWN	10.02 MB	2012-12-13	
Bombus_impatiens_pipeline.tgz		Software	UNKNOWN	4.89 MB	2012-12-13	
Rhodobacter_sphaeroides_pipeline.tgz		Software	UNKNOWN	4.89 MB	2012-12-13	
Staphylococcus_aureus_pipeline.tgz		Software	UNKNOWN	4.33 MB	2012-12-13	
YH_pipeline.tgz	YH	Software	UNKNOWN	7 MB	2012-12-13	
readme.txt		Readme	TEXT	0.29 KB	2012-12-13	

http://gigadb.org/dataset/100044

Tools and data



Genome Assembly Gold-Standard Evaluations

http://gage.cbcb.umd.edu/data/index.html

***Staphylococcus aureus*: Data download page**

- Library 1: Fragment
  - Avg Read length: 101bp
  - Insert length: 180bp
  - # of reads: 1,294,104
  - Fastq read file 1
  - Fastq read file 2

- Library 2: Short jump library
  - Avg Read length: 37bp
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  - # of reads: 3,494,070
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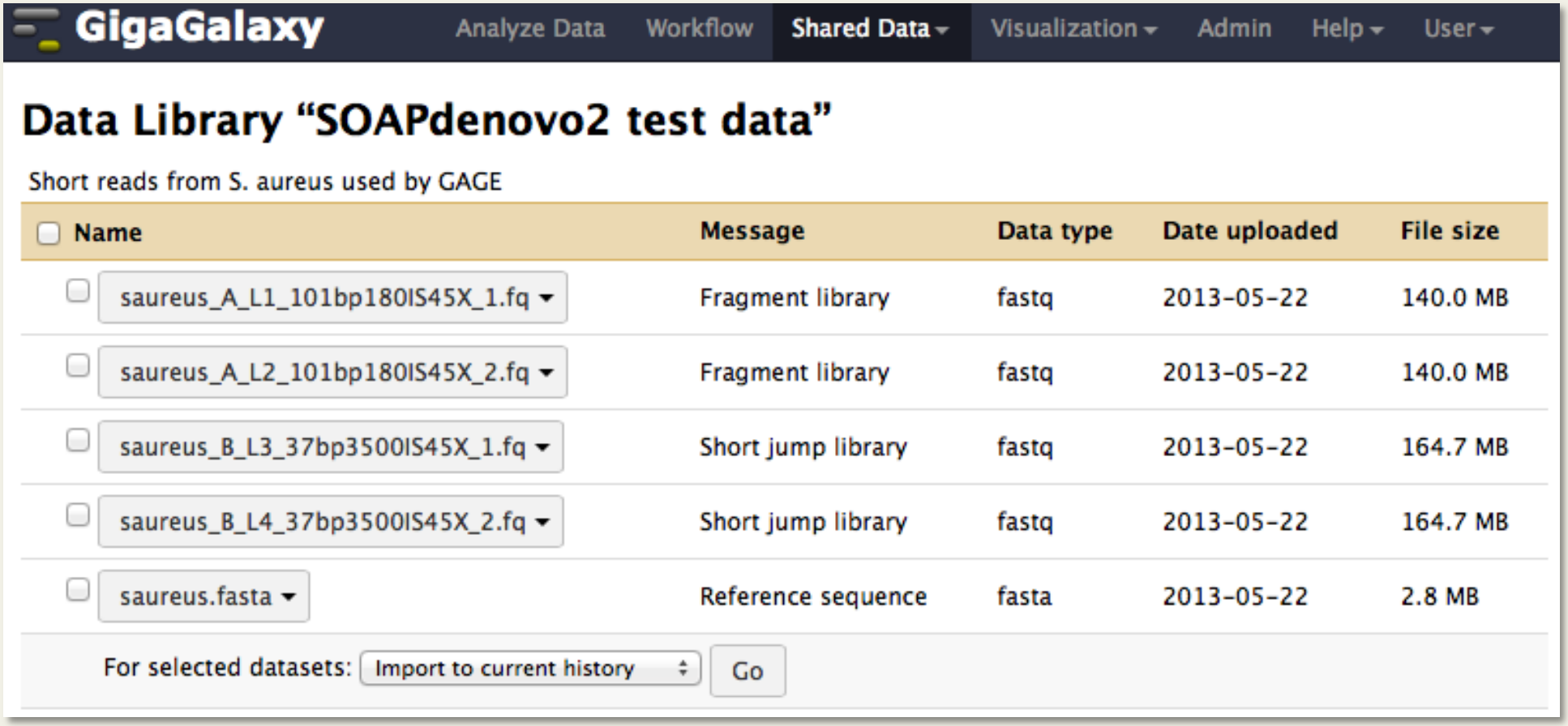
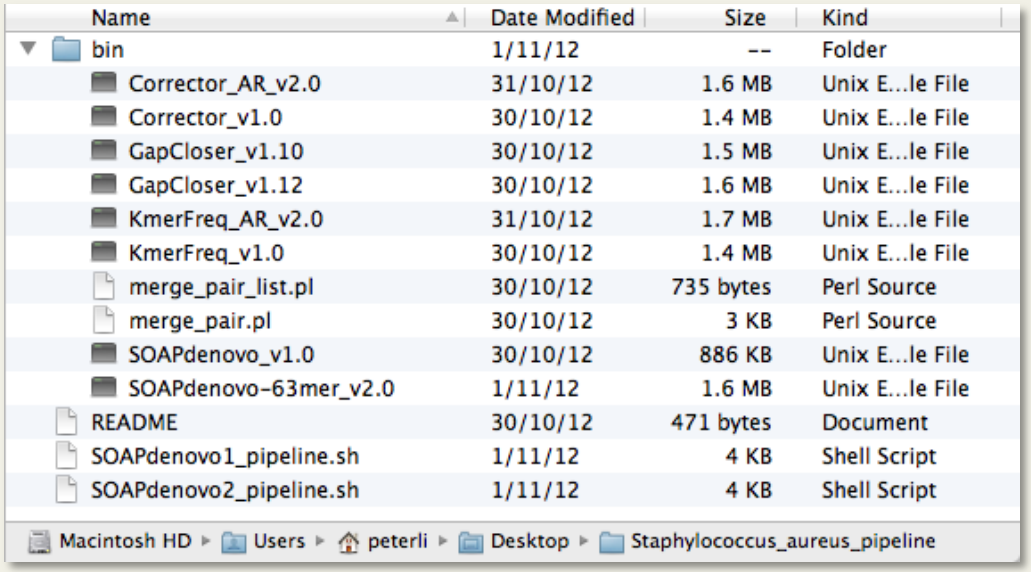
  - Fastq read file 2

Data in GigaGalaxy



Integration of SOAPdenovo2 into GigaGalaxy



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GapCloser_v1.10	30/10/12	1.5 MB	Unix E...le File
GapCloser_v1.12	30/10/12	1.6 MB	Unix E...le File
KmerFreq_AR_v2.0	31/10/12	1.7 MB	Unix E...le File
KmerFreq_v1.0	30/10/12	1.4 MB	Unix E...le File
merge_pair_list.pl	30/10/12	735 bytes	Perl Source
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SOAPdenovo_v1.0	30/10/12	886 KB	Unix E...le File
SOAPdenovo-63mer_v2.0	1/11/12	1.6 MB	Unix E...le File
README	30/10/12	471 bytes	Document
SOAPdenovo1_pipeline.sh	1/11/12	4 KB	Shell Script
SOAPdenovo2_pipeline.sh	1/11/12	4 KB	Shell Script

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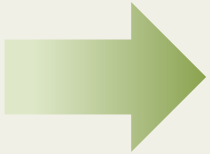

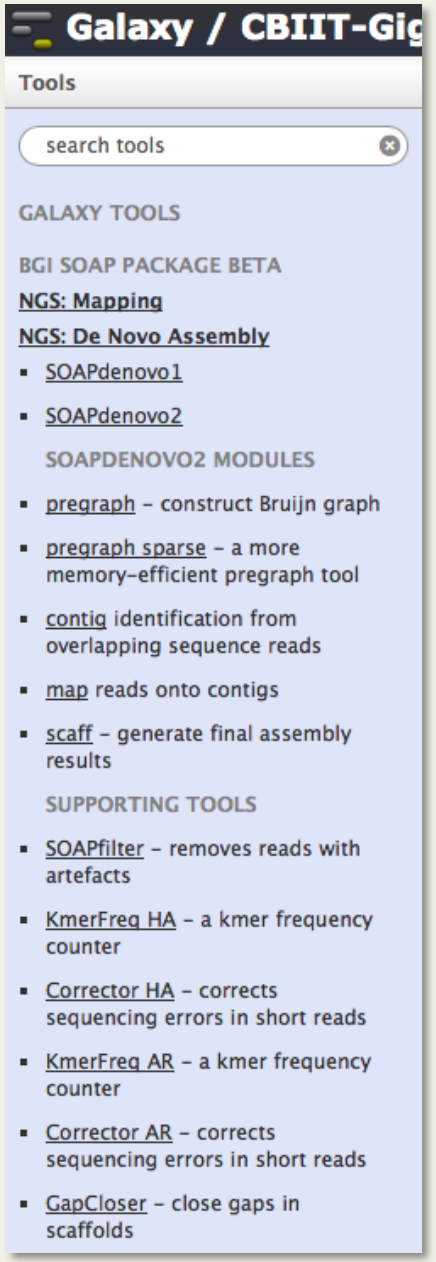

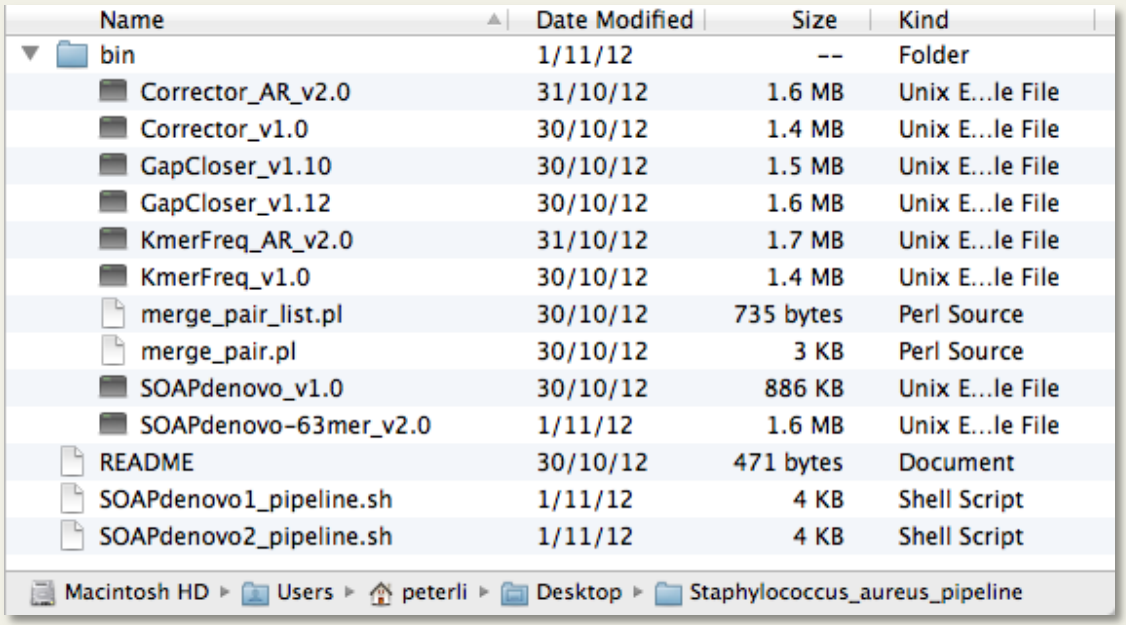

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GapCloser_v1.10	30/10/12	1.5 MB	Unix E...le File
GapCloser_v1.12	30/10/12	1.6 MB	Unix E...le File
KmerFreq_AR_v2.0	31/10/12	1.7 MB	Unix E...le File
KmerFreq_v1.0	30/10/12	1.4 MB	Unix E...le File
merge_pair_list.pl	30/10/12	735 bytes	Perl Source
merge_pair.pl	30/10/12	3 KB	Perl Source
SOAPdenovo_v1.0	30/10/12	886 KB	Unix E...le File
SOAPdenovo-63mer_v2.0	1/11/12	1.6 MB	Unix E...le File
README	30/10/12	471 bytes	Document
SOAPdenovo1_pipeline.sh	1/11/12	4 KB	Shell Script
SOAPdenovo2_pipeline.sh	1/11/12	4 KB	Shell Script

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Downloaded pipeline is missing two tools for reproducibility

Required pipeline

Short reads

KmerFreq_AR

Corrector_AR

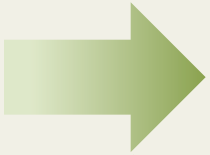
SOAPdenovo2

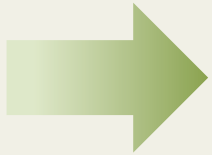
GapCloser

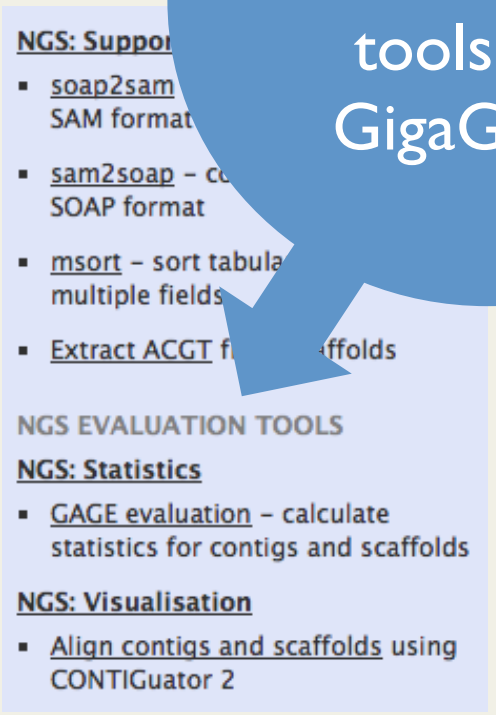
ExtractACGT

GAGE eval

Table 2 N50 & corrected N50 scores







Need to add two extra tools into GigaGalaxy

SOAPdenovo2 *S. aureus* pipeline

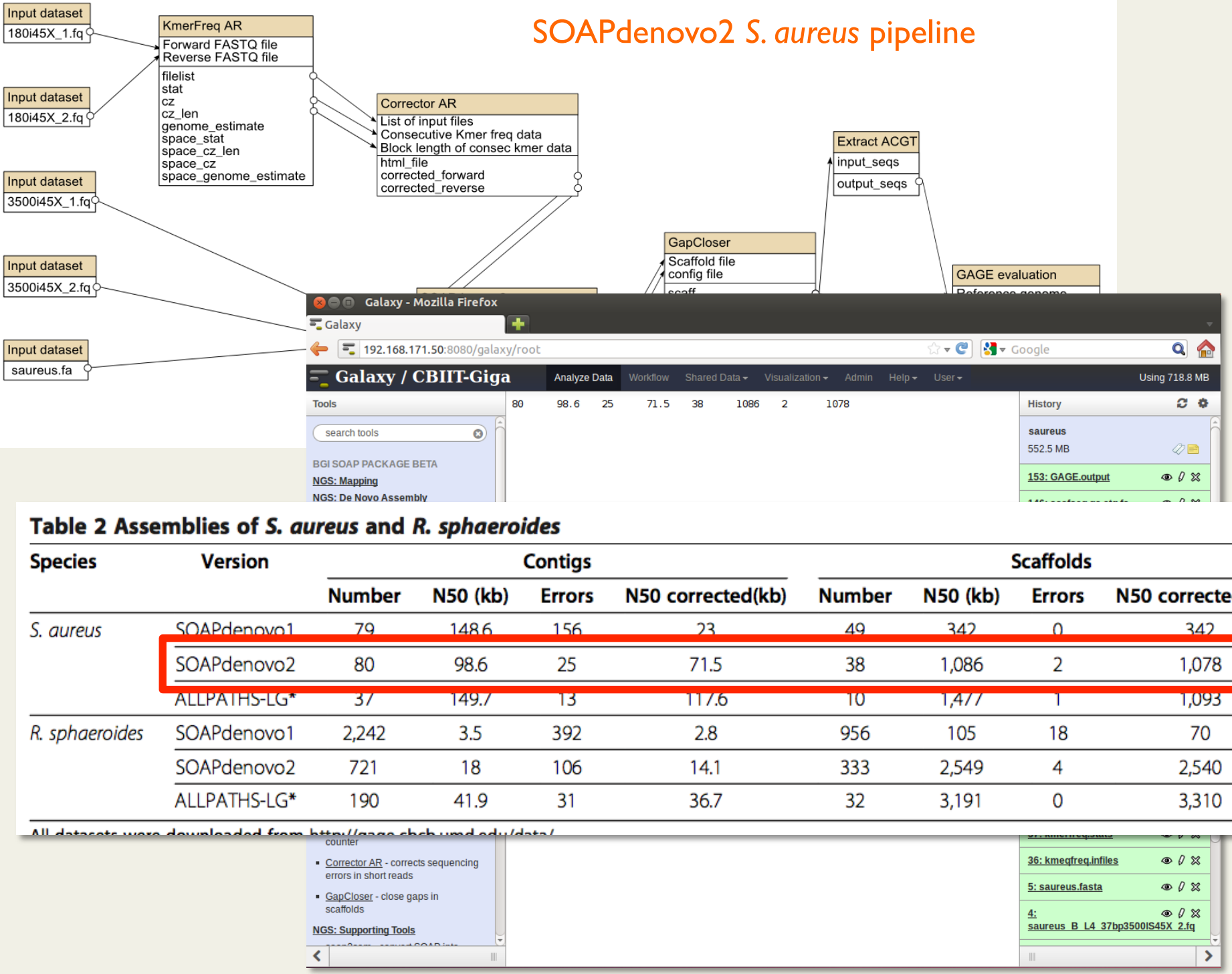


Table 2 Assemblies of *S. aureus* and *R. sphaeroides*

Species	Version	Contigs				Scaffolds			
		Number	N50 (kb)	Errors	N50 corrected(kb)	Number	N50 (kb)	Errors	N50 corrected (kb)
S. aureus	SOAPdenovo1	79	148.6	156	23	49	342	0	342
	SOAPdenovo2	80	98.6	25	71.5	38	1,086	2	1,078
	ALLPATHS-LG*	37	149.7	13	117.6	10	1,477	1	1,093
R. sphaeroides	SOAPdenovo1	2,242	3.5	392	2.8	956	105	18	70
	SOAPdenovo2	721	18	106	14.1	333	2,549	4	2,540
	ALLPATHS-LG*	190	41.9	31	36.7	32	3,191	0	3,310

All datasets were downloaded from http://gage.cbcb.umd.edu/data/

Published and Galaxy-reproduced statistics of genome assemblies of S. aureus and R. sphaeroides

Published

Species	Tool	Contigs				Scaffolds			
		Number	N50 (kb)	Errors	N50 corrected (kb)	Number	N50 (kb)	Errors	N50 corrected (kb)
S. aureus	SOAPdenovo1	79	148.6	156	23	49	342	0	342
	SOAPdenovo2	80	98.6	25	71.5	38	1086	2	1078
	ALL-PATHS-LG	37	149.7	13	117.6	10	1477	1	1093
R. sphaeroides	SOAPdenovo1	2242	3.5	392	2.8	956	105	18	70
	SOAPdenovo2	721	18	106	14.1	333	2549	4	2540
	ALL-PATHS-LG	190	41.9	31	36.7	32	3191	0	3310

Reproduced

Species	Tool	Contigs				Scaffolds			
		Number	N50 (kb)	Errors	N50 corrected (kb)	Number	N50 (kb)	Errors	N50 corrected (kb)
S. aureus	SOAPdenovo1	79	148.6	156	23	49	342	0	342
	SOAPdenovo2	80	98.6	25	71.5	38	1086	2	1078
	ALL-PATHS-LG	37	149.7	13	119.0	11	1477	1	1093
R. sphaeroides	SOAPdenovo1	2241	3.5	400	2.8	956	106	24	68
	SOAPdenovo2	721	18	106	14.1	333	2549	4	2540
	ALL-PATHS-LG	190	41.9	30	36.7	32	3191	0	0

Published Workflows

search name, annotation, owner, and tag

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obedoya_reina_2013: Example 1B: aye-aye FST		gigascience			Jan 23, 2014
obedoya_reina_2013: Example 1C: aye-aye diversity		gigascience			Jan 23, 2014
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rluo_2012: Example 2: soapdenovo2 rsphaeroides		gigascience			Jan 30, 2014
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rluo_2012: Example 6: ALLPATHS-LG rsphaeroides		gigascience			Feb 10, 2014

GigaGalaxy | Analyze Data | Workflow | Shared Data | Visualization | Admin | Help | User | Using 105.3 GB

Published Pages | gigascience | SOAPdenovo2 S. aureus

Pipeline: Luo et al., (2012) SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. *GigaScience* 1:18.

A new version of SOAPdenovo was published in *GigaScience* late in 2012. In this paper, Luo and colleagues described improvements made to their *de novo* genome assembler which was tested on a number of short read data sets including the YH Asian genome. Through our new GigaGalaxy platform, we have made available Galaxy workflows that replicates the data analysis procedures used by Luo et al., (2012) to assemble genomes from short read data sets obtained from *S. aureus* and *R. sphaeroides*. Specifically, these two workflows replicate the metrics shown in Table 2 of the GigaScience paper:

Table 2 Assemblies of *S. aureus* and *R. sphaeroides*

Species	Version	Contigs					
		Number	N50 (kb)	Errors	N50 corrected(kb)	Number	N5
S. aureus	SOAPdenovo1	79	148.6	156	23	49	
	SOAPdenovo2	80	98.6	25	71.5	38	1
	ALLPATHS-LG*	37	149.7	13	117.6	10	1
R. sphaeroides	SOAPdenovo1	2,242	3.5	392	2.8	956	
	SOAPdenovo2	721	18	106	14.1	333	2
	ALLPATHS-LG*	190	41.9	31	36.7	32	3

Workflow

The pipeline that reproduces the above *S. aureus* results requires the following steps:

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http://galaxy.cbiit.cuhk.edu.hk/u/gigascience/p/soapdenovo2-s-aureus

Observations

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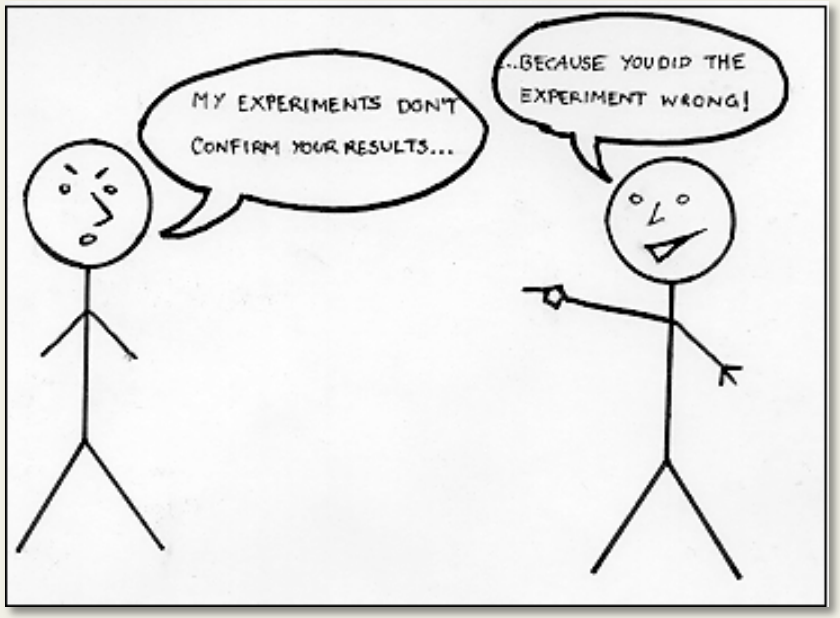
F1000Research 2014, 3:102 Last updated: 27 MAY 2014

RESEARCH ARTICLE

Transient acid treatment cannot induce neonatal somatic cells to become pluripotent stem cells [v1; ref status: indexed, http://f1000r.es/3dq]

Mei Kuen Tang[1], Lok Man Lo[1], Wen Ting Shi[1], Yao Yao[1], Henry Siu Sum Lee[2], Kenneth Ka Ho Lee[1]

[1]Key Laboratory for Regeneration Medicine, School of Biomedical Sciences, Chinese University of Hong Kong, Shatin, Hong Kong
[2]Faculty of Life Sciences, University of Manchester, Manchester, M13 9PL, UK



http://www.cf.ac.uk/socsi/contactsandpeople/harrycollins/image-36548-web.gif

Thanks to:

(GIGA)n SCIENCE team:

Peter Li
Huayan Gao
Chris Hunter
Jesse Si Zhe
Nicole Nogoy
Laurie Goodman
Amye Kenall (BMC)

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Shaoguang Liang (BGI-SZ)
Tin-Lap Lee (CUHK)
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