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# GigaGalaxy: A GigaSolution for reproducible and sustainable genomic data publication and analysis

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Today's next generation sequencing (NGS) experiments generate substantially more data and are more broadly applicable to previous high-throughput genomic assays. Despite the plummeting costs of sequencing, downstream data processing and analysis create financial and bioinformatics challenges for many biomedical scientists. It is therefore important to make NGS data interpretation as accessible as data generation. GigaGalaxy (http://galaxy.cbiit.cuhk.edu.hk) represents a NGS data interpretation solution towards the big sequencing data challenge. We have ported the popular Short Oligonucleotide Analysis Package (http:// soap.genomics.org.cn) as well as supporting tools such as Contiguator2 (http://contiguator.sourceforge.net) into the Galaxy framework, to provide seamless NGS mapping, de novo assembly, NGS data format conversion and sequence alignment visualization. Our vision is to create an open publication, review and analysis environment by integrating GigaGalaxy into the publication platform at GigaScience and its GigaDB database that links to more than 40 TBs of genomic data. We have begun this effort by re-implementing the data procedures described by Luo et al., (GigaScience 1: 18, 2012) as Galaxy workflows so that they can be shared in a manner which can be visualized and executed in GigaGalaxy. We hope to revolutionize the publication model with the aim of executable publications, where data analyses can be reproduced and reused.

**Keywords**: Galaxy, workflows, reproducible research, genome assembly, next generation sequencing, *GigaScience* 

## Background

#### **Growing replication gap:**

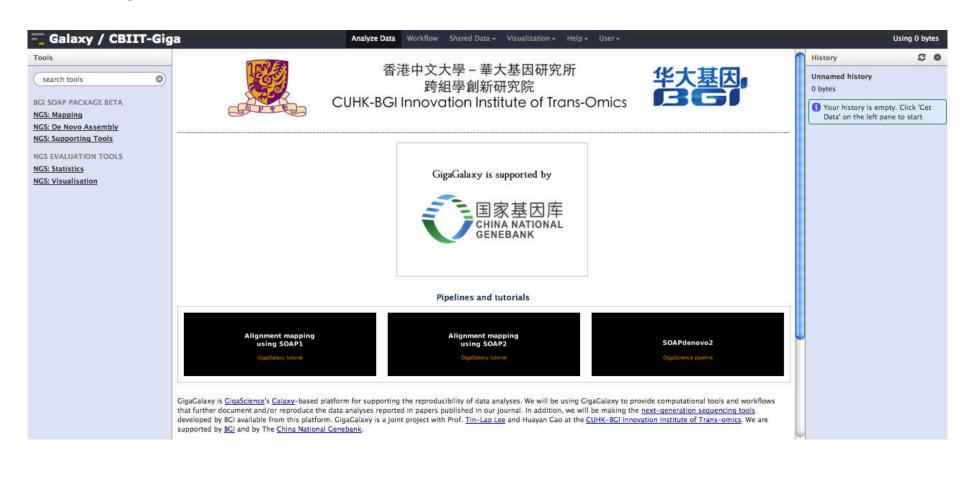
- 10/18 microarray papers cannot be reproduced
- Ioannidis: "Most Published Research Findings Are False"
- >15X increase in retracted papers in last decade
- Lack of incentives to make data/methods available

#### GigaSolution: deconstructing the paper

Combine and integrate (via citable DOIs):

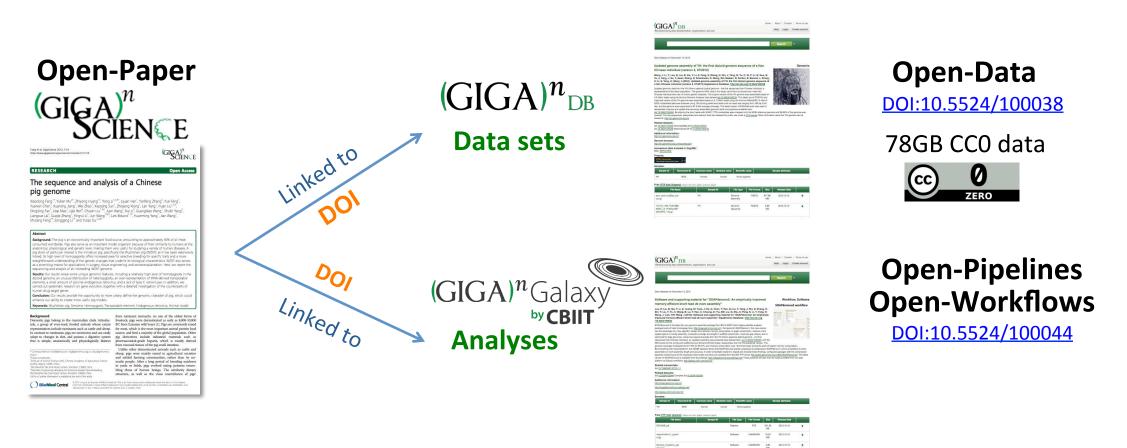


#### **GigaGalaxy: screenshot**

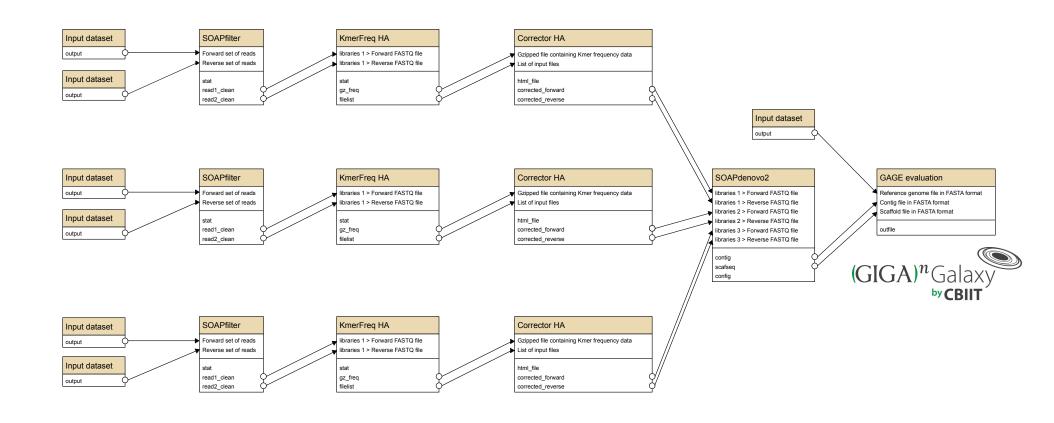


#### **Example: SOAPdenovo2**

#### Linking papers to data and analyses

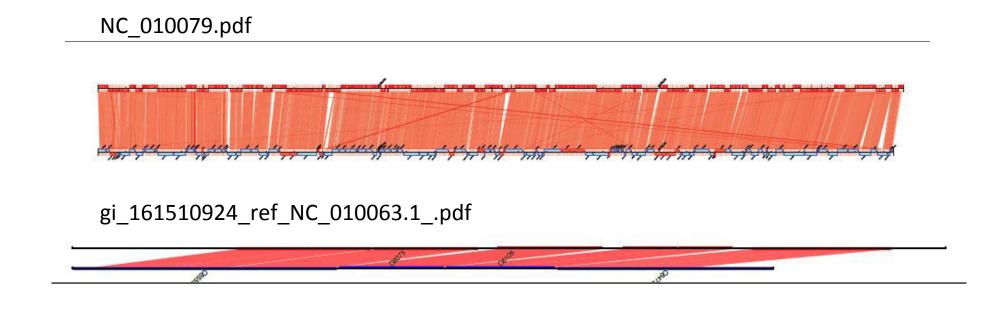


# Implement paper pipelines in GigaGalaxy



### **Visualization of results:**

e.g. GAGE metrics and CONTIGuator 2 outputs:



#### References

- 1. Ioannidis et al., Repeatability of published microarray gene expression analyses. Nature Genetics 2009 41: 14
- 2. Science publishing: The trouble with retractions *Nature* 2011 478, 26-28 3. Ioannidis J. Why Most Published Research Findings Are False. PLoS Med 2005 2(8): e124.
- 4. Sneddon et al., GigaDB: promoting data dissemination and reproducibility. *Database* 2014: bau018 5. Luo et al., SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler

#### GigaScience 2012, 1:18 **Acknowledgements**





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- 6. Wang, J; et al., (2012): Updated genome assembly of YH: the first diploid genome sequence of a Han Chinese individual (version 2, 07/2012). GigaScience Database. <a href="http://dx.doi.org/10.5524/100038">http://dx.doi.org/10.5524/100038</a>.
- 7. Luo, R; et al., (2012): Software and supporting material for "SOAPdenovo2: An empirically improved
- memory-efficient short read de novo assembly". GigaScience Database. http://dx.doi.org/10.5524/100044 8. Galardini et al.:CONTIGuator: a bacterial genomes finishing tool for structural insights on draft genomes.
- *Source Code for Biology and Medicine* 2011 6:11. 9. GigaGalaxy code in GitHub under ASL v3.0 open source license <a href="https://github.com/gigascience">https://github.com/gigascience</a>



doi:10.6084/m9.figshare.713512

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