

# Connecting Galaxy to tools with alternative storage and compute models

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<https://github.com/chapmanb/bcbio-nextgen>

<http://j.mp/bcbiolinks>

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Community > Implementation

# Validation > Replication

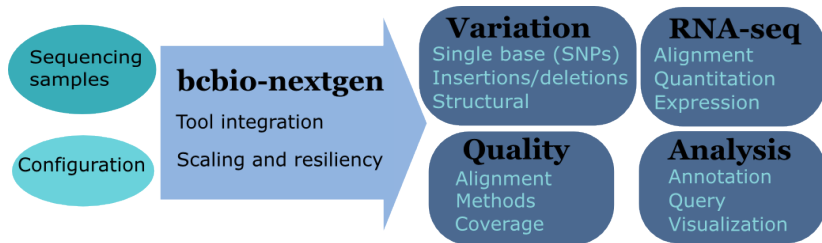
Genome in a Bottle: <http://www.genomeinabottle.org/>

ICGC-TCGA DREAM: <https://www.synapse.org/#!/Synapse:syn312572>

SMaSH: <http://smash.cs.berkeley.edu/>

Scaling > Configurability

# Overview



<https://github.com/chapmanb/bcbio-nextgen>

- Aligners: bwa-mem, novoalign, bowtie2
- Variation: FreeBayes, GATK, MuTect, SnpEff, VEP, GEMINI
- RNA-seq: tophat, STAR, cufflinks, HTSeq
- Quality control: fastqc, bamtools, RNA-SeQC
- Manipulation: bedtools, bcftools, biobambam, sambamba, samblaster, samtools, vcflib

- Validation – outputs + automated evaluation
- Tool integration
- Multi-platform support
- Scaling

# bcbio as a tool

<https://github.com/chapmanb/bcbio-nextgen/tree/master/config/galaxy>



# Storage

<https://github.com/chapmanb/bcbio-nextgen-vm>

<https://github.com/chapmanb/cloudbiolinux>

# Summary

- Focus: Community, Validation, Scaling
- Practical tool: bcbio-nextgen  
<https://github.com/chapmanb/bcbio-nextgen>
- Galaxy