

EUR
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JAAR | YEARS
IMPACT



iReport: HTML reporting in Galaxy

Saskia Hiltemann

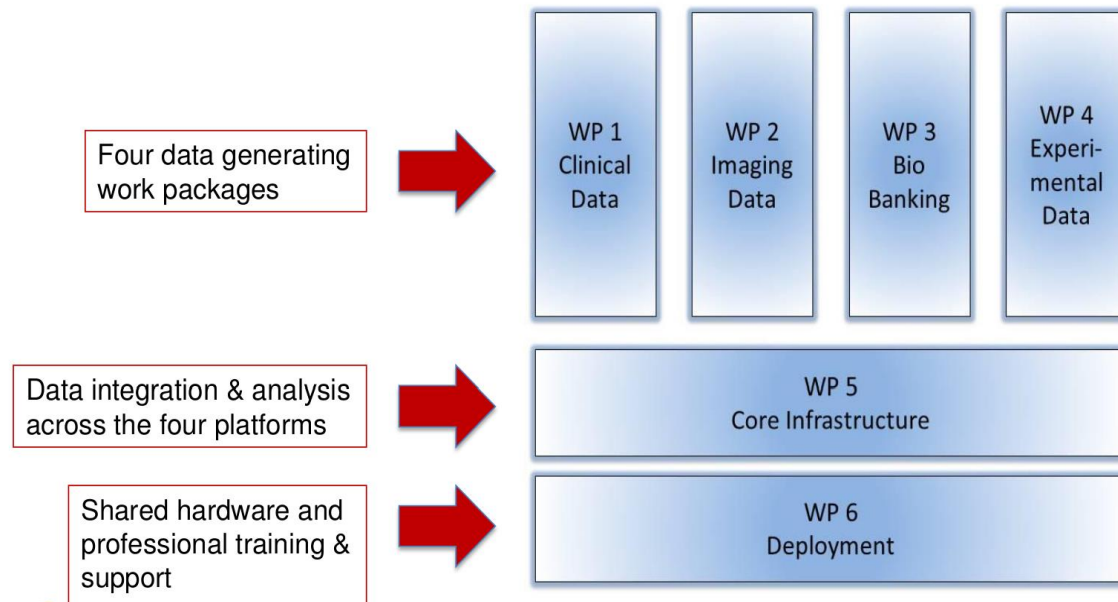
Erasmus University Medical Center,
Rotterdam, The Netherlands

s.hiltemann@erasmusmc.nl

CTMM TraIT project

Translational Research IT (TraIT)

aims to develop a long-lasting IT infrastructure for translational medicine that will facilitate the collection, storage, analysis, archiving, sharing and securing of the data generated in the CTMM's operational translational research projects.



Motivation: CGtag pipeline

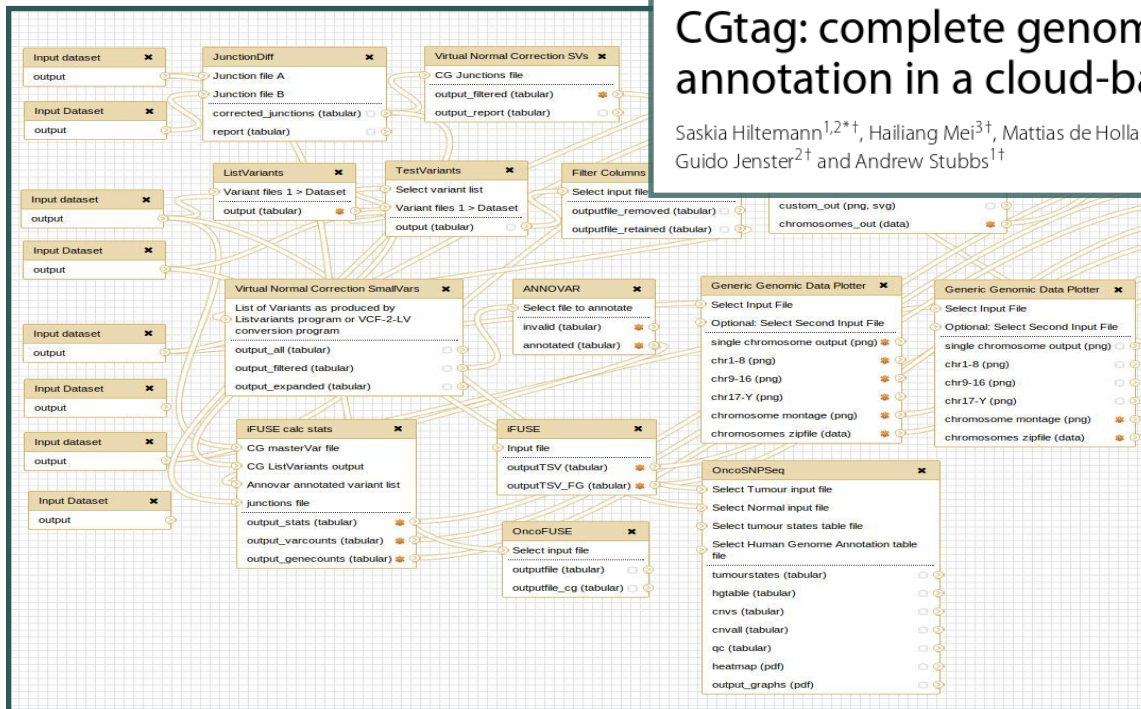
Pipeline for downstream analysis of Complete Genomics data

TECHNICAL NOTE

Open Access

CGtag: complete genomics toolkit and annotation in a cloud-based Galaxy

Saskia Hiltemann^{1,2*†}, Hailiang Mei^{3†}, Mattias de Hollander^{4†}, Ivo Palli^{1†}, Peter van der Spek^{1†}, Guido Jenster^{2†} and Andrew Stubbs^{1†}



Workflow has a lot of outputs, wanted to combine them into a single view.

Solution: iFUSE2

Created iFUSE2, an HTML output for the CGtag pipeline

- Display images, tables, summary statistics, etc.
- Tab per subject (SV, small variants, CNV, ..)
- Javascript and jQuery for interactivity (sortable, searchable tables, image zoom, etc..)

The screenshot displays the Galaxy CMM-TraIT Demo Galaxy interface. The main view is titled "Genome Overview" and includes a "Whole Genome Plot" and a "Chromosome Overview Plot". Below these plots is a table of genomic features and a mutation heatmap. A search bar is visible above the data table.

FEATURE	11/Tv	het/bom
CDS	2.99	1.22
INTERGENIC	2.07	0.64
INTRON	2.22	1.44
UTR	2.15	1.52
DONOR	2.81	1.09
TSS-UPSTREAM	2.08	1.59
ACCEPTOR	2.42	1.46
SYNONYMOUS	5.20	1.30
MISSENSE	2.14	1.07
NONSENSE	1.93	0.66

Junction CG ID	Gene Left name 2	Gene Right name 2	Junction LeftChr	Junction LeftStrand	Junction LeftPosition	Junction LeftStart	Junction LeftEnd	Gene Left name	Junction RightChr	Junction RightStrand	Junction RightPosition	Junction RightStart	Junction RightEnd	C
1038	SPTBN2	SPTBN1	chr10	-	81316262	81316262	81316387	NM_001098666	chr10	+	81374560	81374560	81374811	NM_0
2173	TRIPK4	POPDC1	chr20	-	30729766	30729766	30730208	NM_014742	chr20	-	30817675	30817686	30817675	NM_0

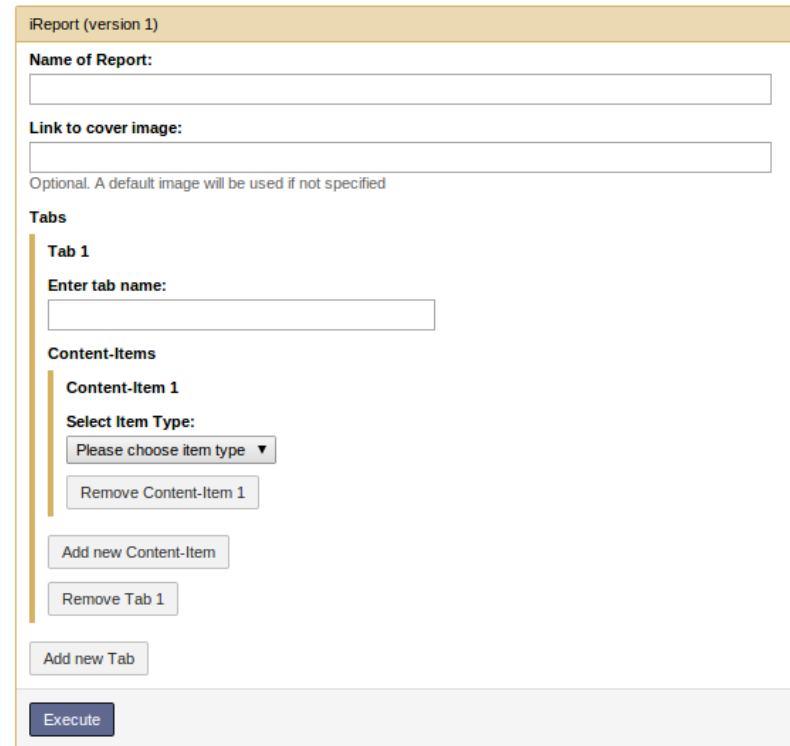
Idea: General tool to easily build such a report page for any workflow

iReport: Create HTML reports for any workflow

Galaxy Tool to create iFUSE2-like HTML reports

Basic structure

- Cover Page (title and cover image)
- Report Page consisting of any number of tabs, each containing one or more *content items*.
- Content items can be:
 - Text
 - Images
 - Tables
 - PDF files
 - Links



iReport (version 1)

Name of Report:

Link to cover image:

Optional. A default image will be used if not specified

Tabs

Tab 1

Enter tab name:

Content-Items

Content-Item 1

Select Item Type:

iReport: Demo

An iReport explaining iReports (live version of my slides) can be viewed at:
<http://galaxy.ctmm-trait.nl/u/saskia-hiltemann/h/gcc2014-ireport-about-ireport>
tinyurl: tinyurl.com/llrzz9w

Import history, go to *Analyze Data*, and view (eye) dataset 94: HTML report: iReport Tutorial

You should now see the cover page:

The screenshot shows the Galaxy web interface. The top navigation bar includes 'Galaxy / CTMM-Trait Demo Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Admin', 'Help', and 'User'. The left sidebar contains a 'Tools' menu with categories like 'Get Data', 'CGTAG', 'CGAtools', 'Annotation', 'Visualisation', 'File Manipulation', 'iReport', 'GENERAL TOOLS', and 'Workflows'. The main content area displays the 'iReport: iReport Tutorial' cover page, which features the Galaxy Community Conference logo (a sailboat) and the text 'GALAXY COMMUNITY CONFERENCE BALTIMORE, MD | JUNE 30 - JULY 2, 2014'. A link 'Click here to view report' is visible. The right sidebar shows the 'History' panel with a list of reports, including 'GCC2014: iReport about iReport' (77.5 MB) and a list of numbered HTML reports (11-17).

tinyurl.com/llrzz9w

iReport: Cover Page

Title of report is specified by user

URL to a **cover image** may be specified by user, otherwise default image is used

The screenshot displays the Galaxy web interface for a report titled "iReport: iFUSE2". The main content area features the Erasmus MC logo (University Medical Center Rotterdam) and the text "Erasmus Bioinformatics" above a blue DNA double helix image. A link "Click here to view report" is visible below the title. The left sidebar contains a "Tools" menu with categories like "Get Data", "CGTAG", "CGAtools", "Annotation", "Visualisation", "File Manipulation", "iReport", "GENERAL TOOLS", "Filter and Sort", "Admin Tools", "VCF tools", and "Workflows". The right sidebar shows a "History" panel with a list of recent reports, including "CGtag with iReport example for Mariska" (5.4 GB) and several "iFUSE" reports with various file names and sizes.

iReport : Text

Text File from history can be specified, will be printed verbatim
Text Field Text can be added directly into a text field in the tool wrapper

Content-Items

Content-Item 1

Select Item Type:

Text Field

Text to display.:

```
<h3> iReport: HTML reporting in Galaxy </h3> iReport is a Galaxy tool for the easy creation of HTML reports from workflow outputs. An iReport consists of a cover page, and a tab-based report page.
```

```
<strong>Cover Page</strong>
```

Users specify a title for their iReport, and optionally a link to a cover image. If no cover image is specified, a default image is used. An example (the cover page for this report) is shown below. Clicking on the image or on the link above it, will take the user to the main report page.

can explicitly add whitespace adding \n in your text for a newline

Insert break after item?:

Input is sanitized, only a few html formatting tags are allowed (h1-h6, strong, em)
\t and \n to explicitly enter whitespace

iReport: Images

Specify image file from history (supported formats: jpeg, png, svg)

Specify image width (0 for original size)

- if image is scaled down, a jQuery zoom-on-mouseover effect is added

After every content item, user can explicitly add a break (
) to force elements to be placed beneath one another, otherwise let browser decide layout.

Content-Item 5

Select Item Type:

Image ▼

Image File:

53: Campus_Map.jpg ▼

Supported formats: png, jpg, svg. If image is scaled by choice of width, zoom-on-mousover effect is added.

Width (in pixels):

1000

enter 0 to keep original size

Insert break after item?:



Remove Content-Item 5

iReport: Images



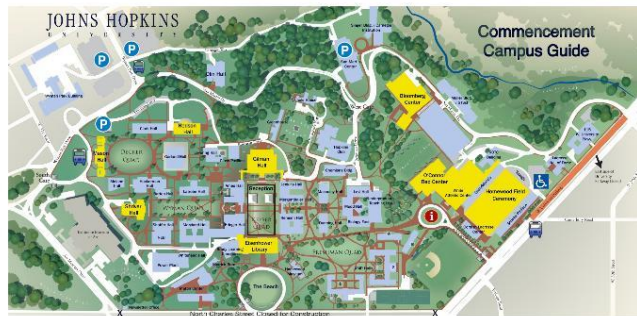
Introduction	Text	Images	Links	PDF files	Tables	Parting words
--------------	------	--------	-------	-----------	--------	---------------

Images can also be added to the tabs. Currently supported formats are: png, jpg, svg.

Users specify a width for their image, and the image is scaled accordingly. To keep the original size, enter a width of z. A break can be explicitly inserted after every item, to force images to appear below one another. If this option is not chosen below each other.



For image that are scaled down, a (jQuery) zoom-on-mouseover effect is added:



Next up.. Links!



Introduction	Text	Images	Links	PDF files	Tables	Parting words
--------------	------	--------	-------	-----------	--------	---------------

Images can also be added to the tabs. Currently supported formats are: png, jpg, svg.

Users specify a width for their image, and the image is scaled accordingly. To keep the original size, enter a width of z. A break can be explicitly inserted after every item, to force images to appear below one another. If this option is not chosen below each other.



For image that are scaled down, a (jQuery) zoom-on-mouseover effect is added:



Next up.. Links!

iReport: Tables

Table input must be tab-delimited file. File is assumed to have a 1-line header (all lines starting with hash symbol (#) are ignored)

jQuery library **datatables** (<https://datatables.net>) used to create html tables which are searchable, sortable, and paginated (if desired).

Introduction Text Images Links PDF files **Tables** Parting words

Tables can displayed as well. The input file must be a tab-delimited file.

Lines starting with # character are ignored. The first non-empty line not starting with # is assumed to be the header (exception is the VCF file header lines starting with #CHROM, which is correctly detected despite beginning with hash symbol)

Fancy tables

The *fancy table* option creates a table which is paginated, searchable and sortable.

The jQuery library [datatables](#) is used for this.

An example of such a *fancy* table can be found below.

Show 10 entries

Search:

Cars	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
AMC Javelin	15.2	8	304.0	150	3.15	3.435	17.30	0	0	3	2
Cadillac Fleetwood	10.4	8	472.0	205	2.93	5.250	17.98	0	0	3	4
Camaro Z28	13.3	8	350.0	245	3.73	3.840	15.41	0	0	3	4
Chrysler Imperial	14.7	8	440.0	230	3.23	5.345	17.42	0	0	3	4
Dodge Challenger	15.5	8	318.0	150	2.76	3.520	16.87	0	0	3	2
Ferrari Dino	19.7	6	145.0	175	3.62	2.770	15.50	0	1	5	6
Fiat 128	32.4	4	78.7	66	4.08	2.200	19.47	1	1	4	1
Duster 360	14.3	8	360.0	245	3.21	3.570	15.84	0	0	3	4
Datsun 710	22.8	4	108.0	93	3.85	2.320	18.61	1	1	4	1
Fiat X1-9	27.3	4	79.0	66	4.08	1.935	18.90	1	1	4	1

Showing 1 to 10 of 31 entries

Previous Next



iReport: Tables with links

Column from table can be used to create **hyperlinks**, by providing column number, url prefix and suffix. For example, if a column contains gene names, adding prefix www.genecards.org/cgi-bin/carddisp.pl?gene= generates a link to the corresponding gene cards entry.

Content-Item 6

Select Item Type:

Table

Table File:

78: genest.tsv

must be a tab-delimited file with a 1-line header

Fancy table?:

If selected, will create, sortable, searchable, paginated table. Otherwise not (for small

create url links from one of the columns in your table?:

Yes

For example: from column with gene names, link to genecards page

Column to turn in to weblinks:

c1

URL prefix:

this will be placed before value in column to form the weblink. e.g. for genecards use: http://www.genecards.org/cgi-bin/carddisp.pl?gene=

URL suffix:

this will be placed before value in column to form the weblink. e.g. For genecards, the

Archive with files to link to:

Selection is Optional

Optional. Only if you want to link column entries to local files instead of websites

Insert break after item?:

Remove Content-Item 6

Weblinks from column entries

Column values can also be used to generate weblinks. For instance, in the following table, the column containing gene names has been turned into a series of links to corresponding genecards entries. This can be achieved by specifying the column number, along with a url prefix and url suffix, which will be added before and after the value in the column to form the weblink.

Show 10 entries

gene-name	chromosome	start	stop
A1BG	19	58858172	58864865
A1CF	10	52566322	52645435
A2GC1B	2	130831108	130886795
A21D1	13	101183801	101241782
A2M	12	9220308	9268825
A2ML1	12	8975174	9029379
A4GALT	22	43088127	43117304
A4GNT	3	137842560	137851229
AAAS	12	53701241	53715412
AACS	12	125549925	125627871

Showing 1 to 10 of 20,089 entries



Weblinks from column entries

Column values can also be used to generate weblinks. For instance, in the following table, the column containing gene names has been turned into a series of links to corresponding genecards entries. This can be achieved by specifying the column number, along with an url prefix and url suffix, which will be added before and after the value in the column to form the weblink.

The screenshot shows the GeneCards website interface. At the top, there are logos for GeneCards, Weizmann Institute of Science, and LifeMap Sciences. Below the logos, there is a navigation bar with links for Home, GeneCards Guide, Suite, Terms and Conditions, About Us, User Feedback, and Mirror sites. A search bar is present with the text "Set Analyses: GeneAtlas, GeneDecks" and a search button. The main content area displays the gene entry for A1BG Gene, protein-coding, with the Gene ID: GC19M058858 and the title Alpha-1-B Glycoprotein. The gene name "A1BG" is highlighted in red.

tinyurl.com/llrzz9w

iReport: PDF files



Galaxy / CTMM-TraIT Demo Galaxy

Analyze Data Workflow Shared Data Visualization Admin Help User

Tools

search tools

Get Data

CGTAG

CGAtools

Annotation

Visualisation

File Manipulation

iReport

Admin Virtual Normal Preprocessing

Admin Virtual Normal Correction

GENERAL TOOLS

Filter and Sort

Admin Test Tools

Admin iPER test

VCF tools

Workflows

- All workflows

Introduction Text Images Links PDF files Tables Parting words

PDF files from history can also be added. Simply specify the file, and depending on your browser setup, the file will be either displayed within the tab, or a link to the file will be generated, allowing the file to be opened in your default pdf viewer or downloaded to your computer.

For example, the pdf file of the CGtag paper published in GigaScience, can be viewed/downloaded below.

History

Copy of 'GCC2014: iReport at iReport' (active items only)

17.3 MB

Tags:

Add tags

Annotation:

Click here to edit annotation

95: HTML report: iReport Tutorial

94: HTML report: iReport Tutorial

87: pictures.dat

80: mtcars.tsv

78: genest.tsv

73: cgtag.pdf

62: weblink.png

55: campus.jpg

53: Campus_Map.jpg

51: Johns-Hopkins-University-Logo.jpg

40: textfileinput.txt

31: textfileinput.txt

26: textfield_screenshot.png

19: coverpage_screenshot.png

8: workflow_CGtag_with_iReport.png

Hiltemann et al. *GigaScience* 2014, 3:1
<http://www.gigascejournal.com/content/3/1/1>

(GIGA)ⁿ SCIENCE

TECHNICAL NOTE Open Access

CGtag: complete genomics toolkit and annotation in a cloud-based Galaxy

Saskia Hiltemann^{1,2*†}, Hailiang Mei^{3†}, Mattias de Hollander^{4†}, Ivo Palli^{1†}, Peter van der Spek^{1†}, Guido Jenster^{2†} and Andrew Stubbs^{1†}

Abstract

Background: Complete Genomics provides an open-source suite of command-line tools for the analysis of their CG-formatted mapped sequencing files. Determination of, for example, the functional impact of detected variants, requires annotation with various databases that often require command-line and/or programming experience; thus, limiting their use to the average research scientist. We have therefore implemented this CG toolkit, together with a number of annotation, visualisation and file manipulation tools in Galaxy called CGtag (Complete Genomics Toolkit and Annotation in a Cloud-based Galaxy).

Findings: In order to provide research scientists with web-based, simple and accurate analytical and visualisation applications for the selection of candidate mutations from Complete Genomics data, we have implemented the open-source Complete Genomics tool set, CGATools, in Galaxy. In addition we implemented some of the most popular command-line annotation and visualisation tools to allow research scientists to select candidate pathological

iReport: Links

Link to web address

- specify url and link text

Link to file in history

- specify history item and link text
- specify if link is another iReport (use as kind of lab notebook)

Link to files in archive in history

- specify archive history item (e.g. zip file of per-chromosome plots)
- link will be created to each file in archive
- supported archives formats: zip, bz2, tar, gz, tar.gz

Content-Item 4

Select Item Type:

web location to link to :

url to link to

link text:

text to display as a link

Insert break after item?:

Supported formats: zip, gz, tar, bz2

Link to files in archive

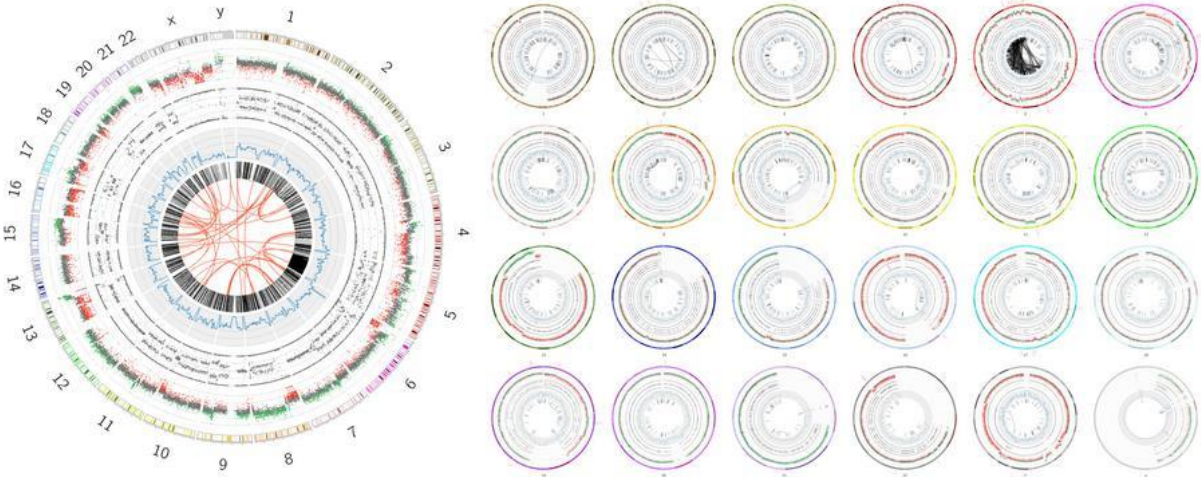
Often my tools output an archive of files (for instance an archive with 26 images, one per chromosome). iReports can take this as input and generate a series of links to each of the contained files. Currently supported archives: zip, tar, gz, tar.gz, bz2

Below is an example with an archive containing images of all the speakers of the conference: [AlbanLermine](#) [AndrewLonie](#) [AngelPizarro](#) [AnushkaBrownley](#) [BradChapman](#) [Hackathon](#) [JamesReaney](#) [JohnChiltonSmaller](#) [MikaelLoaec](#) [OlivierInizan](#) [PatrickCombes](#) [PeterCock](#) [PeterLi](#) [PratikJagtap](#) [RaviMadduri](#) [Salzberg](#) [SarahDiehl](#) [SaskiaHiltemann](#) [SebastianSchaaf](#) [VivienDeshaies](#) [YoungkiKim](#) [anton](#) [dan](#) [greg](#) [james](#) [marten](#) [mike](#) [nuwan](#)

iReport example: iFUSE2



Genome Overview | Structural Variants | B-allele Frequency | Coverage | Virtual Normal



Chromosome plots: [chr01](#) [chr02](#) [chr03](#) [chr04](#) [chr05](#) [chr06](#) [chr07](#) [chr08](#) [chr09](#) [chr10](#) [chr11](#) [chr12](#) [chr13](#) [chr14](#) [chr15](#) [chr16](#) [chr17](#) [chr18](#) [chr19](#) [chr20](#) [chr21](#) [chr22](#) [chrX](#) [chrY](#)

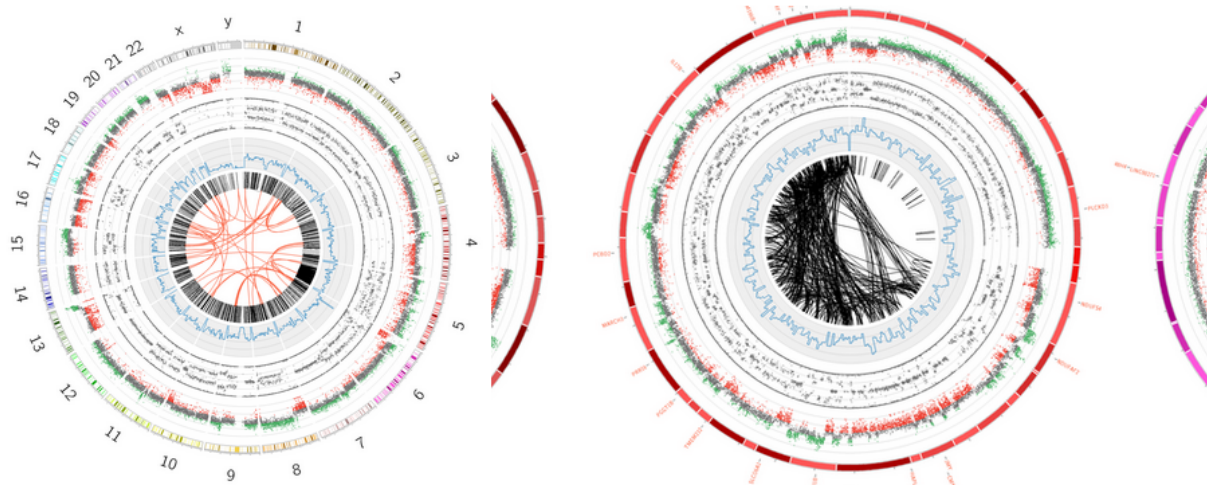
Metric	Whole Genome	Exonic
Structural Variants	2,415	999
Small variants	279,466	2,250
SNP	131,248	1,663
INS	75,703	277
DEL	48,978	149
SUB	23,536	161
Ti/Tv ratio	1.8048	1.76246
Het/Hom ratio	1.21596	1.26153

	All Variants	snps	ins	del	sub
Whole Genome	279,465	131,248	75,703	48,978	23,536
exonic;splicing	1	1	0	0	0
intergenic	159,127	78,580	39,360	26,835	14,352
downstream	1,741	691	568	347	135
intronic	102,604	43,510	32,048	19,310	7,736
UTR5;UTR3	1	1	0	0	0
ncRNA_splicing	1	1	0	0	0
ncRNA_intronic	8,294	3,982	2,119	1,398	795
UTR3	2,060	887	654	393	126
upstream	2,342	1,267	488	412	175
ncRNA_exonic	469	299	91	51	28
UTR5	874	592	135	99	48
ncRNA_UTR3	33	9	15	8	1
upstream;downstream	90	47	22	17	4
ncRNA_UTR5	10	5	1	3	1
splicing	38	13	16	7	2
exonic	1,780	1,363	186	98	133

Gene	All Variants	snps	ins	del	sub
PTPRD	287	139	73	63	12
CSMD1	236	146	40	32	18
EYS	221	118	54	26	23
CNTNAP2	207	103	50	41	13
DLG2	199	98	48	33	20
LRPIB	181	88	42	28	23
RBFOX1	178	74	53	39	12
NRG1	178	104	41	25	8
MACROD2	175	67	64	37	7
CTNNA3	170	90	46	24	10
MAGI2	154	69	44	29	12

iReport example: iFUSE2

Genome Overview | Structural Variants | B-allele Frequency | Coverage | Virtual Normal



Chromosome plots: [chr01](#) [chr02](#) [chr03](#) [chr04](#) [chr05](#) [chr06](#) [chr07](#) [chr08](#) [chr09](#) [chr10](#) [chr11](#) [chr12](#) [chr13](#) [chr14](#) [chr15](#) [chr16](#) [chr17](#) [chr18](#) [chr19](#) [chr20](#) [chr21](#) [chr22](#) [chrX](#) [chrY](#)

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UTR3	2,060	887	654	393	126
upstream	2,342	1,267	488	412	175
ncRNA_exonic	469	299	91	51	28
UTR5	874	592	135	99	48
ncRNA_UTR3	33	9	15	8	1
upstream;downstream	90	47	22	17	4
ncRNA_UTR5	10	5	1	3	1
splicing	38	13	16	7	2
exonic	1,780	1,363	186	98	133

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PTPRD	287	139	73	63	12
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EYS	221	118	54	26	23
CNTNAP2	207	103	50	41	13
DLG2	199	98	48	33	20
LRP1B	181	88	42	28	23
RBFOX1	178	74	53	39	12
NRG1	178	104	41	25	8
MACROD2	175	67	64	37	7
CTNNA3	170	90	46	24	10
MAGI2	154	69	44	29	12



iReport example: iFUSE2

Genome Overview | **Structural Variants** | B-allele Frequency | Coverage | Virtual Normal

Fusion Gene Candidates:

Show 10 entries Search:

Junction CG.ID	Related Junctions	Associated Junctions	Shared Genes	Gene Mismatch	Single Event	Fusion Gene	Left Position in CDS	Right Position in CDS	Left Position in Exon	Right Position in Exon	Gene Left.name2	Gene Right.name2	Gene Left.name	Gene Left.chrom	Gene Left.strand	Gene Left.txStart	Gene Left.txEnd
244	rj119	NA	sg160	yes	interchromosomal	same orientation	yes	yes	no	yes	UNK	LSM12	NM_001080419	chr17	+	71292514	7133348
761	rj1734	NA	sg1220	yes	inversion	same orientation	yes	yes	no	no	UNC5D	ANK1	NM_080872	chr8	+	35212516	3577172
837	rj1915	NA	sg264	yes	inversion	same orientation	yes	no	no	no	CDKAL1	DCDC2	NM_017774	chr6	+	20642666	2134061
899	rj1304	NA	sg1437	yes	inversion	same orientation	yes	yes	no	yes	AP3S1	LMAN2	NM_001284	chr5	+	115205517	11527767
1517	rj38	NA	sg39	yes	interchromosomal	same orientation	yes	yes	no	no	GRID2	TEC	NM_001510	chr4	+	93444572	9491267
1565	rj39	NA	sg40	yes	inversion	same orientation	yes	no	no	yes	RGNEF	ZFP62	NM_001080479	chr5	+	72957738	7327357
1567	rj41	NA	sg2422	yes	inversion	same orientation	yes	yes	no	no	CWC27	SLIT3	NM_005869	chr5	+	64100510	6435034
1570	rj44	NA	sg2422	yes	inversion	same orientation	yes	yes	yes	no	MAP1B	EBF1	NM_005909	chr5	+	71438873	7154115
1585	rj41	NA	sg2422	yes	inversion	same orientation	yes	yes	no	no	CWC27	FBXL17	NM_005869	chr5	+	64100510	6435034
1609	rj67	NA	sg71	yes	inversion	same orientation	yes	yes	no	no	CHNG	HJURP	NM_005199	chr2	+	233112680	23311928

Showing 1 to 10 of 48 entries Previous Next

All breakpoints:

Show 10 entries Search:

Junction CG.ID	Related Junctions	Associated Junctions	Shared Genes	Gene Mismatch	Single Event	Fusion Gene	Left Position in CDS	Right Position in CDS	Left Position in Exon	Right Position in Exon	Gene Left.name2	Gene Right.name2	Gene Left.name	Gene Left.chrom	Gene Left.strand	Gene Left.txStart	Gene Left.txEnd
70	rj1674	NA	sg1870	NA	inversion	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
103	rj12	NA	sg13	NA	inversion	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
104	rj13	NA	sg14	NA	inversion	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
105	rj14	NA	sg15	NA	inversion	NA	NA	yes	NA	no	NA	OPHN1	NA	NA	NA	NA	NA
109	rj15	NA	sg16	no	inversion	opposing	yes	yes	no	no	IL1RAPL1	IL1RAPL1	NM_014271	chrX	+	28515601	2988393
195	rj92	NA	sg97	NA	interchromosomal	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
240	rj145	NA	sg110	no	inversion	opposing	yes	no	no	no	TMPRSS2	TMPRSS2	NM_005656	chr21	-	41758347	4180195
241	rj151	NA	sg156	NA	inversion	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
242	rj154	NA	sg159	no	inversion	opposing	yes	yes	no	no	APP	APP	NM_201413	chr21	-	26174731	2646500
244	rj119	NA	sg160	yes	interchromosomal	same orientation	yes	yes	no	yes	UNK	LSM12	NM_001080419	chr17	+	71292514	7133348

Showing 1 to 10 of 2,433 entries Previous Next

iReport example: iFUSE2

Genome Overview

Structural Variants

B-allele Frequency

Coverage

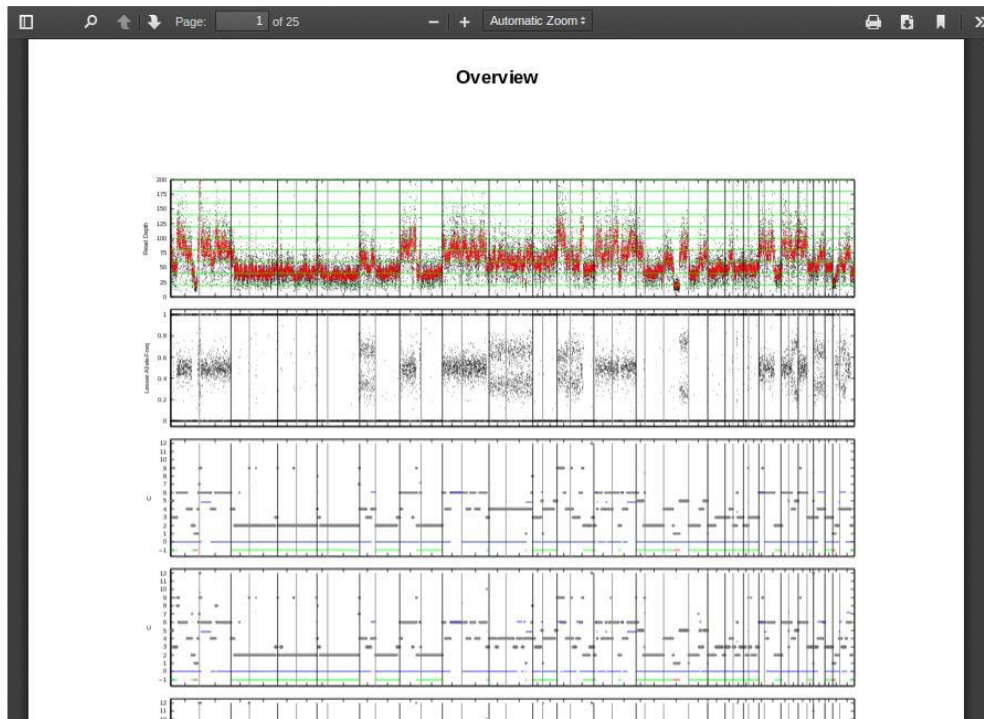
Virtual Normal

OncoSNPseq

OncoSNP-SEQ is an analytical tool for characterising copy number alterations and loss-of-heterozygosity (LOH) events in cancer samples from (Complete Genomics) whole genome sequencing data. It was originally developed by Dr. Yau at Department of Mathematics, Imperial College London.

OncoSNP-SEQ contains the following novel features:

- Loci classified into one of a number of copy number aberration states, each state describes a particular form of copy number alteration and LOH event.
- Ability to model both normal DNA contamination and intra-tumour heterogeneity jointly.
- Estimates baseline haploid read level for polyploid samples.
- Inference using Bayesian methods allowing uncertainty in estimates to be characterised.



Parting Words

iReport is very flexible, but can become somewhat cumbersome for large reports, therefore ideally used as last step in workflow (create iReport once, use often)

Additional Features

- add support for large tables (client-side database solution?)
- add additional content items (suggestions welcome)

To Galaxy Team

- insert items anywhere in repeat parameter?
- remember scroll position on select and repeat parameters?

Poster number 8 for additional information/questions 😊

tinyurl.com/llrzz9w



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The Hyve

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