Medical Genetics at Oslo University Hospital

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courses@CRG: NEXTFLOW: Reproducible in Silico Genomics
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Oslo University Hospital

- One of northern Europe's largest hospitals with 1500 beds, 22,000 employees, 22B NOK annual budget
- Responsible for patient treatment (1.2 million treatments^{2016}), medical research (1980 papers^{2015}) and medical education (121 PhDs^{2015})

Department of Medical Genetics

- Norway's largest med genetics department
- 200 employees
- 34,301 molecular genetic tests and 1935 cytogenetic tests in 2015.
  - 480 with HTS in 2016
  - ~150 per month now (August 2017)

High throughput sequencing for diagnosis of rare disease

- HTS project group established in 2012 to bring HTS into clinical diagnostics
- Monogenic/rare disease
- Co-located with Norwegian sequencing centre (national core facility for research)
- Current staff is
  - 10 bioengineers / molecular biologists in lab / interpretation
  - 10 bioinformaticians
    - Pharma/bioinf^{PhD}, chem/bioinf^{PhD}, 2xcomputer-eng/bioinf^{PhD}, computer-eng/medical-eng^{PhD}, 2xmathematicians^{PhD}, 3xsoftware-eng (2xfullstack, bigdata)

Different pipelines on different seq machines

4 x HiSeqX
1 x HiSeq3000
2 x HiSeq2500

2 x NextSeq 500

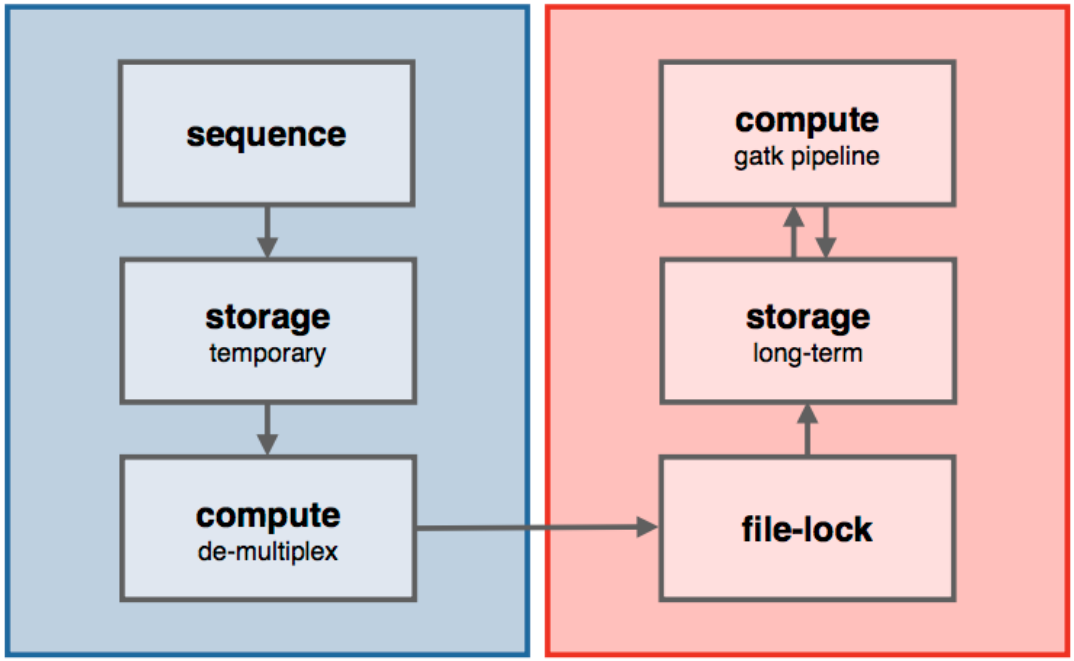
3 x MiSeq

- **Whole exome sequencing** (Agilent SureSelect) – HiSeq 2500
- ~~**"Targeted" trios** (Illumina TruSightOne , ~ 5000 genes) – NextSeq 500 – trio sequencing~~
- **Targeted Cancer** (Illumina custom capture kit, 17 genes) – MiSeq
- **Whole genome sequencing** – HiSeq X

	Exome		Targeted Cancer	Trio
Capture Kit	Agilent SureSelect		Nextera Rapid Capture Kit	Illumina TruSightOne
Sequencing	HiSeq2500, HiSeq3000		MiSeq	NextSeq500
Gene Panels	BB (22 genes) Bindevev (44 genes) CDG1 (25 genes) CED (4 genes) Ciliopati (115 genes) CorticalMalf (138 genes) EB (20 genes) EEogPU (57 genes) Ekto (34 genes) HBOC (2 genes) HBOCogLYNCH (6 genes) HBOCUTV (7 genes) HSPogHA (51 genes) Iktyose (40 genes)	Immunsvikt (307 genes) Jeune (14 genes) Joubert (24 genes) KFM (58 genes) Leber (19 genes) LYNCH (4 genes) LYNCHUTV (11 genes) Meckel (11 genes) MELANOM (3 genes) Mitokon (231 genes) NPHPogSLSN (21 genes) PCD (28 genes)	KREFT17 (17 genes)	TrioPU (755 genes)
File Outputs	• full vcf (330MB) • sliced vcf (1.5MB for EEogPU) • bam (25GB) • xlsx • coverage report PDF		• full vcf (600KB) • sliced vcf (500KB) • bam (135MB) • xlsx • coverage report PDF	• 1x full vcf (70MB) • 1x sliced vcf (13MB) • 3x bam (2GB) • 1x xlsx • 1x coverage report PDF

Local and remote infrastructure

Hospital internal network

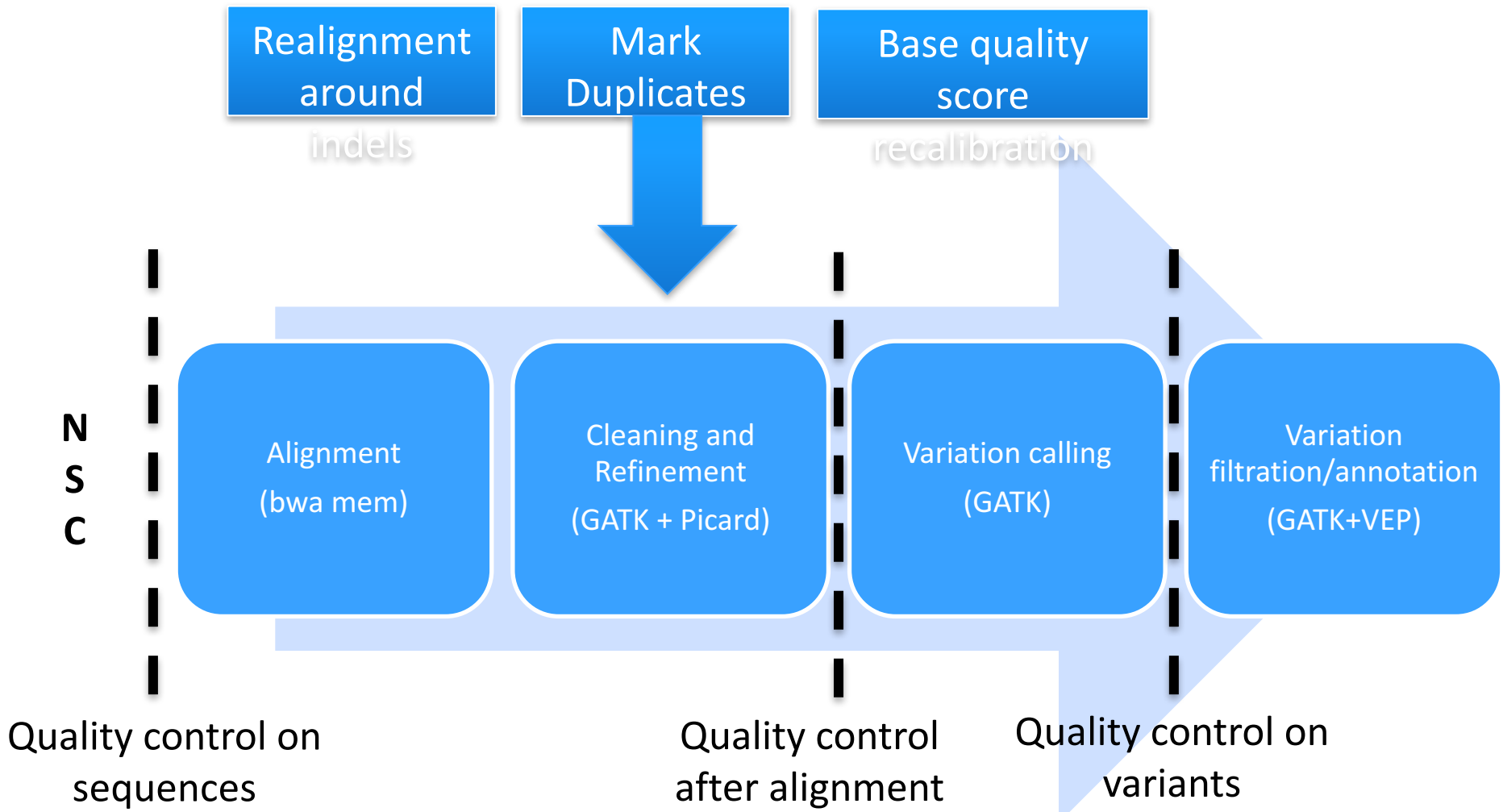


Develop env

National Sequencing Center (NSC):
own server

University secure HPC:
Air-gapped cluster with 2 factor authentication

Variant calling - workflow



Quality control

Read quality:
>80% of fq1 at least Q30
>80% of fq2 at least Q30

Coverage:
>90% of targets >= 10x
>80% of targets >= 20x
Median target coverage > 75x

Variants:
Total number of mutations in range [35000, 55000]
Number of nonsense mutations < 160
Tr/Ti ratio in range [2, 3]

SNP fingerprinting test – Comparing HTS against Taqman array to detect potential sample swaps or contaminations
WES: 23 sites, allow up to 8 undetermined and one mismatch
Custom cancer: 16 sites, allow 4 undetermined but no mismatch
Trios: N.A., use trio relationships for qc instead

GIAB Reference materials and data

Genome in a bottle consortium (GIAB), hosted by National Institute of Standards and Technology (NIST)

Reference materials:
NA12878: an EUR sample from 1000 Genome project

Data:
High-confidence whole genome variant calls which are integrated from data sequenced by different sequencers and sequencing centers

We use this to validate/evaluate pipeline, lab changes, and do trend analysis.

Variant annotation

- Ensembl Variant Effect Predictor (VEP)
- VCF databases (HGMD, Clinvar, ExAC…)
- Local variant frequency database
- All annotation data must be available locally (infrastructure has no Internet access)
- Custom annotation for variants with potential to affect RNA splicing

Variant interpretation: Excell sheets

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	CHR	POS	REF	ALT	Gene	HGVSc	HGVSp	Consequence	Klasse	Variant	ExAC	1000g	ESP6500_EA	ESP6500_AA	inDB_alleleF
3	7	147335933	C	CT	CNTNAP2 (AR)	NM_014141.5:c.1898-265_1898-264insT	N/A	intron_variant			N/A	N/A	N/A	N/A	N/A
4	X	119676896	GA	G	CUL4B (XR)	NM_003588.3:c.1311-9delT	N/A	intron_variant			N/A	N/A	N/A	N/A	0.0026
5	2	38878328	A	T	DYRK1A (AD)	NM_001396.3:c.1547-74A>T	N/A	intron_variant			N/A	0.004	N/A	N/A	0.0051
6	9	140637837	G	T	EHMT1 (AD)	NM_024757.4:c.838G>T	NP_079033.4:p.Val280Phe	missense_variant			0.003	N/A	N/A	N/A	0.0422
7	9	140637826	G	T	EHMT1 (AD)	NM_024757.4:c.827G>T	NP_079033.4:p.Cys276Phe	missense_variant			N/A	N/A	N/A	N/A	N/A
8	5	161524944	GA	G	GABRG2 (AD)	NM_000816.3:c.548+81delA	N/A	intron_variant			N/A	N/A	N/A	N/A	0.0013
9	1	153790495	A	T	GATAD2B (AD)	NM_020699.2:c.729+21T>A	N/A	intron_variant			0.000	N/A	N/A	N/A	0.0013
10	16	56226638	G	GCA	GNAO1 (AD)	NM_020988.2:c.161+110_161+111insCA	N/A	intron_variant			N/A	N/A	N/A	N/A	N/A
11	16	9934689	AAG	A	GRIN2A (AD)	NM_000833.3:c.1498-34_1498-33delCT	N/A	intron_variant			N/A	N/A	N/A	N/A	0.009
12	2	149241063	C	A	MBD5 (AD)	NM_018328.4:c.2845+58C>A	N/A	intron_variant			0.004	0.002	N/A	N/A	0.0064
13	2	149240657	GT	G	MBD5 (AD)	NM_018328.4:c.2519-21delT	N/A	intron_variant			N/A	N/A	N/A	N/A	N/A
14	X	153357591	G	A	MECP2 (XD)	NM_004992.3:c.26+51C>T	N/A	intron_variant			0.001	N/A	N/A	N/A	N/A
15	X	153357589	C	A	MECP2 (XD)	NM_004992.3:c.26+53G>T	N/A	intron_variant			N/A	N/A	-:0.060	-:0.044	0.0217
16	2	51125819	AAATT	A	NRXN1 (AR)	NM_001135659.1:c.931+23184_931+2318	N/A	intron_variant			N/A	-:0.038	N/A	N/A	0.0473
17	X	67429834	CT	C	OPHN1 (XR)	NM_002547.2:c.832+160delA	N/A	intron_variant			N/A	N/A	N/A	N/A	N/A
18	20	8665502	GA	G	PLCB1 (AR)	NM_015192.3:c.863-76delA	N/A	intron_variant			N/A	N/A	N/A	N/A	N/A
19	17	46022824	CT	C	PNPO (AR)	NM_018129.3:c.364-100delT	N/A	intron_variant			N/A	-:0.003	N/A	N/A	0.0102
20	17	17700037	AAGG	A	RAI1 (AD)	NM_030665.3:c.3776_3778delAGG	NP_109590.3:p.Glu1261del	inframe_deletion			0.003	-:0.001	-:0.009	-:0.004	0.0051
21	2	166892444	TAAA	T	SCN1A (AD)	NM_001165963.1:c.3429+111_3429+113d	N/A	intron_variant			N/A	N/A	N/A	N/A	N/A
22	2	166895913	CTTT	C	SCN1A (AD)	NM_001165963.1:c.2589+17_2589+19del	N/A	intron_variant			N/A	N/A	N/A	N/A	N/A
23	2	166895913	CTTT	CT	SCN1A (AD)	NM_001165963.1:c.2589+17_2589+19del	N/A	intron_variant			N/A	N/A	N/A	N/A	N/A
24	2	228567111	AT	A	SLC19A3 (AR)	NM_025243.3:c.-2-76delA	N/A	intron_variant			N/A	T:0.381	N/A	N/A	N/A
25	X	135115669	GA	G	SLC9A6 (XD)	NM_001042537.1:c.1727+18delA	N/A	intron_variant			N/A	N/A	N/A	N/A	0.0038
26	X	135067675	G	C	SLC9A6 (XD)	NM_001042537.1:c.14G>C	NP_001036002.1:p.Gly5Ala	missense_variant			N/A	N/A	N/A	N/A	0.0013
27	9	2096706	A	T	SMARCA2 (AD)	NM_003070.3:c.2933A>T	NP_003061.3:p.Tyr978Phe	missense_variant			0.000	0.000	N/A	N/A	0.0013
28	1	44303786	C	CAAAAA	ST3GAL3 (AR)	NM_006279.3:c.210-105_210-104insAAAA	N/A	intron_variant			N/A	-:0.219	N/A	N/A	N/A
29	9	130414090	T	C	STXBP1 (AD)	NM_003165.3:c.87+159T>C	N/A	intron_variant			N/A	0.005	N/A	N/A	0.0141
30	9	130423271	CA	C	STXBP1 (AD)	NM_003165.3:c.326-109delA	N/A	intron_variant			N/A	N/A	N/A	N/A	0.0448
31	6	33402884	T	G	SYNGAP1 (AD)	NM_006772.2:c.510-45T>G	N/A	intron_variant			0.002	N/A	N/A	N/A	0.0077
32	6	33402852	CAAAAAAAAA	C	SYNGAP1 (AD)	NM_006772.2:c.510-76_510-68delAAAAA	N/A	intron_variant			N/A	N/A	N/A	N/A	N/A
33	6	33408465	TTC	T	SYNGAP1 (AD)	NM_006772.2:c.1677-40_1677-39delTC	N/A	intron_variant			N/A	N/A	N/A	N/A	0.0077
34	6	33408890	ATG	A	SYNGAP1 (AD)	NM_006772.2:c.1914-59_1914-58delTG	N/A	intron_variant			N/A	N/A	N/A	N/A	N/A

Automation system

Overview

- Data is delivered from sequencing center to us.
- Data is copied onto TSD, our computing/storage system for sensitive data (@ University of Oslo)
- Automation automatically system picks up the new data and starts processing the data.
- We copy out the variant files and reports, and send an email to the lab that the results are ready for interpretation.

Health:

#5 genAP-test-NA12878-EEogPU_OUS_medGen_v02_b37

Process | Log | Version | Raw | Admin

Log output:

```
==========================================
          SINGLESAMPLE PIPELINE
==========================================
Sample          : test_sample
Project         : Diag-excap01-2015-02-19
Sequence date   : 2015-02-26
Read 1          : Diag-excap30-NA12878-EEogPU-v01-KIT-Av5_GCCAAT_L002_R1_001.fastq.gz (Size: 808666935
Read 2          : Diag-excap30-NA12878-EEogPU-v01-KIT-Av5_GCCAAT_L002_R1_001.fastq.gz (Size: 823060514
Capturekit      : agilent_sureselect_v05
Genepanel       : EEogPU_OUS_medGen_v02_b37

Output path     : /net/tsd-evs.tsd.usit.no/p22/data/colossus/vcpipe/testdata/repo/analysis/genAP-test-
Cores           : 6
==========================================

[warm up] executor > slurm
[67/9d170f] Submitted process > ss_mapping (1)
Starting job 75093 ("nf-ss_mapping_1") on c1-2 at Tue May 12 21:05:57 CEST 2015
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
#!/bin/bash -ue
```

Close

Analyses

Filter

Next

genAP-test-NA12878-Iktyose_OUS_medGen_v02_b37 — 12/05/2015 21:06

genAP-test-NA12878-Bindevev_OUS_medGen_v02_b37 — 12/05/2015 21:06

genAP-test-NA12878-Ciliopati_OUS_medGen_v03_b37 — 12/05/2015 21:06

genAP-test-NA12878-HSPogHA_OUS_medGen_v01_b37 — 12/05/2015 21:07

Oslo univers

#2 Diag-Cardio-NA12878-Cardio-v02

Process | Log | Version | Raw | QC | Admin

Tested QC parameters

BaseQuality	
q30_bases_pct	91.47
CalculateHsMetrics	
PCT_TARGET_BASES_10X	0.9881
MEAN_TARGET_COVERAGE	188.42
CollectAlignmentSummaryMetrics	
PCT_PF_READS_ALIGNED	0.9991
LowCoverageRegions	
failedRegionCount	173
VcfQuality	
contamination	1
skewedRatio	0.0068
tiTvRatio	3.7736
variants	258

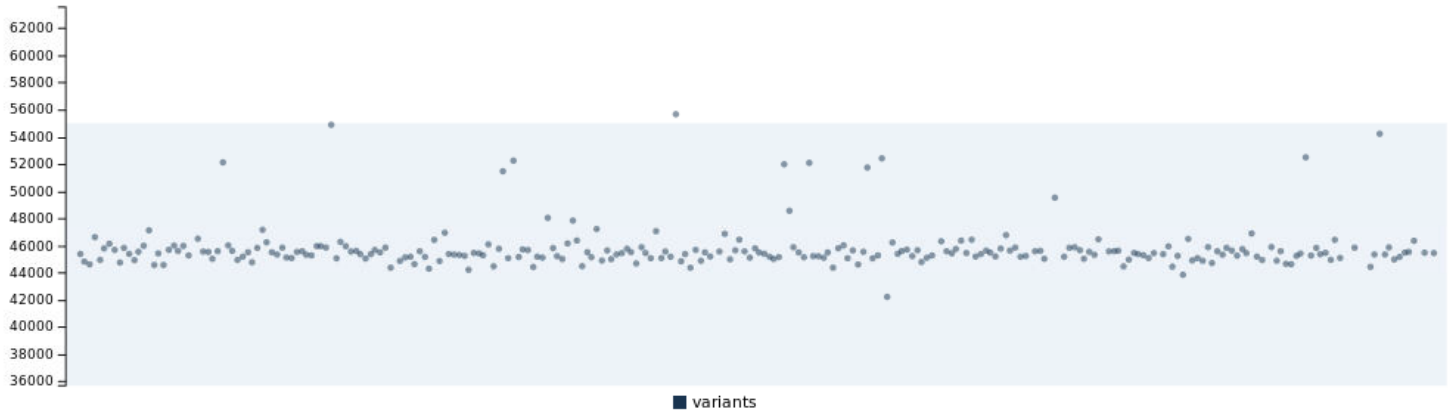
Raw QC parameters


```
{
    "BaseQuality": [
        true,
        {
            "mean_qual_score": 35.87,
            "one_mismatch_index_pct": 1.28,
            "perfect_index_reads_pct": 98.72,
            "q30_bases_pct": 91.47,
            "reads": 629331
        }
    ],
    "CalculateHsMetrics": [
        true,
        {
            "AT_DROPOUT": 2.891694,
            "BAIT_DESIGN_EFFICIENCY": 1,
            "BAIT_SET": "illumina_trusightcardio_v01",
            "BAIT_TERRITORY": 571897,
            "FOLD_80_BASE_PENALTY": 2.141088,
            "FOLD_ENRICHMENT": 3966.607407,
```

vcpipe dashboard Overview Metrics

Select metric: exome: variants

avg: 45,775.762 stdev: 1,660.389 min: 42,199.000 max: 55,663.000



Analysis: trio

Capture kit: illumina_trusightone_v01

Metrics: tiTvRatio

Overview

- Almost everything fully automated. Striving for full automation.
- User interface shows status (complete, failed, etc) of each sample, quality control plots and log.
- Everything is logged and reproducible.
- All data is “snapshotted”, we know exactly what software, genepanel and databases were used for every run.
- Can theoretically process >300 exomes samples per day using whole cluster (but shared with others).
- In practice we only run ~150 per month, but increasing.

Code

vcpipe

All pipeline related code
(pipeline, automation, qc, ++)

Separate Git repo

Tools

vcpipe-bin

All thirdparty tools
Precompiled binaries (linux)

Separate Git repo

Data

vcpipe-bundle

All data files used in pipeline.
GATK bundle/captureKits/
genepanels/annotation++

Separate Git + Git annex repo

Sample/analysis metadata

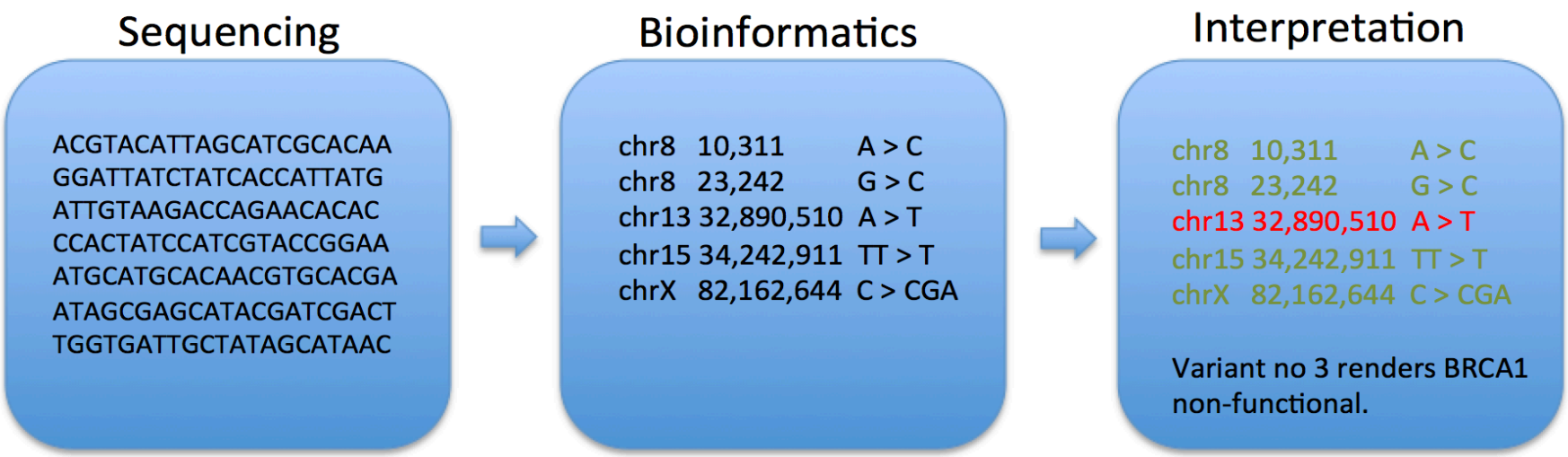
Diag-excap01-123456789.sample


```
{
  "index": "GCCAAT",
  "lane": 3,
  "stats": {
    "one_mismatch_index_pct": 2.24,
    "reads": 121434860,
    "mean_qual_score": 34.98,
    "q30_bases_pct": 88.94,
    "perfect_index_reads_pct": 97.76
  },
  "sequencer_id": "D00132",
  "project": "Diag-excap01-2015-02-19",
  "reads": [
    {
      "length": 123456789,
      "file": "Diag-excap01-123456789-EEogPU-v02-KIT-Av5_GCCAAT_L007_R1_001.fastq.gz",
      "md5": "d41d8cd98f00b204e9800998ecf8427e"
    },
    {
      "length": 123456789,
      "file": "Diag-excap01-123456789-EEogPU-v02-KIT-Av5_GCCAAT_L007_R2_001.fastq.gz",
      "md5": "d41d8cd98f00b204e9800998ecf8427e"
    }
  ],
  "flowcell": "A",
  "sample_id": "123456789",
  "capturekit": "agilent_sureselect_v05",
  "sequence_date": "2015-02-26",
  "name": "Diag-excap01-123456789"
}
```

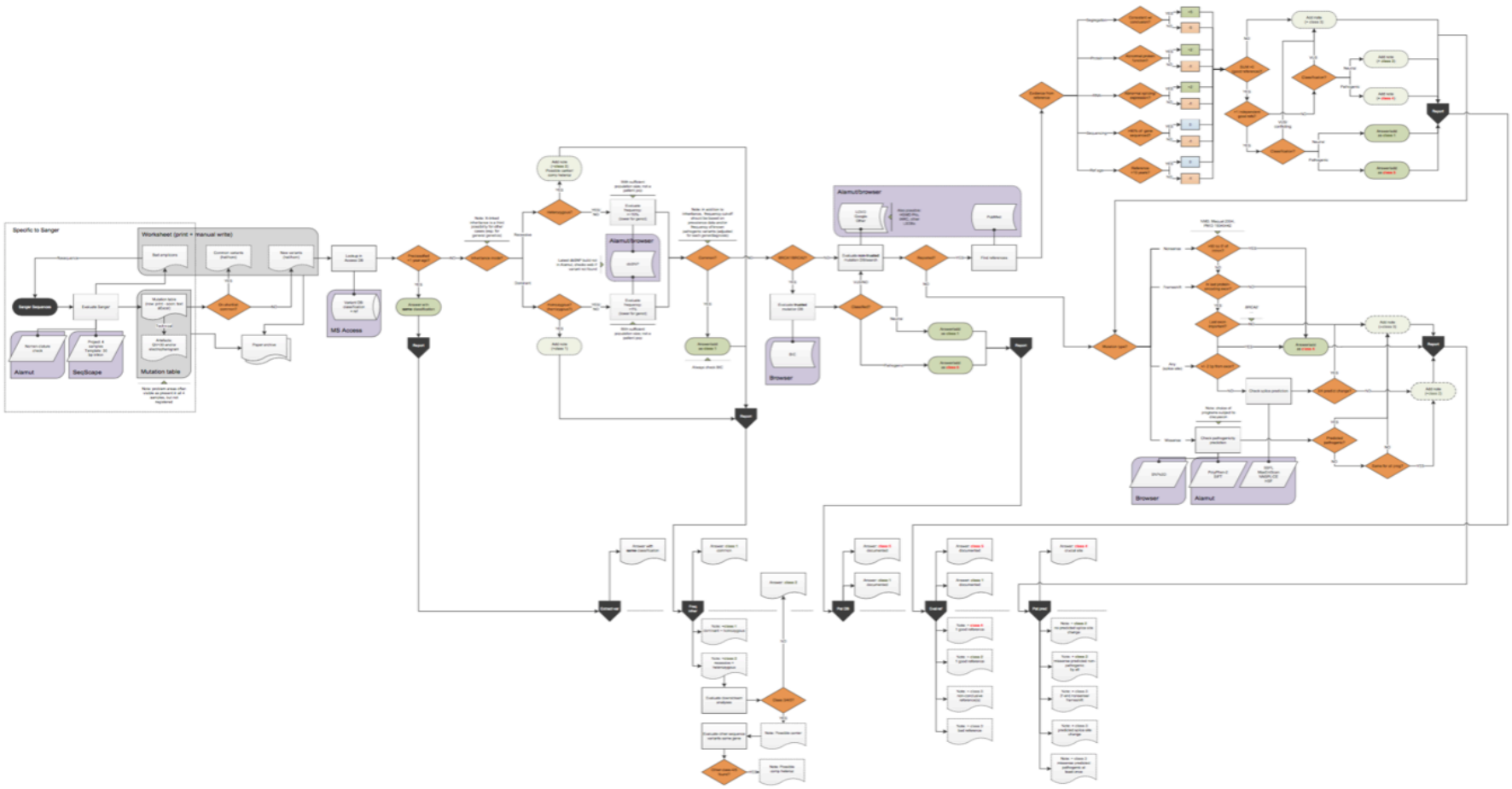

Diag-excap01-123456789-EEogPU-v02.analysis


```
{
  "params": {
    "genepanel": "EEogPU-v02"
  },
  "type": "singlesample",
  "name": "Diag-excap01-123456789-EEogPU-v02",
  "samples": [
    "Diag-excap01-123456789"
  ]
}
```

Bioinformatics for support of variant interpretation



Decision support for variant interpretation

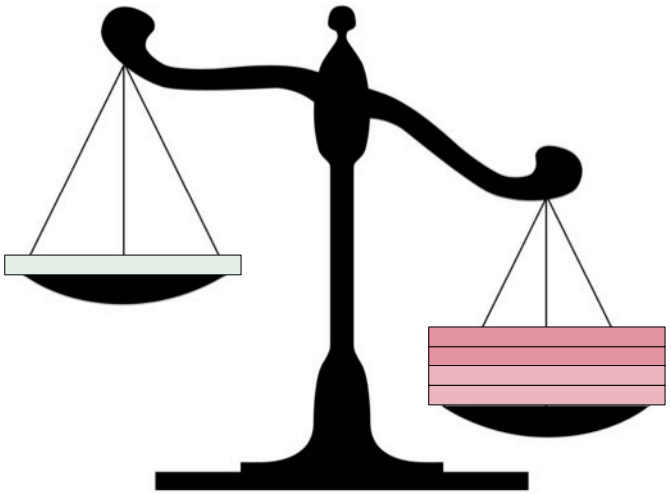


Rules-based interpretation

Pathogenic *Examples*

Protein destroyed
In sick child only
Small protein change
Predicted pathogenic
Predicted benign
Not inherited
High population frequency

Benign



ACMG guidelines

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ACMG STANDARDS AND GUIDELINES | Genetics inMedicine

Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology

Sue Richards, PhD[1], Nazneen Aziz, PhD[2,16], Sherri Bale, PhD[3], David Bick, MD[4], Soma Das, PhD[5], Julie Gastier-Foster, PhD[6,7,8], Wayne W. Grody, MD, PhD[9,10,11], Madhuri Hegde, PhD[12], Elaine Lyon, PhD[13], Elaine Spector, PhD[14], Karl Voelkerding, MD[13] and Heidi L. Rehm, PhD[15]; on behalf of the ACMG Laboratory Quality Assurance Committee

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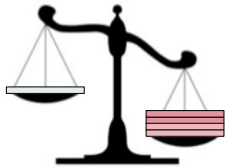


rules from ACMG

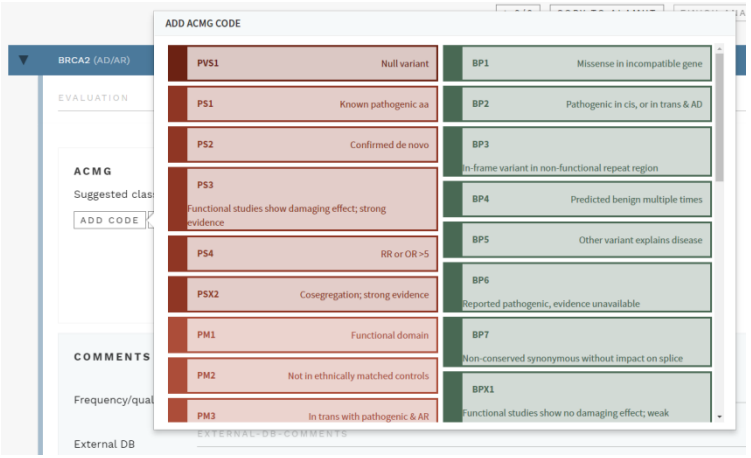
Classification	Rule	Colour
Pathogenic	(i) 1 Very strong (PVS1) AND	
	(a) ≥1 Strong (PS1–PS4) OR	
	(b) ≥2 Moderate (PM1–PM6) OR	
	(c) 1 Moderate (PM1–PM6) and 1 supporting (PP1–PP5) OR	
	(d) ≥2 Supporting (PP1–PP5)	
	(ii) ≥2 Strong (PS1–PS4) OR	
	(iii) 1 Strong (PS1–PS4) AND	
	(a) ≥3 Moderate (PM1–PM6) OR	
	(b) 2 Moderate (PM1–PM6) AND ≥2 Supporting (PP1–PP5) OR	
	(c)1 Moderate (PM1–PM6) AND ≥4 supporting (PP1–PP5)	
Likely pathogenic	(i) 1 Very strong (PVS1) AND 1 moderate (PM1–PM6) OR	
	(ii) 1 Strong (PS1–PS4) AND 1–2 moderate (PM1–PM6) OR	
	(iii)1 Strong (PS1–PS4) AND ≥2 supporting (PP1–PP5) OR	
	(iv) ≥3 Moderate (PM1–PM6) OR	
	(v) 2 Moderate (PM1–PM6) AND ≥2 supporting (PP1–PP5) OR	
	(vi)1 Moderate (PM1–PM6) AND ≥4 supporting (PP1–PP5)	
Benign	(i) 1 Stand-alone (BA1) OR	
	(ii) ≥2 Strong (BS1–BS4)	
Likely benign	(i) 1 Strong (BS1–BS4) and 1 supporting (BP1–BP7) OR	
	(ii) ≥2 Supporting (BP1–BP7)	
Uncertain significance	(i) Other criteria shown above are not met OR	
	(ii) the criteria for benign and pathogenic are contradictory	

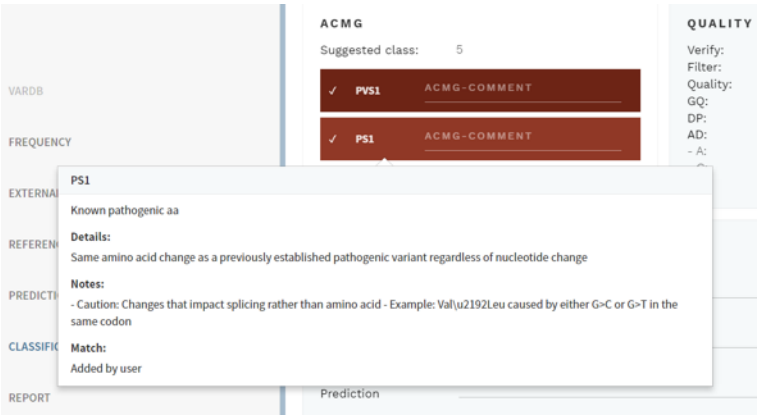
E||A

- Stepwise interpretation and presentation of annotation information
- Curating a database of classified variants
- Decision support based on suggested ACMG criteria adapted to local procedures
- Support for evaluation of litteratue references

ACMG in ELLA

- Mark annotation with relevant ACMG codes
  - Automatic
  - Manually
- Easy access to explanations
- Suggest a clinical classification





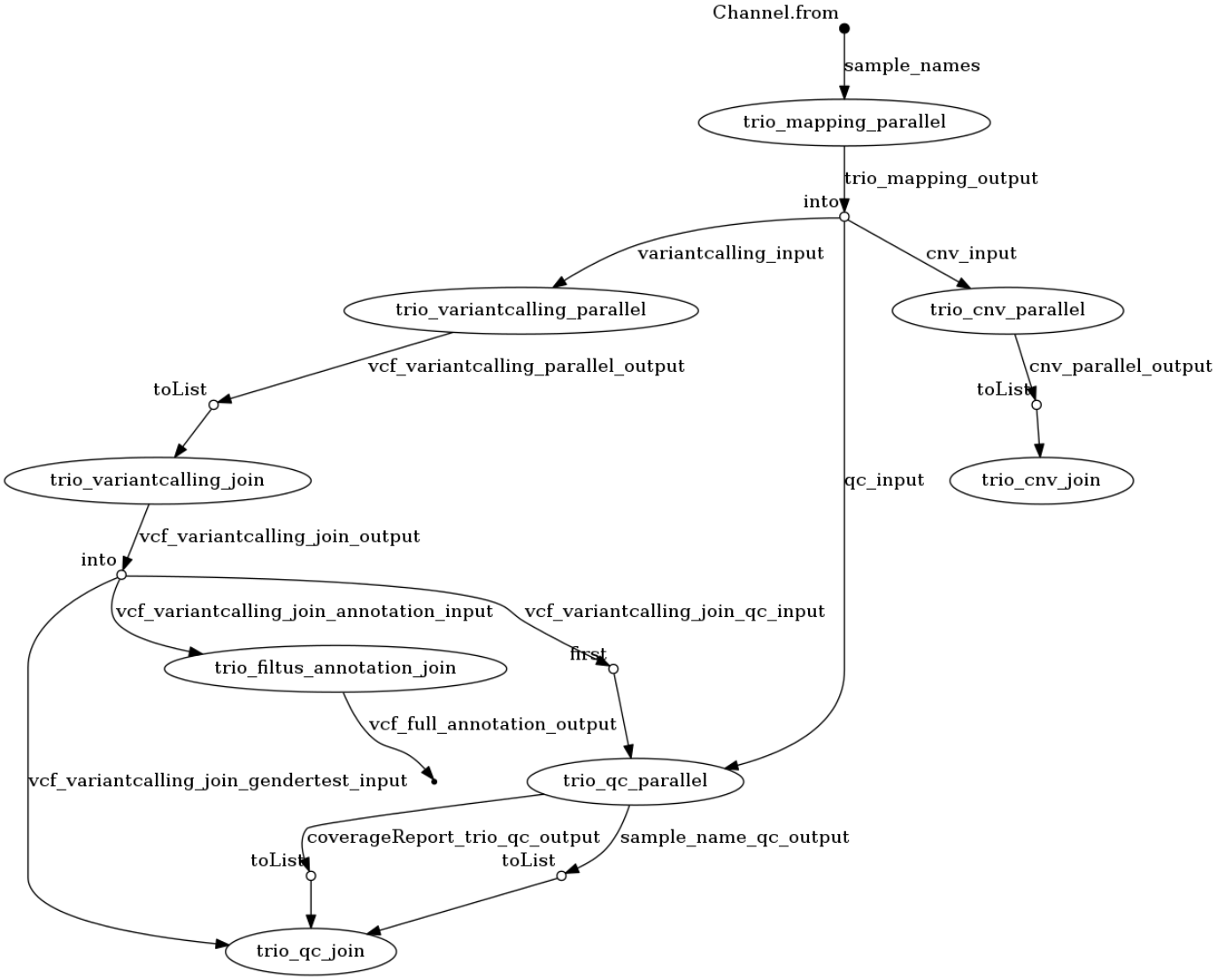
Projects

- Norvariome – Norwegian variant database
- Scandinavian frequency database
- Standardise variant interpretation procedures
- Human Phenotype Ontology (HPO) <-> variant prioritization
- integrate pharmacogenomics

Summary

- The diagnostic bioinformatics group develops and runs the computational analyses that enables the interpretation of a patient's variants
- Pipelines and automation
- ELLA - Decision support for variant interpretation
- Norvariome – Database of consented samples and data sharing

Pipeline s



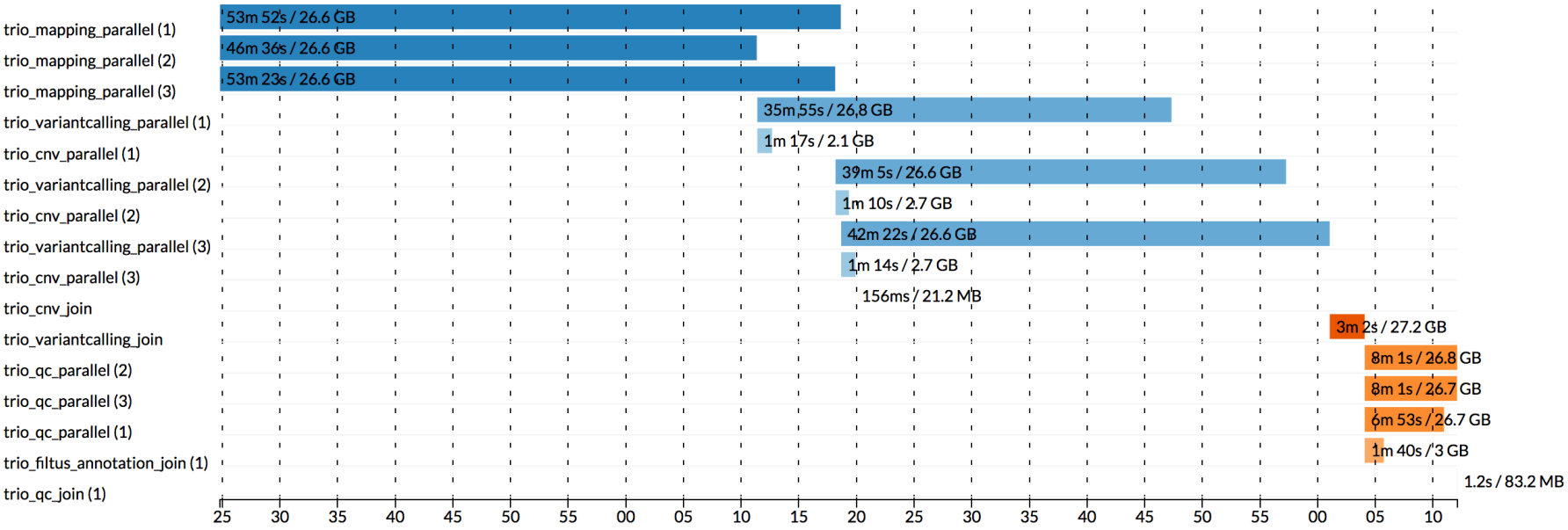
nextflow run <script-name> --with-dag [filename]

Timeline report

nextflow run <pipeline name> **-with-**timeline [file name]

Processes execution timeline

Launch time: 14 Sep 2017 10:24
Elapsed time: 1h 47m 22s



Created with Nextflow -- http://nextflow.io

```
process {
    executor='slurm'
    clusterOptions = "--account=p22 --mem-per-cpu=3140"
    time = { '6h' * task.attempt }
    cpus = { 6 * task.attempt }

    $target_mapping {
        time = { '1h' * task.attempt }
    }

    $target_variantcalling {
        time = { '1h' * task.attempt }
    }

    $trio_excap_qc_parallel {
        time = { '2h' * task.attempt }
        cpus = { 4 * task.attempt }
    }

}
trace {
  enabled = true
  fields =
'task_id,hash,native_id,process,tag,name,status,exit,module,container,attempt,submit,start,comple
te,duration,realtime,%cpu,%mem,rss,vmem,peak_rss,peak_vmem,rchar,wchar,syscr,syscw,read_bytes,wri
te_bytes'
}
```

```
errorStrategy 'retry'
maxRetries 1
```

```
//////////////////////////////
// SNP fingerprinting test
//////////////////////////////

process exome_fingerprinting {
    echo true

errorStrategy 'retry'
    maxRetries 1
    storeDir "$variantcalling_storage_path"

    input:
    set file(bam_file), file(bai_file) from bam_fingerprinting_input
    file(qc_json) from qc_signal_output

    when:
    taqman_check == 'true'

    script:

"""
"""

}
```

Codebase

- Three repos version controlled by git:
  - Source Code: python, nextflow, bash
  - Binaries compiled for target architecture (RHEL6)
  - Data bundle (+git-lfs)
    - bundle.json : key-value dict where values are rel path to data

```
{
    "captureKit": {
          "TSCarV1": {
            "contamination_test": "captureKit
            "noslop_bed": "captureKit/illumin
            "noslop_list": "captureKit/illumi
        },
        //…
    },
    "clinicalGenePanels": {
        "BB_v02": {
            "noslop": "clinicalGenePanels/BB_
            "report_config": "clinicalGenePan
            "slop2": "clinicalGenePanels/BB_v
            "slop20": "clinicalGenePanels/BB_
            "transcripts": "clinicalGenePanel
        },
        //...
},
    "cnv": {
        "cnvScan-bundle": "cnv/cnvScan"
    },
    "funcAnnot": {
        "VEP": {
            "cache": "funcAnnot/VEP/cache"
        },
        "snpeff": {
            "dataDir": "funcAnnot/snpEff/data
        }
    },
```

Early in nf:

```
/*
 * We import the old JsonSlurperClassic instead of JsonSlurper
 * because the latter is not thread safe.
*/
import groovy.json.JsonSlurperClassic

bundle_json = new File(bundle_path + '/' + 'bundle.json')
bundle = new JsonSlurperClassic().parse(bundle_json)
```

In process body:

```
param_transcripts = [bundle_path, bundle['clinicalGenePanels'][genepanel]['transcripts']].join(File
```

In process script:

```
script:
"""
gatk -T HaplotypeCaller \
      -R ${bundle_reference_fasta} \
      -I ${bam_file} \
      --dbsnp ${bundle_knownSites_dbsnp} \
      --emitRefConfidence GVCF \
      -variant_index_type LINEAR \
      -variant_index_parameter 128000 \
      --bamOutput haplotypeCaller.temp.bam \
      --bamWriterType CALLED_HAPLOTYPES \
      -L ${bundle_path}/${bundle['clinicalGenePanels'][genepanel]['slop20']} \
      -o trash.vcf
"""
```

Pre-checks

Pipeline.nf

```
import Util;

Util.checkPedigree(analysis)
Util.checkSamples(analysis, full_config)
Util.checkGenePanel(genepanel, bundle, full_config, keys=["noslop", "report_config",
"slop2", "slop20", "transcripts"])
Util.checkCaptureKits(analysis, bundle, full_config, keys=["noslop_list"])

bundle_reference_index_bwa = bundle_path + '/' + bundle.reference.index.bwa
Util.checkFile(bundle_reference_index_bwa)
```

Util.groovy

```
class Util {

static def checkFile(def path, def size = null, def md5 = null) {
        def File file = new File(path)
        if (!file.exists()) {
            throw new Exception("File " + path + "doesn't exist.")
        }
        if (size != null && size > 0 && file.length() != size) {
            throw new Exception("Size of file " + path + "doesn't
match. File is " + file.length() + ", but should be " + size)
        }
    }
```

JIRA

Jira Software | Dashboards | Projects | Issues | Boards | Create | ui qc

Requests from lab for 1.9 AMG-873 OPEN | TSD problems AMG-304 OPEN

AMG
AMG

- Backlog
- Active sprints
- Releases
- Reports
- Issues
- Components

PROJECT SHORTCUTS

- Add shortcut

SOURCE CODE

- git.ousamg.io
- Add source code

- Project settings

AMG / AMG-882

Metrics UI improvements

Edit | Comment | Assign | Close Issue | Reopen Issue | Admin

Details

Type:	Task	Status:	RESOLVED (View workflow)
Priority:	Medium	Resolution:	Done
Affects Version/s:	None	Fix Version/s:	1.9
Labels:	None		

People

Assignee:	Hugues Fontenelle
Reporter:	Hugues Fontenelle
Votes:	0
Watchers:	3 Stop watching this issue

Description

git-branch: **882-ui-metrics**

A few months ago, the UI would take *a few minutes* (aka eternity) when requesting **metrics** such as `nonsenseCount` to be displayed in a graph.
As of today this request crashes the UI.

Dates

Created:	24/Aug/17 8:36 PM
Updated:	Just now
Resolved:	6 days ago

Attachments

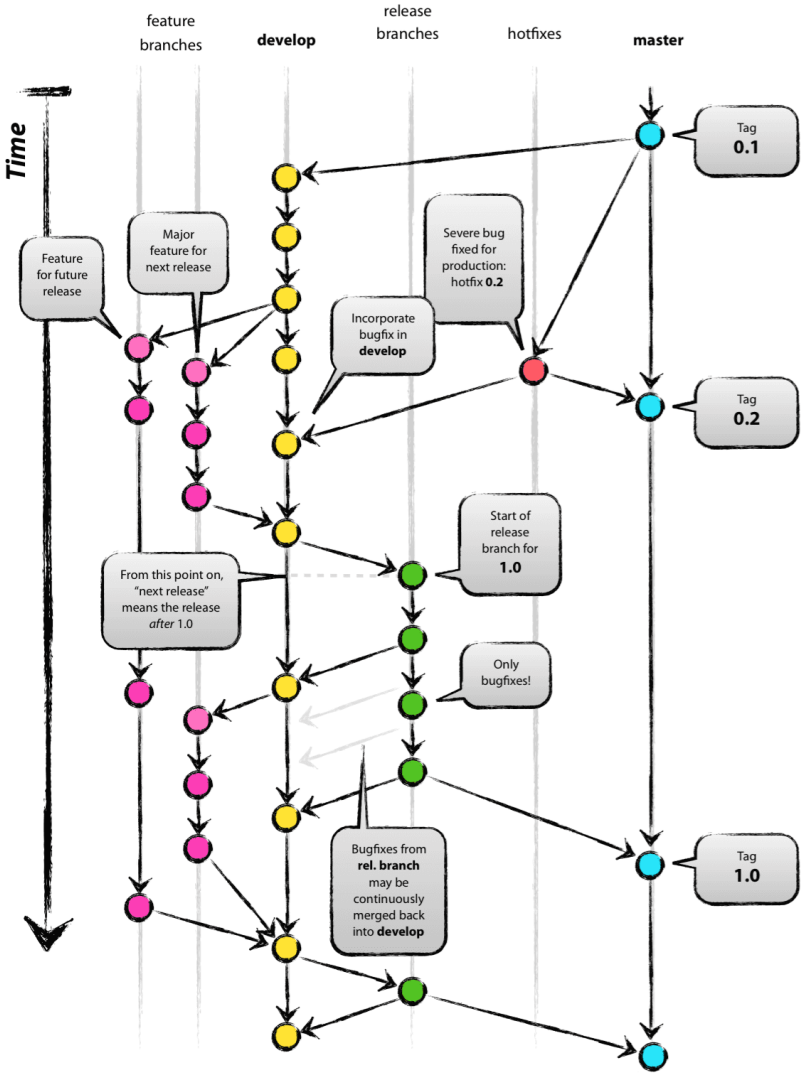
Drop files to attach, or browse.

Screen Shot 2017-08-24 at | Screen Shot 2017-08-25 at | Screen Shot 2017-09-07 at

Agile

View on Board

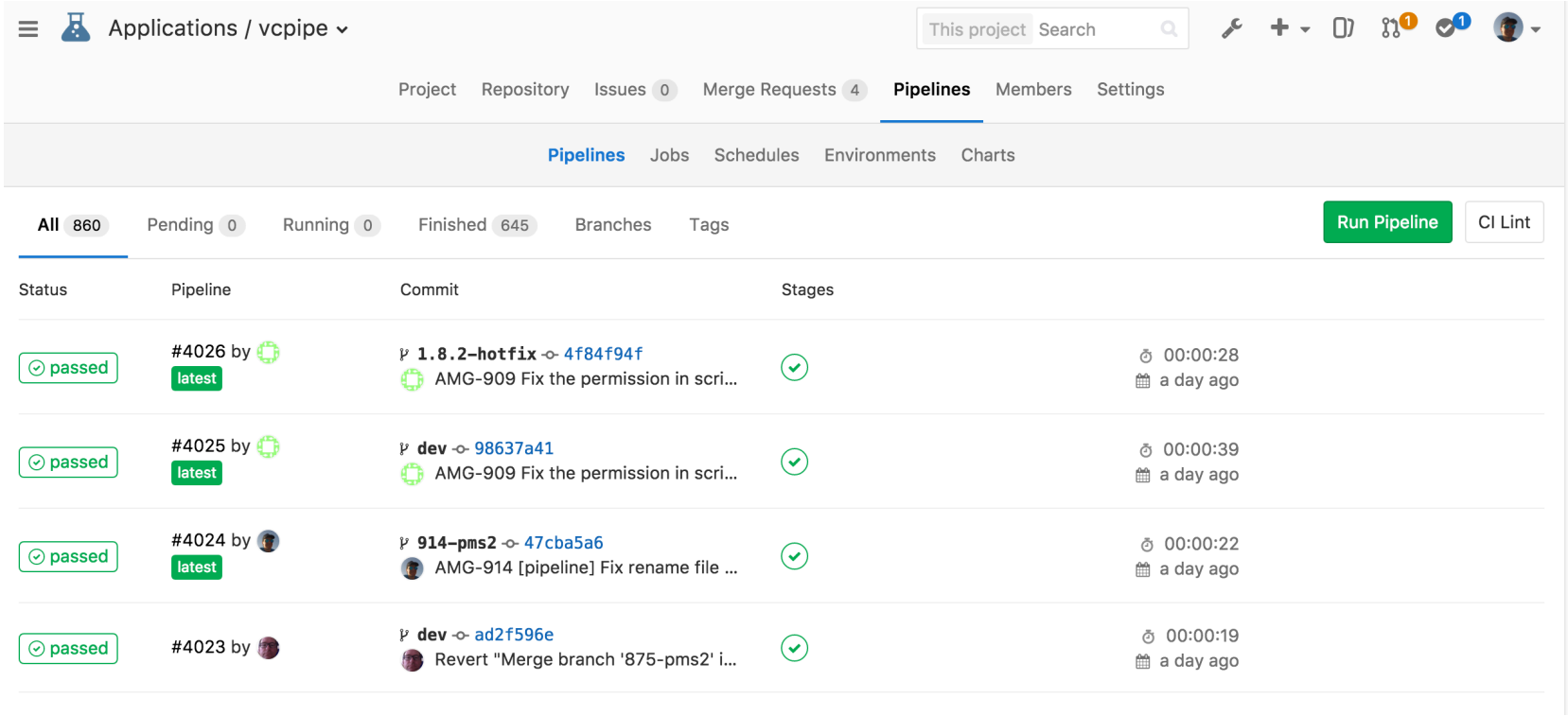
Git workflow



http://nvie.com/posts/a-successful-git-branching-model/

CI

- On each commit:
  - Unit tests
  - Linting
- At release: regression tests
  - pipeline run
  - variants called vs gold standard
  - variant filtered



Acknowledgements

- All the people that should be thanked are being thanked hereafter: Thank you ☺
- Thank you for attending