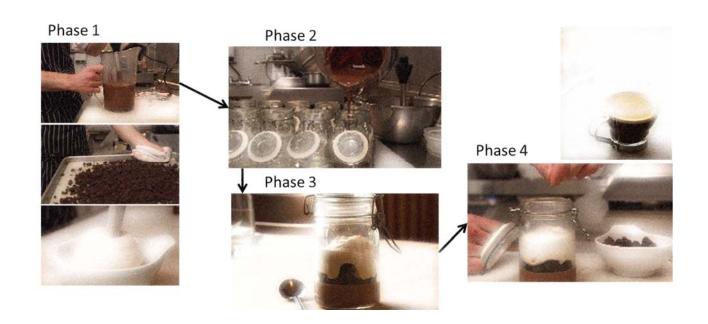
La genèse d'un pipeline d'assemblage de génomes bactériens ou comment travailler en équipe pour optimiser une analyse à haut débit!



Aujourd'hui, on parle d'informatique!



Breathing life into the future* Donnez le souffle de vie^{MD}



Evolutionary and Genomic Microbiology



< Archive

PERSPECTIVE ARTICLE

Front. Microbiol., 29 September 2015 | http://dx.doi.org/10.3389/fmicb.2015.01036







3,460 Am score 35



(Oop

SHARE ON



SUPPLEMENTAL DATA

Table 1.XLSX

D-1- Ch--+1 CCV

Clinical utilization of genomics data produced by the international *Pseudomonas aeruginosa* consortium

🕍 Luca Freschi¹†, 👤 Julie Jeukens¹†, 🌘 Irena Kukavica-Ibrulj¹†, 🎑 Brian Boyle¹, 🜘 Marie-Josée Dupont¹, 🜘 Jérôme Laroche¹, 🕛 Stéphane Larose¹, 👤 Halim Maaroufi¹, 🍨 Joanne L. Fothergill², 👤 Matthew Moore², 🌉 Geoffrey L. Winsor³, 🍨 Shawn D. Aaron⁴, 👤 Jean Barbeau⁵, 🚇 Scott C. Bell⁶, 🚇 Jane L. Burns⁷, 🌘 Miguel Camara⁸, 👰 André Cantin⁹, 🎆 Steve J. Charette^{1,10,11}, 👰 Ken Dewar¹², 🚳 Éric Déziel¹³, 🚇 Keith Grimwood¹⁴, 🧝 Robert E. W. Hancock¹⁵, 🚇 Joe J. Harrison¹⁶, 🜇 Stephan Heeb⁸, 🚇 Lars Jelsbak¹⁷, 👤 Baofeng Jia¹⁸, 🐧 Dervla T. Kenna¹⁹, 👢 Timothy J. Kidd^{20,21}, 👤 Jens Klockgether²², 👢 Joseph S. Lam²⁵, 👢 Iain L. Lamont²⁴, 💽 Shawn Lewenza¹⁶, 🔙 Nick Loman²⁵, 🔝 François Malouin⁹, 🌘 Jim Manos²⁶, 🚇 Andrew G. McArthur¹⁸, 🔝 Josie McKeown⁸, 📱 Julie Milot²⁷, 🛊 Hardeep Naghra⁸, 🥊 Dao Nguyen^{12,28}, 🛊 Sheldon K. Pereira¹⁸, 🛊 Gabriel G. Perron²⁹, 🛊 Jean-Paul Pirnay⁵⁰, 🔮 Paul B. Rainey^{51,52}, 🔛 Simon Rousseau¹², 🔮 Pedro M. Santos⁵³, 🔮 Anne Stephenson⁵⁴, 🔮 Véronique Taylor²³, 🔮 Jane F. Turton¹⁹, 🐧 Nicholas Waglechner¹⁸, 🐧 Paul Williams⁸, 🐧 Sandra W. Thrane¹⁷, 🐧 Gerard D. Wright¹⁸, 🐧 Fiona S. L. Brinkman³, 酮 Nicholas P. Tucker³5, 👤 Burkhard Tümmler²2, 👤 Craig Winstanley² and 👩 Roger C. Levesque¹*

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²Institute of Infection and Global Health, University of Liverpool, Liverpool, UK

Department of Molecular Biology and Biochemistry, Simon Fraser University, Vancouver, BC, Canada

⁴Ottawa Hospital Research Institute Ottawa ON Canada

... et d'histoire!: de fin 2013 à aujourd'hui

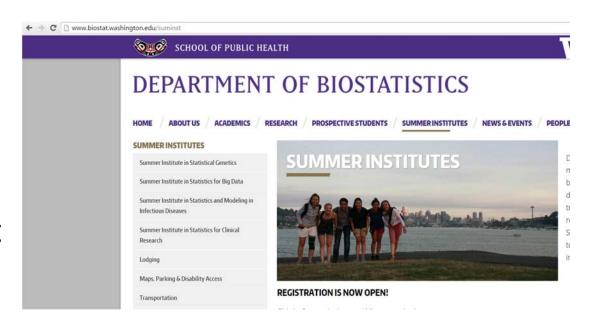
- Phase 1
 - Déménager sur Katak + paralléliser l'analyse
- Phase 2
 - > Faciliter la vie de l'utilisateur
- Phase 3
 - > Pipeline «intelligent», changement de serveur, etc.
- Phase 4

Objectifs

- Assembler plusieurs dizaines de génomes bactériens à la fois
- Aligner ces nouveaux génomes sur des génomes de référence
- Minimiser les interventions de l'utilisateur

Mes compétences en programmation (2005-2011)

- (Avant 2005, quasi rien)
- Au Marchand depuis mai 2005!
- Quelques formations courtes sur R (analyses de données microarray)
- Un module sur R au SISG2007
- Un peu de bash (serveurs) et beaucoup de R durant mon doc (les débuts du RNA-Seq!)





Mes compétences en programmation

(2011-2016)

- Pas mal tous les cours de bioinfo IBIS
- CSHL
 Advanced
 sequencing
 technologies
 nov. 2013
- Beaucoup de «Katak» depuis 1 an









JORGE CHAM @THE STANFORD DAILY

phd.stanford.edu

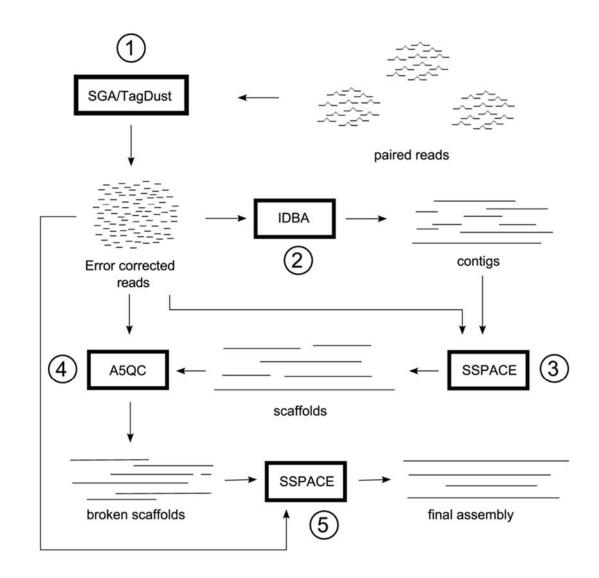


Phase 1, décembre 2013, Julie Jeukens Google

- Projet pilote pour le projet 1000 génomes de Pseudomonas
- 20 génomes

Phase 1

- Test de différents assembleurs
- A5 pipeline
 (Tritt et al.
 2012. PLOS
 ONE),
 disponible sur
 Katak(/prg,
 modifié)



Phase 1

- Sur mon portable (Linux)
- Fichier texte avec des instructions et des lignes de commandes en bash (à copier-coller)
- Tâches:
 - Assembler les génomes en série (2-3 h/génome)
 - Calculer/trier/extraire des statistiques d'assemblage
 - Aligner les nouveaux génomes sur des références (nucmer) et compiler les résultats

Historia na beneral THE RESERVE AND THE PARTY NAMED IN ----



Phase 2, printemps 2014, Jérôme Laroche

- Installation sur Katak
- Paralléliser: plusieurs génomes à la fois pour l'étape de l'assemblage avec A5 (la plus longue)
- Format: soumission avec SGE + 7 fichiers .sh
 - 01_PrepDir.sh
 - 02_A5assembly.sh
 - 03_ConcatCSV.sh
 - 04_ScaffoldDepth.sh
 - 05_AlignToRef.sh
 - 06_StatAlignRefs.sh
 - 07_MvResults.sh

Phase 3, hiver 2014-2015, Luca Freschi

- Fichier texte de configuration à éditer au préalable
- Analyse complète (incluant la soumission SGE) contrôlée par une seule commande: do_analysis.py
- Git: logiciel de gestion de versions

Phase 3:

- Ça marche... mais...
 - Bugs d'architecture de dossier
 - Copie manuelle de fichiers finaux
 - Mémoire
 - Etc.



Phase 4, janvier 2015, Luca et Julie

- Mise à jour après plusieurs mois d'utilisation et de prise de notes sur les manques et les irritants
- Nouvelle composante: projet Salmonelle



Phase 4

- Beaucoup de petites corrections dans les scripts existants
- Paralléliser toutes les étapes plus longues
- Choix du projet (pseudo ou salmo)
- Réduction au maximum de l'intervention de l'utilisateur
- Tout est contrôlé par A5driver.pl



Non! Le A5-bus-driver!!

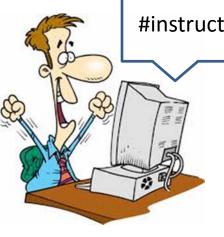
Nombre de passagers = nombre de génomes (= nombre de cœurs ;)

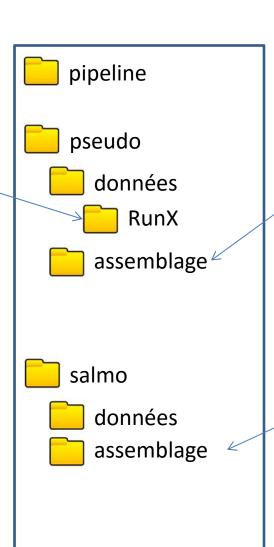
Le résultat!



cd RunX A5-bus-driver.pl

#instructions







ipcd.ibis.ulaval.ca



salfos.ibis.ulaval.ca



Lancer l'assemblage

- jujeu2@katak:~/pseudo1000/miseq_data/Run12a> A5-bus-driver.pl
- ::I found the configuration.py file --OK
- ::Please choose a project [pseudo|salmo], default -- pseudo
- >>pseudo
- ::Project: pseudo
- ::I have detected that you are analyzing the run Run12a
- ::How many genomes do you want to assemble in parallel? -- default: 16
- >>16
- ::Writing all changes on configuration.py
- --sed -i -e 's@run=.*@run="Run12a\/"@' configuration.py
- --sed -i -e 's@dir genomes=.*@dir genomes="/project/rclevesq/pseudo/Pseudo1000/miseq data/Run12a\/"@' configuration.py
- --sed -i -e 's@tasks=.*@tasks=16@' configuration.py
- --sed -i -e 's@dir refs=.*@dir refs="/project/rclevesq/pseudo/Pseudo1000/reference genomes/"@' configuration.py
- --sed -i -e 's@dir_refs=.*@dir_refs="/project/rclevesq/pseudo/Pseudo1000/reference_genomes/"@' configuration.py
- ::Printing current variables -- so you can check if everything is ok
- dir scripts="/project/rclevesq/users/lfreschi/pseudo/pipeline lfreschi current/"
- dir_genomes="/project/rclevesq/pseudo/Pseudo1000/miseq_data/Run12a/"
- dir doc="/home/lfreschi/pseudo/doc/"
- dir refs="/project/rclevesq/pseudo/Pseudo1000/reference genomes/"
- tasks=16
- smp=1
- project="/project/rclevesq/pseudo/Pseudo1000/data pseudo/"
- run="Run12a/"
- ::Do you want to start the analysis now [y/n]? -- default: n
- >>n
- ::Bye!

Regarder les résultats

jujeu2@katak:~/pseudo1000/miseq_dat	ca/Run12a> 1s		
configuration.py	Set12aA9_S9	Set12aB9_S21_L001_R2_001.fastq.gz	Set12aD10_S46_L001_R1_001.fastq.gz
configuration.pyc	Set12aA9 S9 L001 R1 001.fastq.gz	Set12aC10 534	Set12aD10 S46 L001 R2 001.fastq.gz
FastqSummaryF1L1.txt	Set12aA9 S9 L001 R2 001.fastq.gz	Set12aC10 S34 L001 R1 001.fastq.gz	Set12aD11_547
logs	Set12aB10_522	Set12aC10_S34_L001_R2_001.fastq.gz	Set12aD11_S47_L001_R1_001.fastq.gz
queue	Set12aB10_S22_L001_R1_001.fastq.gz	Set12aC11 535	Set12aD11_S47_L001_R2_001.fastq.gz
Set12aA10_510	Set12aB10_S22_L001_R2_001.fastq.gz	Set12aC11_S35_L001_R1_001.fastq.gz	
Set12aA10_S10_L001_R1_001.fastq.gz		Set12aC11_S35_L001_R2_001.fastq.gz	Set12aD12_S48_L001_R1_001.fastq.gz
Set12aA10_S10_L001_R2_001.fastq.gz	Set12aB11_S23_L001_R1_001.fastq.gz	Set12aC12_536	Set12aD12_S48_L001_R2_001.fastq.gz
Set12aA11_511	Set12aB11_S23_L001_R2_001.fastq.gz	Set12aC12_S36_L001_R1_001.fastq.gz	Set12aD1_537
Set12aA11_S11_L001_R1_001.fastq.gz	Set12aB12_524	Set12aC12_S36_L001_R2_001.fastq.gz	Set12aD1_S37_L001_R1_001.fastq.gz
Set12aA11_S11_L001_R2_001.fastq.gz	Set12aB12_S24_L001_R1_001.fastq.gz	Set12aC1_S25	Set12aD1_S37_L001_R2_001.fastq.gz
Set12aA12 512	Set12aB12_S24_L001_R2_001.fastq.gz	Set12aC1 S25 L001 R1 001.fastq.gz	Set12aD2 538
Set12aA12_S12_L001_R1_001.fastq.gz	Set12aB1_513	Set12aC1 S25 L001 R2 001.fastq.gz	Set12aD2_S38_L001_R1_001.fastq.gz
Set12aA12_S12_L001_R2_001.fastq.gz	Set12aB1_S13_L001_R1_001.fastq.gz	Set12aC2_526	Set12aD2_S38_L001_R2_001.fastq.gz
Set12aA1_51	Set12aB1_S13_L001_R2_001.fastq.gz	Set12aC2_S26_L001_R1_001.fastq.gz	Set12aD3_539
Set12aA1_S1_L001_R1_001.fastq.gz	Set12aB2_S14	Set12aC2_S26_L001_R2_001.fastq.gz	Set12aD3_S39_L001_R1_001.fastq.gz
Set12aA1_S1_L001_R2_001.fastq.gz	Set12aB2_S14_L001_R1_001.fastq.gz	Set12aC3_527	Set12aD3_S39_L001_R2_001.fastq.gz
Set12aA2_52	Set12aB2_S14_L001_R2_001.fastq.gz	Set12aC3_S27_L001_R1_001.fastq.gz	Set12aD4_S40
Set12aA2_S2_L001_R1_001.fastq.gz	Set12aB3_\$15	Set12aC3_S27_L001_R2_001.fastq.gz	Set12aD4_S40_L001_R1_001.fastq.gz
Set12aA2_S2_L001_R2_001.fastq.gz	Set12aB3_S15_L001_R1_001.fastq.gz	Set12aC4_528	Set12aD4_S40_L001_R2_001.fastq.gz
Set12aA3_53	Set12aB3_S15_L001_R2_001.fastq.gz	Set12aC4_S28_L001_R1_001.fastq.gz	Set12aD5_S41
Set12aA3_S3_L001_R1_001.fastq.gz	Set12aB4_\$16	Set12aC4_S28_L001_R2_001.fastq.gz	Set12aD5_S41_L001_R1_001.fastq.gz
Set12aA3_S3_L001_R2_001.fastq.gz	Set12aB4_S16_L001_R1_001.fastq.gz	Set12aC5_529	Set12aD5_S41_L001_R2_001.fastq.gz
Set12aA4_54	Set12aB4_S16_L001_R2_001.fastq.gz	Set12aC5_S29_L001_R1_001.fastq.gz	Set12aD6_542
Set12aA4_S4_L001_R1_001.fastq.gz	Set12aB5_\$17	Set12aC5_S29_L001_R2_001.fastq.gz	Set12aD6_S42_L001_R1_001.fastq.gz
Set12aA4_S4_L001_R2_001.fastq.gz	Set12aB5_S17_L001_R1_001.fastq.gz	Set12aC6_530	Set12aD6_S42_L001_R2_001.fastq.gz
Set12aA5_\$5	Set12aB5_S17_L001_R2_001.fastq.gz	Set12aC6_S30_L001_R1_001.fastq.gz	Set12aD7_S43
Set12aA5_S5_L001_R1_001.fastq.gz	Set12aB6_\$18	Set12aC6_S30_L001_R2_001.fastq.gz	Set12aD7_S43_L001_R1_001.fastq.gz
Set12aA5_S5_L001_R2_001.fastq.gz	Set12aB6_S18_L001_R1_001.fastq.gz	Set12aC7_531	Set12aD7_S43_L001_R2_001.fastq.gz
Set12aA6_S6	Set12aB6_S18_L001_R2_001.fastq.gz	Set12aC7_S31_L001_R1_001.fastq.gz	Set12aD8_544
Set12aA6_S6_L001_R1_001.fastq.gz	Set12aB7_519	Set12aC7_S31_L001_R2_001.fastq.gz	Set12aD8_S44_L001_R1_001.fastq.gz
Set12aA6_S6_L001_R2_001.fastq.gz	Set12aB7_S19_L001_R1_001.fastq.gz	Set12aC8_\$32	Set12aD8_S44_L001_R2_001.fastq.gz
Set12aA7_57	Set12aB7_S19_L001_R2_001.fastq.gz	Set12aC8_S32_L001_R1_001.fastq.gz	Set12aD9_S45
Set12aA7_S7_L001_R1_001.fastq.gz	Set12aB8_\$20	Set12aC8_S32_L001_R2_001.fastq.gz	Set12aD9_S45_L001_R1_001.fastq.gz
Set12aA7_S7_L001_R2_001.fastq.gz	Set12aB8_S20_L001_R1_001.fastq.gz	Set12aC9_533	Set12aD9_S45_L001_R2_001.fastq.gz
Set12aA8_58	Set12aB8_S20_L001_R2_001.fastq.gz	Set12aC9_S33_L001_R1_001.fastq.gz	Statistics
Set12aA8_S8_L001_R1_001.fastq.gz	Set12aB9_S21	Set12aC9_S33_L001_R2_001.fastq.gz	WG_411gnments
Set12aA8_S8_L001_R2_001.fastq.gz	Set12aB9_S21_L001_R1_001.fastq.gz	Set12aD10_546	
jujeu2@katak:~/pseudo1000/miseq_dat	a/Run12a>		

2 fichiers résumés: Assembly_stats.csv

File Name		Scaffolds		Genome S			Scaffold		7377	TO A CONTRACT TO STATE OF THE S	Reads		s passing		Raw
Set12aA10_S10	37				768454				254584634	196426792	77.16	38.96	30.06	29	19
Set12aA11_S11	54			1559844		1037806			298771132		78.39	44.20	34.65	33	23
et12aA12_S12	54			1456967		750856		96.14	213816575	164379610	76.88	31.63	24.31	23	14
et12aA1_S1	36			1275041				97.59	216026365	170020201	78.70	33.07	26.02	25	16
Set12aA2_S2	40			1118602		1000		96.71	224044158	174732466	77.99	34.27	26.72	25	17
Set12aA3_S3	42			1154946			676884	95.50	202902421	154092006	75.94	31.04	23.57	23	15
Set12aA4_S4	37			1304876		961164		96.97	279633151	215772026	77.16	42.78	33.01	32	22
Set12aA5_S5	42			1118791		1083618			314512636		77.44	48.09	37.24	36	25
Set12aA6_S6	41			1213340		982620		92.88	281170178	212504823	75.58	43.01	32.51	31	22
et12aA7_S7	44				615787	889090		97.40	256615537	201074883	78.36	39.26	30.76	29	21
Set12aA8_S8	38	100		1693787			100000000000000000000000000000000000000	97.11	258721206		77.58	40.04	31.06	30	20
Set12aA9_S9	38			1119279				96.70	210998561	163951868	77.70	32.29	25.09	24	16
Set12aB10_S22	39		6795047		579437	1105954			309995369	242176840	78.12	45.62	35.64	34	25
Set12aB11_S23	33	100 miles	6791188		600730			97.68	253072933	199025060	78.64	37.26	29.31	28	20
Set12aB12_S24	49		6786301		425321			95.87	195082340	147938059	75.83	28.75	21.80	21	14
Set12aB1_S13	49			1554067		803404		97.31	228509010	178116864	77.95	33.82	26.36	25	16
Set12aB2_S14	45		6759636	1723252	650085	1098310	1059674	96.48	313803856		76.19	46.42	35.37	33	23
et12aB3_S15	57	34 6	6763802	1442974	525188	928356	890977	95.97	260617557	201833816	77.44	38.53	29.84	28	19
et12aB4_S16	52	21 6	6763457	1733750	771247	1136430	1114980	98.11	322385583	257486484	79.87	47.67	38.07	36	25
et12aB5_S17	41	18 6	6958392	1006921	630591	988248	953473	96.48	280006787	213089789	76.10	40.24	30.62	29	19
et12aB6_S18	48	17 6	6963155	1486079	665142	1107370	1066654	96.32	320732507	245003738	76.39	46.06	35.19	34	24
Set12aB7_S19	51	18 6	6961613	1091951	737267	1071900	1037903	96.83	311784990	238648620	76.54	44.79	34.28	32	23
et12aB8_S20	47	17 6	6958739	1732063	681947	1026746	997828	97.18	293667637	229869248	78.28	42.20	33.03	32	23
et12aB9_S21	50	14 6	6716548	1446270	938712	803290	773624	96.31	228044483	173643382	76.14	33.95	25.85	25	16
Set12aC10_S34	96	40 7	7006586	1201753	811664	899142	876464	97.48	261687149	204342139	78.09	37.35	29.16	28	19
et12aC11_S35	56	34 6	6820892	962520	429283	840040	818392	97.42	240201112	187831613	78.20	35.22	27.54	27	18
et12aC12_S36	50	23 6	6816131	1962507	429687	782842	758451	96.88	223839862	174115680	77.79	32.84	25.54	25	17
Set12aC1_S25	65	33 7	7033028	831540	640402	814472	795342	97.65	232223548	183289246	78.93	33.02	26.06	25	16
et12aC2_S26	52	19 7	7028181	1105694	592523	926512	900716	97.22	261331053	205158722	78.51	37.18	29.19	28	19
Set12aC3_S27	52	21 7	7024063	1314378	591526	942018	912876	96.91	261882277	206702178	78.93	37.28	29.43	28	19
Set12aC4_S28	57	25 7	7030507	1419607	664650	923668	902733	97.73	261544145	207481439	79.33	37.20	29.51	28	20
Set12aC5 S29	100	48 7	7027941	1189888	311445	840774	810881	96.44	238696540	183436709	76.85	33.96	26.10	25	17
et12aC6 S30	87	47 7	7010067	1783282	416245	957024	923946	96.54	266874947	211360464	79.20	38.07	30.15	29	20
Set12aC7 S31	55	33	4994239	1551648	413371	1031590	1009983	97.91	293114413	243547441	83.09	58.69	48.77	46	33
et12aC8 S32	95	42 7	7004625	1135008	579094	869080	847085	97.47	250105883	196782633	78.68	35.71	28.09	27	19
et12aC9 S33	161	88	11990452		824268	391287	847102	824970	97.39 2	41283610 19	2650255	79.84	20.12	16.07	15
et12aD10 S46	57		6816421	772370	414372	881444	853890	96.87	255181607	196103877	76.85	37.44	28.77	28	20
et12aD11 S47	46			1441280			788833	97.73	227500326		78.66	33.40	26.27	25	17
et12aD12 S48	37			1013512		27.7	816067	97.31	232225561	184288443	79.36	34.14	27.09	26	17
et12aD1 S37	46			1110037		649074	631413	97.28	186580718		78.85	27.38	21.59	21	14
Set12aD2 S38	52			1274754		100000000000000000000000000000000000000		97.28	209462301	163785576	78.19	29.97	23.44	22	15
Set12aD3 S39	54				449994			97.41	215534412		77.65	31.61	24.54	23	16

2 fichiers résumés: Assembly_stats.csv

F	N50 Raw r	reads EC Re	ads	% read:	passing	EC	Raw nt	EC nt	% nt pa	ssing EC	Raw cov EC cov	Median cov
.42	254584634	196426792	77.16	38.96	30.06	29	19	6530302	66.3	A5-miseq	20150522	
.19	298771132	234216497	78.39	44.20	34.65	33	23	6755151	66.2	A5-miseq	20150522	
.14	213816575	164379610	76.88	31.63	24.31	23	14	6749379	66.2	A5-miseq	20150522	
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.40	256615537	201074883	78.36	39.26	30.76	29	21	6531581			20150522	
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.87	255181607	196103877	76.85	37.44	28.77	28	20	6809910			20150522	q 20130322
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	215534412	167355570	77.65	31.61	24.54	23	16	6808730				
.41					20.47	16.37	15	9	1166838		20150522 61.6 A5-mise	~ 201E0E22
0418	97.66 24171	19337	1354	80.00	20.47	10.3/	15	9	1100038	1	oi.o Ab-Mise	q 20150522
	ted to katak.ibis.u	laval ea								CCLI2	120 she have	IS no 140.44
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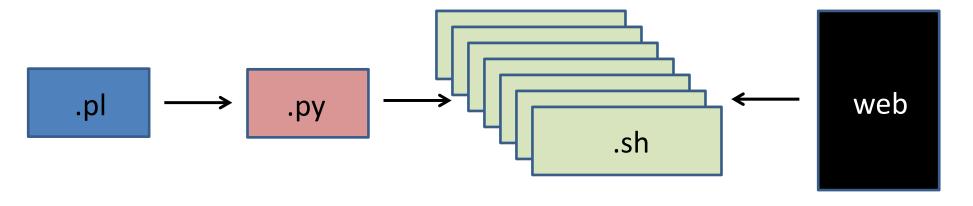
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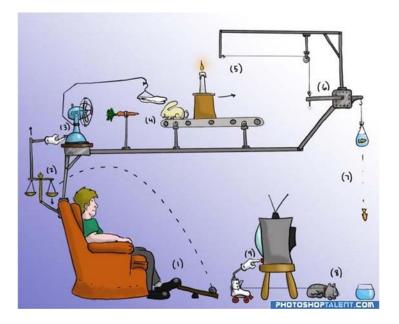
2 fichiers résumés: PercentAlignAll

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Mais...





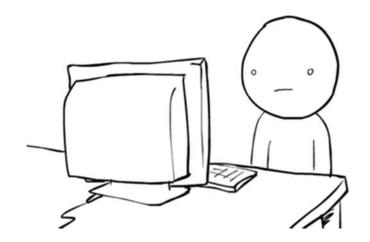


Conclusion

Objectifs atteints!

En fait...

- Ma faute: Mise à jour de A5
- Pas ma faute: soumission avec Slurm



Autres ajouts potentiels au pipeline

Merci!







Nouveau site web!!! http://rclevesque.ibis.ulaval.ca/fr/accueil-2/