FUSIONCloud[™]

FusionCloud[™] is a secure and compliant bioinformatics platform for analyzing nextgeneration sequencing (NGS) data from the ONETest[™] assays developed by Fusion Genomics for sensitive multiplexed microbial identification. Operating behind Fusion-Cloud[™] is a proprietary bioinformatics pipeline to infer the type, subtype, and strain of microbes from NGS data.

FUSIONCloud[™] offers:

- 1 Simple and intuitive data analysis workflow
- 2 Best-in-class project and run management tools
- Bioinformatics applications for microbe typing, consensus sequence reconstruction, mutation calling, and geographical and phylogenetic analysis
- 4 Secure and compliant data storage

FusionCloud[™], backed by the IBM SoftLayer[®] infrastructure, allows rapid on-demand scaling of computational power for data analysis. Where required by regulatory considerations FusionCloud[™] also supports geographic segmentation of data. All data is stored in compliance with HIPPA, CLIA, 21 CFR parts 11, 58, and 493.

FusionCloud[™] provides data encryption, discrete access control, auditing and monitoring. All analyses and results are versioncontrolled for reproducibility. FusionCloud[™] produces key QA/QC library metrics, type(s)/subtype(s)/strain(s) detected, consensus sequence(s) reconstructed per target region (e.g., hemagglutinin and neuraminidase genes in the case of the ONETest[™] Influenza Sentinel assay), and mutations plus their corresponding amino acid substitutions (**Figures 1 and 2**). Additionally, heterogeneous data from widely used databases—including the NCBI Influenza Virus Resource—are integrated to facilitate downstream analysis (e.g., drug resistance variant annotation and phylogenetic analysis of outbreak strains).



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fusiongenomics.com



Figure 1: Overview of the bioinformatics pipeline for microbe typing on FusionCloud™.

Genotype: ha A	Subtype: A H3	Closest strain name: A/Thailand/CU370/2008	Closest strain ID: FJ912984	Genotype: na A	Subtype: A N2	Closest strain name: A/Thailand/CU_B657/2009	Closest strain ID: GQ902827
NNNNNNNNNNNNNN	INNNATG		NNNNGAGCAAAAGCAG	GGAGTAA <mark>A</mark> GATG			
AAG ACT ATC ATT	GCT TTG AGC TAC AT	FT CTA TGT CTG GTT TTC GC	T CAA AAA CTT CCT GGA AAT GAC AAC AGC ACG	AAT CCA AAT CAA A	AAG ATA ATA ACG A	TT GGC TCT GTT TCT CTC ACC ATT 7	ACC ACA ATA TGC TTC TTC ATG CAA CTT
GCA ACG CTG TGC	CTT GGG CAC CAT GG	CA GTA CCA AAC GGA ACG AT	A GTG AAA ACA ATC ACG AAT GAC CAA ATT GAA	GCC ATC TTG ATA A	ACT GTA ACA T	TG CAT TTC AAG CAA TAT GAA TTC A	AAC TCC CCC CCA AAC AAC CAA GTG ATG
GTT ACT AAT GCT	ACT GAG CTG GTT CA	A G A G T TCC TCA <mark>ACA</mark> GGT GA	A ATA TGC GAC AGT CCT CAT CAG ATC CTT GAT	CTG TGT GAA CCA A	ACA ATA ATA GAA A	GA AAC ATA ACA GAG ATA GTG TA T (TG ACC AAC ACC ACC ATA GAG AAG GAA
GGA GAA AAC TGC .	ACA CTA ATA GAT GO	CT CTA TTG GGA GAC CCT CA	IG TGT GAT GGC TTC CAA AAT AAG AAA TGG GAC	ATA TGC CCC AAA	CTA GCA GAA TAC A	GA 🗚 TGG TCA AAG CCG CAA TGT 🤅	AC ATT ACA GGA TTT GCA CCT TTT TCT
CTT TTT GTT GAA	CGC AGC AAA GCC TA	AC AGC AAC TGT TAC CCT TA	IT GAT GTG CCG GAT TAT GCC TCC CTT AGG TCA	AAG GAC AAT TCG	TT AGG CTT TCC G	CT GGT GGG GAC ATC TGG GTG ACA A	AGA GAA CCT TAT GTG TCA TGC GAT CCT
CTA GTT GCC TCA	TCC GGC ACA CTG GF	AG TTT AAC AAT GAA AGC TT	C AAT TGG ACT GGA GTC ACT CAA AAC GGA ACA	GAC AAG TGT TAT (CAA TTT GCC CTT G	GA CAG GGA ACA ACG CTA AAC AAC O	JTG CAT TCA AAT AAC ACA GTA CGT GAT
AGC TCT GCT TGC	ATA AGG <mark>AAA</mark> TCT AA	AT AAC AGT TTC TTT AGT AG	SA TT G AAT TGG TTG ACC CAC TTA AAA TTC AAA	AGG ACC CCT TAT (CGG ACT CTA TTG A	TG AAT GAG TTA GGT GTT CCT TTT C	AT CTG GGG ACC AAG CAA GTG TGC ATA
TAC CCA GCA TTG	AAC GTG ACT ATG CO	CA AAC AAT GAA CAA TTT GA	AC AAA TTG TAC ATT TGG GGG GTT CAC CAC CCG	GCA TGG TCC AGC	F AC AGT TGT CAC G	AT GGA AAA GCA TGG CTG CAT GTT 1	GT ATA ACG GGG GAT GAT AAA AAT GCA
GGT ACG GAC AAT	GAC CAA ATC TTC CT	rg tat gC t c aa <mark>gca</mark> tca gg	SA AGA ATC ACA GT C T CT ACC AAA <mark>AGA</mark> AGC CAA	ACT GCT AGC TTC A	ATT TAC AAT GGG A	GG CTT GTA GAT AGT GTT GTT TCA 7	AGG TCC AAA GAA ATC CTC AGG ACC CAG
CAA ACT GTA ATC	CCG AAT ATC GGA <mark>TC</mark>	T AGA CCC AGA GTA AGG AA	T ATC CCT AGC AGA ATA AGC ATC TAT TGG ACA	GAG TCA GAA TGC (GTT TGT ATC AAT G	GA ACT TGT ACA GTA GTA ATG ACT O	JAT GG G A G T GCT <mark>TCA</mark> GGA AAA GCT GAT
ATA GTA AAA CCG	GGA <mark>GAC</mark> ATA CTT TI	rg att aac agc aca ggg 🗛	T CTA ATT GCT CCT AGG GGT TAC TTC AAA ATA	ACT AAA ATA CTA 1	FTC ATT GAG GAG G	GG AAA ATC GTT CAT ACT AGC ACA 7	TG TCA GGA AGT GCT CAG CAT GTC GAG
CGA AGT GGG AAA	AGC TCA ATA ATG 🗚	A TCA GAT GCA CCC ATT GG	C AAA TGC AAT TCT GAA TGC ATC ACT CCA AAT	GAG TGC TCC TGC	PAT CCT CGA TAT C	CT GGT GTC AGA TGT GTC TGC AGA C	JAC AAC TGG AAA GGC TCC AAT AGG CCC
GGA AGC ATT CCC	AAT GAC AAA CCA TI	FC CAA AAT GTA AAC AGG AT	C ACA TAC GGG GCC TGT CCC AGA TAT GTT AAG	ATC GTA GAT ATA A	AAC ATA AAG GAT C	AT AGC ATT GTT TCC AGT TAT GTG 7	AGT TCA GGA CTT GTT GGA GAC ACA CCC
CAA AAC ACT CTG	AAA TTG GCA ACA GO	G G ATG CGA <mark>AAT</mark> GTA <mark>CCA</mark> GA	IG AAA CAA ACT AGA GGC ATA TTT GGC GCA ATC	AGA AAA AAC GAC A	AGC TCC AGC AGT A	GC CAT TGT TTG GAT CCT AAC AAT O	JAA GAA GGT GGT CAT GGA GT G AAA GGC
GCG GGT TTC ATA	GAA AAT GGT <mark>TGG</mark> G <mark>A</mark>	NG GGA ATG ATG GAT GGT TG	G TAC GGT TTC AGG CAT CAA AAT TCT GAG GGA	TGG GCC TTT GAT (GAT GGA <mark>AAT</mark> GAC G	TG TGG ATG <mark>GGA</mark> AGA ACG ATC <mark>AGC</mark> O	JAG AAA TCA CGC TTA GGG TAT GAA ACC
AGA GGA CAA GCA	GCA GAT CTC AAA AG	GC ACT CAA GCA GCA AT <mark>C</mark> GA	IT CAA ATC AAT GGG AAG CTG AAT AGA TTG ATC	TTC AAA GTC ATT (GAA GGC TGG TCC A	AC CCT AAG TCC AAA TTG CAG ATA A	AAT AGG CAA GTC ATA GTT GAC AGA GGT
GGG AAA ACC AAC	GAG AAA TTC CAT CA	AG ATT GAA AAA GAA TTC TC	CA GAA GTC GAA GGG AGG ATT CAG GAC CTT GAG	AAT AGG TCC GGT 1	TAT TCT GGT ATT T	TC TCT GTT GAA GGC AAA AGC TGC A	ATC AAT CGG TGC TTT TAT GTG GAG TTG
AAA TAT GTT GAG	GAC ACC AAA ATA GA	AT CTC TGG TCA TAC AAC GC	G GAG CTT CTT GTT GCC CTG GAG AAC CAA CAT	ATA AGG GGA AGG A	AAA GAG <mark>A</mark> AA ACT G	AA GTC TTG TGG ACC TCA AAC AGT #	ATT GTT GTG TTT TGT GGC ACC TCA GGT
ACA ATT GAT CTA	ACT GAC TCA GAA AT	rg aac aaa ctg ttt gaa aa	A ACA AAG AAG CAA CTG AGG GAA AAT GCT GAG	ACA TAT GGA ACA (GGC TCA TGG CCT G	AT GGG GCG GAC ATC AAT CTC ATG C	CT ATA TAA
GAT ATG GGC AAT	GGT TGT TTC AAA AT	FA TAC CAC AAA TGT GAC AA	IT GCC TGC ATA GGA TCA ATC AGA AAT GGA ACT	GCTTTCGCAATTTTAG	AAAAAAACTNNNNNNNN	NNNNNNNN	
TAT GAC CAC GAT	GTA TAC AGA GAT GA	AA GCA TTA AAC AAC CGG TI	C CAG ATC AAG GGA GTT GAG CTG AAG TCA GGG				
TAC AAA GAT TGG	ATC CTA TGG ATT TO	CC TTT GCC ATA TCA TGT TT	T TTG CTT TGT GTT GCT TTG TTG GGG TTC ATC				
ATG TGG GCC T GC	CAA AAA GGC AAC AT	FT AGG TGC AAC ATT TGC AT	T TGA				
GTGCATTAAAAAACACCCTTGTTTCNNNNNNNN							

Figure 2: Variants in the hemagglutinin (HA) and neuraminidase (NA) genes viewed in FusionCloudTM. In this example, the closest reference strains were identified for HA and NA, and then the variants were reported relative to their sequences (listed in tables on the right). The 5' and 3' end sequences outside the triplet block structure are untranslated regions. Codons with non-synonymous variants are highlighted in orange.

Learn more

For more information about **FUSION**Cloud[™] and the **ONE**Test[™] system, please visit: **WWW.FUSIONGENOMICS.COM**

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