



# Standard Operating Procedure (SOP) For Nucleotide Data Submission to INSACOG SARS-COV-2 Genome Analysis Web Portal Version\_0.1 2022

#### **INSACOG SARS-COV-2 Genome Analysis Web Portal**

IBDC developed a web portal for analysis SARS-COV-2 sequencing data for genome assembly and lineage prediction. The portal is accessible at <u>https://ibdc.rcb.res.in/covid-</u>

## <u>portal/</u>

### **STEP1: User registration**

Access to SARS-COV-2 data analysis portal requires user registration.

- 1. Click on the 'Data Analysis' button on the web page https://ibdc.rcb.res.in/covid-portal/.
- 2. Provide all the relevant details.

3. Upon completion of registration an email notification would be sent to the registered email ID with FTP credentials for FASTQ raw read upload.

### STEP2: Login to Data Analysis Portal, Upload data and perform analysis

1. Login to the Data analysis portal with registered email ID and Password (A).

2. Use FTP credentials available in the Analysis data tab after login to upload NGS raw reads(B).

3. Data need to be uploaded to a directory with name sample\_data by using FileZilla.

Username or email * dibyabhaba.pradhan@ibdc.rcb.res.in	dibyabhabha (Editaccount)					
Password *	Analyse Data Analysis Reports User D	betails				
Remember me		Analyse Data				
·	FTP Host	ibdc.rcb.res.in				
V I'm not a robot	FTP Username	1800153				
	FTP Password	5x0yy0s				
Login	FTP Access URL	Click To Analyse				
Don't have an account? Signup Now » Lost your password?	Note: Please upload data using above credentials via any FTP Client and click "Click TO Analyse"					
Α		B				

c) Run analysis by selecting either pair end or single end read

1						
	Name	Data Type	Action	Size	Date	Time
	result				17/10/22	08:34
•	sample_data	Illumina PE reads (fastq.gz) ~	Analysis is in progress.		17/10/22	09:02
	С					

#### STEP3: Results summary, visualization and download

1. An email notification would be sent upon completion of analysis. The results can be accessed through the analysis report tab. Summary of results visible in analysis report includes QC, alignment bam file, FASTA sequence generated, Variant list, Circos plot and lineages (D, E, F). The analysis details can also be downloaded through the link shared through result generated email.

				Analy	<u>/sis Re</u>	<u>ports</u>						
ID Sample ID	DATAQC Forward Rev	erse High Quality Read	High Quality S Mapped Reads	MAPPI Genome coverage (%)	NG Mean depth(X)	Mean base quality	Mean map quality	Alignment file(bam)	VARIANT S	VISUALIS ATION	CONSENSUS	CLASSIFI Clade
99 INCOV2074 85 68	View Vie	w 3004026	1828488	98.8295	2185.12	34.9	41.6	Download	View / Downlo ad	View / Downlo ad	Download	21L (Omicro n)
997 INCOV2074 03 68	View Vie	w 3004026	1828488	98.8295	2185.12	34.9	41.6	Download	View / Downlo ad	View / Downlo ad	Download	21L (Omicro n)
97 INCOV2074 03 69	View Vie	w 3119556	1857625	98.241	2219.89	34.9	41.6	Download	View / Downlo ad	View / Downlo ad	Download	21L (Omicro n)
Known Variant NC DIKKnown Variant NC UNKnown Variant NC Known Variant NC DIKKnown Variant NC DIKKnown Variant NC	045512.2 241 045512.2 678 045512.2 2790 045512.2 3007 045512.2 3760 045512.2 3760 045512.2 4184 045512.2 4184 045512.2 6190	T upstream.gene variant 6 missanse variant 7 missense variant 7 synomymous variant 8 missense variant 8 missense variant 7 missense variant 9 synomymous variant 6 synomymous variant	OFFIAD OFFIAD S5   D_SHIISKY OFFIAD 37   D_TR-SLIP OFFIAD 23   D_TR-SLIP OFFIAD 23   D_TR-SLIP OFFIAD 25   D_TR-SLIP OFFIAD 25   D_TR-SLIP OFFIAD 26   D_FALISTSAIN OFFIAD 29   D_ALISTSAIN OFFIAD 34   D_SHOTOPHN OFFIAD 34   D_SHOTOPHN OFFIAD 25   D_SHOTOPHN OFFIAD 25   D_SHOTOPHN OFFIAD 54	o			à	ONT	-	-		

Note: The Genome analysis portal is presently available for Illumina Single End and Pair End Data analysis