



Bioinformatics Associate/Analyst Elective 1: Open-Source language Programming, 2: Dry Lab Genomic Pipeline Analysis, 3: Dry Lab Meta-Genomics Analysis, 4: Microarray-Based Gene Expression Profiling, 5: Data Interpretation using Artificial Intelligence and Machine Learning

QUALIFICATION FILE

☒ Short Term Training (STT) ☐ Long Term Training (LTT) ☐ Apprenticeship

☒ Upskilling ☒ Dual/Flexi Qualification ☒ For ToT ☒ For ToA

☒ General ☐ Multi-skill (MS) ☐ Cross Sectoral (CS) ☒ Future Skills ☐ OEM

NCrF/NSQF Level: 5

Submitted By:

Life Sciences Sector Skill Development Council

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Section 1: Basic Details

1.	Qualification Name	Bioinformatics Associate/ Analyst Elective 1: Open-Source language Programming 2: Dry Lab Genomic Pipeline Analysis 3: Dry Lab Meta-Genomics Analysis 4: Microarray-Based Gene Expression Profiling 5: Data Interpretation using Artificial Intelligence and Machine Learning	
2.	Sector/s	Life Sciences	
3.	Type of Qualification: ☐ New ☒ Revised ☒ Has Electives/Options ☐ OEM	NQR Code & version of existing/previous qualification: QC-04-LS-00269-2023-V1.1-LSSSDC	Qualification Name of existing/previous version: Bioinformatics Associate/ Analyst
4.	a. OEM Name b. Qualification Name <i>(Wherever applicable)</i>	NA	
5.	National Qualification Register (NQR) Code &Version <i>(Will be issued after NSQC approval)</i>	QG-5-LS-04427-2025-V2-LSSSDC	6. NCrF/NSQF Level: 5
7.	Award (Certificate/Diploma/Advance Diploma/ Any Other <i>(Wherever applicable specify multiple entry/exits also & provide details in annexure)</i>	Certificate	
8.	Brief Description of the Qualification	Bioinformatics Associate, also known as a Bioinformatics Analyst, is multifaceted, requiring a blend of technical expertise and collaborative skills. The job role holder has ability to perform data mining and data transformation using statistical tools and various programming scripts, followed by the reporting and organization of data analysis results in specified templates and formats. This job requires coordination with managers, team members, and cross-functional teams to achieve functional objectives. Additionally, the Bioinformatics Associate may be involved in specialized functions such as Open-Source language programming, Dry Lab Genomic Pipeline Analysis, Dry Lab Meta-genomics Analysis, data quality assessment and filtering, data interpretation and analysis of variants, and the tweaking and customization of pipelines.	

		A fundamental understanding of data analysis, Artificial Intelligence (AI), and Large Language Models (LLMs) is crucial, enabling the meaningful interpretation of data within the field.																																													
9.	Eligibility Criteria for Entry for Student/Trainee/Learner/Employee	a. Entry Qualification & Relevant Experience: <table><tr><th>S. No.</th><th>Academic/Skill Qualification (with Specialization - if applicable)</th><th>Required Experience (with Specialization - if applicable)</th></tr><tr><td>1.</td><td>Completed 2nd year of 3-year/ 4-years</td><td>Graduation in Science subjects/ Bioinformatics/ Biotechnology</td></tr><tr><td>2.</td><td>Completed 2nd year of 3-year/ 4-years</td><td>B Tech in Biotechnology/ Bioinformatics/ Biomedical Engineering/ Computational Science</td></tr></table> b. Age: As per government Norms						S. No.	Academic/Skill Qualification (with Specialization - if applicable)	Required Experience (with Specialization - if applicable)	1.	Completed 2nd year of 3-year/ 4-years	Graduation in Science subjects/ Bioinformatics/ Biotechnology	2.	Completed 2nd year of 3-year/ 4-years	B Tech in Biotechnology/ Bioinformatics/ Biomedical Engineering/ Computational Science																															
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2.	Completed 2nd year of 3-year/ 4-years	B Tech in Biotechnology/ Bioinformatics/ Biomedical Engineering/ Computational Science																																													
10.	Credits Assigned to this Qualification, Subject to Assessment (as per National Credit Framework (NCrF))	Minimum Credit :16 Maximum Credit: 31			11. Common Cost Norm Category (I/II/III) (wherever applicable): II																																										
12.	Any Licensing requirements for Undertaking Training on This Qualification (wherever applicable)	NA																																													
13.	Training Duration by Modes of Training Delivery (Specify Total Duration as per selected training delivery modes and as per requirement of the qualification)	☒ Offline ☐ Online ☒ Blended <table><tr><th>Training Delivery Modes</th><th>Theory (Hours)</th><th>Practical (Hours)</th><th>OJT Mandatory (Hours)</th><th>OJT Recommended (Hours)</th><th>Total (Hours)</th></tr><tr><td colspan="6">Offline Mode</td></tr><tr><td>Classroom</td><td>180:00</td><td>300 :00</td><td>00:00</td><td>00:00</td><td>480:00</td></tr><tr><td colspan="6">OR</td></tr><tr><td>Blended Mode</td><td>180:00</td><td>300 :00</td><td>00:00</td><td>00:00</td><td rowspan="3">480:00</td></tr><tr><td>Offline (As part of blended mode)</td><td>90:00</td><td>300 :00</td><td>00:00</td><td>00:00</td></tr><tr><td>Online (As part of blended mode)</td><td>90:00</td><td>00:00</td><td>00:00</td><td>00:00</td></tr></table> (Refer Blended Learning Annexure for details)						Training Delivery Modes	Theory (Hours)	Practical (Hours)	OJT Mandatory (Hours)	OJT Recommended (Hours)	Total (Hours)	Offline Mode						Classroom	180:00	300 :00	00:00	00:00	480:00	OR						Blended Mode	180:00	300 :00	00:00	00:00	480:00	Offline (As part of blended mode)	90:00	300 :00	00:00	00:00	Online (As part of blended mode)	90:00	00:00	00:00	00:00
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14.	Aligned to NCO/ISCO Code/s (if no code is available mention the same)	NCO-2015/2120.0501 Bioinformatics																																													

15.	Progression path after attaining the qualification		
16.	Other Indian languages in which the Qualification & Model Curriculum are being submitted	English and Hindi	
17.	Is similar Qualification(s) available on NQR-if yes, justification for this qualification	☐ Yes ☒ No URLs of similar Qualifications:	
18.	Is the Job Role Amenable to Persons with Disability	☐ Yes ☒ No If "Yes", specify applicable type of Disability:	
19.	How Participation of Women will be Encouraged	Policy measures are needed to promote the inclusion of educated and working women, especially in science and technology fields, where only 14% of women are hired among micro, small, and medium enterprises despite comprising 43% of Science and technology graduates. The conscious efforts are made by LSSSDC to sensitize organizations and hiring manager for bring Women employees on board by LSSSDC through Industry Associations and Large MNCs on governing Board and have received positive responses and assurance from most of employers in life sciences sector to bring Min. 30% share of Women employees and apprentices in the given occupation and job role. LSSSDC shall also be driving a Diversity and Inclusivity Program with Indian Pharmaceutical Alliance for catalysing the efforts	
20.	Are Greening/ Environment Sustainability Aspects Covered	☒ Yes ☐ No	
21.	Is Qualification Suitable to be Offered in Schools/Colleges	Schools ☐ Yes ☐ No Colleges ☒ Yes ☐ No	
22.	Name and Contact Details of Submitting / Awarding Body SPOC	Name: Mrs. Shivi Chaudhary Email: shivi.chaudhary@lsssd.in Contact No.: + 91 11 41042407/ 408, +91 9315747189 Website: https://www.lsssd.in/	
23.	Final Approval Date by NSQC: 29 September 2025	24. Validity Duration: 3 Year	25. Next Review Date : 29 September 2028

Section 2: Module Summary

NOS/s of Qualifications

(In exceptional cases these could be described as components)

Mandatory NOS/s:

Specify the training duration and assessment criteria at NOS/ Module level. For further details refer curriculum document.

Th.-Theory Pr.-Practical OJT-On the Job Man.-Mandatory Training Rec.-Recommended Proj.-Project

S. No	NOS/Module Name	NOS/Module Code & Version (if applicable)	Core/ Non-Core	NCrF/NS QF Level	Credits as per NCrF	Training Duration (Hours)					Assessment Marks					
						Th.	Pr.	OJT-Man.	OJT-Rec.	Total	Th.	Pr.	Proj.	Viva	Total	Weightage (%) (if applicable)
1.	Compulsory NOS Discuss about life sciences sector and basics of Bioinformatics Occupation	LFS/N3916 v1.0	Core	Level 5	1.0	10	20	-	-	30	30	40	15	15	100	10
2.	Compulsory NOS Utilize Bioinformatics Databases for Data Retrieval and Biological Interpretation	LFS/N3917 v1.0	Core	Level 5	2.0	20	40	-	-	60	40	40	10	10	100	10
3.	Compulsory NOS Apply Computational Bioinformatics Tools for Sequence and Structural Analysis	LFS/N3918 v1.0	Core	Level 5	3.0	30	60	-	-	90	40	40	10	10	100	10
4.	Compulsory NOS Use statistical tool and programming scripts for data mining and transforming data	LFS/N3910 v3.0	Core	Level 5	4.0	40	80	-	-	120	35	45	10	10	100	10
5.	Compulsory NOS Coordinate with Supervisors and Other Cross-functional team members	LFS/N0107 v9.0	Non-Core	Level 5	1.0	10	20	-	-	30	30	40	15	15	100	10

S. No	NOS/Module Name	NOS/Module Code & Version (if applicable)	Core/Non-Core	NCrF/NS QF Level	Credits as per NCrF	Training Duration (Hours)					Assessment Marks					
						Th.	Pr.	OJT-Man.	OJT-Rec.	Total	Th.	Pr.	Proj.	Viva	Total	Weightage (%) (if applicable)
6.	Compulsory NOS Employability Skills (60 hours)	DGT/VSQ/N 0102	Non-Core	Level 5	2.0	30	30	-	-	60	20	30	-	-	50	10
Duration (in Hours) / Total Marks					13	140	250	-	-	390	135	245	30	140	550	60

Elective NOS/s 1: Open Source language Programming

The table lists the modules and their duration corresponding to the Elective NOS of the QP

S. No	NOS/Module Name	NOS/Module Code & Version (if applicable)	Core/Non-Core	NCrF/NS QF Level	Credits as per NCrF	Training Duration (Hours)					Assessment Marks					
						Th.	Pr.	OJT-Man.	OJT-Rec.	Total	Th.	Pr.	Proj.	Viva	Total	Weightage (%) (if applicable)
1.	Elective NOS Computational Programming and Cloud Infrastructure for Bioinformatics	LFS/N3919, v1.0	Core	Level 5	3.0	40	50	-	-	90	30	50	10	10	100	40
Duration (in Hours) / Total Marks					3.0	40	50	-	-	90	30	50	10	10	100	40

Elective NOS/s 2: Dry Lab Genomic Pipeline Analysis

The table lists the modules and their duration corresponding to the Elective NOS of the QP

S. No	NOS/Module Name	NOS/Module Code & Version (if applicable)	Core/ Non-Core	NCrF/NS QF Level	Credits as per NCrF	Training Duration (Hours)					Assessment Marks					
						Th.	Pr.	OJT-Man.	OJT-Rec.	Total	Th.	Pr.	Proj.	Viva	Total	Weightage (%) (if applicable)
1.	Elective NOS Perform DNA-Sequence Data Analysis for Variant Calling in Bioinformatics	LFS/N3920, v1.0	Core	Level 5	2.0	20	40	-	-	60	40	40	10	10	100	15
2.	Elective NOS Perform bulk and single cell transcriptomics Data Analysis for Transcriptomic Interpretation in Bioinformatics	LFS/N3921, v1.0	Core	Level 5	2.0	20	40	-	-	60	30	40	15	15	100	15
3.	Elective NOS Perform Spatial Transcriptomics Analysis for Tissue-Specific Gene Expression Mapping and Visualization	LFS/N3922, v1.0	Core	Level 5	1.0	10	20	-	-	30	30	40	15	15	100	10
Duration (in Hours) / Total Marks				Level 5	5	50	100	-	-	150	100	120	40	40	100	40

Elective NOS/s 3: Dry Lab Meta-genomics Analysis

The table lists the modules and their duration corresponding to the Elective NOS of the QP

S. No	NOS/Module Name	NOS/Module Code & Version (if applicable)	Core/ Non-Core	NCrF/NS QF Level	Credits as per NCrF	Training Duration (Hours)					Assessment Marks					
						Th.	Pr.	OJT-Man.	OJT-Rec.	Total	Th.	Pr.	Proj.	Viva	Total	Weightage (%) (if applicable)
1.	Elective NOS Perform Targeted Microbiome Profiling Using Metagenomic Analysis and Phylogenetic Visualization Tools	LFS/N3923, v1.0	Core	Level 5	3.0	30	60	-	-	90	30	40	15	15	100	40

S. No	NOS/Module Name	NOS/Module Code & Version (if applicable)	Core/ Non-Core	NCrF/NS QF Level	Credits as per NCrF	Training Duration (Hours)					Assessment Marks					
						Th.	Pr.	OJT-Man.	OJT-Rec.	Total	Th.	Pr.	Proj.	Viva	Total	Weightage (%) (if applicable)
Duration (in Hours) / Total Marks					3.0	30	60	-	-	90	30	40	15	15	100	40

Elective NOS/s 4: Microarray-Based Gene Expression Profiling

The table lists the modules and their duration corresponding to the Elective NOS of the QP

S. No	NOS/Module Name	NOS/Module Code & Version (if applicable)	Core/ Non-Core	NCrF/NS QF Level	Credits as per NCrF	Training Duration (Hours)					Assessment Marks					
						Th.	Pr.	OJT-Man.	OJT-Rec.	Total	Th.	Pr.	Proj.	Viva	Total	Weightage (%) (if applicable)
1.	Elective NOS Perform Microarray-Based Gene Expression Profiling and Bioinformatics Analysis for Differential Gene Interpretation	LFS/N3924 v1.0	Core	Level 5	3.0	30	60	-	-	90	30	40	15	15	100	40
Duration (in Hours) / Total Marks					3.0	30	60	-	-	90	30	40	15	15	100	40

Elective NOS/s 5: Data Interpretation using Artificial Intelligence and Machine Learning

The table lists the modules and their duration corresponding to the Elective NOS of the QP

. No	NOS/Module Name	NOS/Module Code & Version (if applicable)	Core/ Non-Core	NCrF/NS QF Level	Credits as per NCrF	Training Duration (Hours)					Assessment Marks					
						Th.	Pr.	OJT-Man.	OJT-Rec.	Total	Th.	Pr.	Proj.	Viva	Total	Weightage (%) (if applicable)
1.	Elective NOS Development and application of Algorithm for AI and ML	LFS/N3925 v1.0	Core	Level 5	1.0	10	20	-	-	30	30	50	10	10	100	20
2.	Elective NOS Apply Machine Learning and Computational Strategies for Big Data interpretation	LFS/N3926 v1.0	Core	Level 5	3.0	30	60	-	-	90	30	40	15	15	100	20
Duration (in Hours) / Total Marks					4	40	80	-	-	120	60	90	25	25	200	40

Assessment - Minimum Qualifying Percentage

Please specify **any one** of the following:

Minimum Pass Percentage – Aggregate at qualification level: 70 % (Every Trainee should score specified minimum aggregate passing percentage at qualification level to successfully clear the assessment.)

Minimum Pass Percentage – NOS/Module-wise: 70 % (Every Trainee should score specified minimum passing percentage in each mandatory and selected elective NOS/Module to successfully clear the assessment.)

Section 3: Training Related

1.	Trainer's Qualification and experience in the relevant sector (in years) (as per NCVET guidelines)	Graduate (B.Tech in Biotechnology / Computer Science) with 6 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology. Or Postgraduate (M.Sc. in Biotechnology / Biology) with 6 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology. Or
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		Postgraduate (Any Science Discipline) with 6 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology. Or At least four (4) years of teaching and/or research experience in a relevant academic or research position (Assistant Professor/ Associate Professor/ Professor) with Recognition of Prior Learning Certification in “Bioinformatics Associate/ Analyst” mapped to QP: “LFS/Q3904, V3.0” post completion of Faculty Development Program of LSSSDC And Certified for Job Role -“Bioinformatics Associate/ Analyst” mapped to QP: “LFS/Q3904, V3.0” with minimum accepted score of 80%. Recommended that the Trainer is certified for the Job Role: “Trainer (VET and Skills)”, mapped to the Qualification Pack: “MEP/Q2601, v3.0” with minimum score of 80%.
2.	Master Trainer’s Qualification and experience in the relevant sector (in years) <i>(as per NCVET guidelines)</i>	Graduate (B.Tech in Biotechnology / Computer Science) with 10 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology. Or Postgraduate (M.Sc. in Biotechnology / Biology) with 10 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology. Or Postgraduate (Any Science Discipline) with 10 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology. Or At least four (4) years of teaching and/or research experience in a relevant academic or research position (Assistant Professor/ Associate Professor/ Professor) with Recognition of Prior Learning Certification in “Bioinformatics Associate/ Analyst” mapped to QP: “LFS/Q3904, V3.0” post completion of Faculty Development Program of LSSSDC And Certified for Job Role -“Bioinformatics Associate/ Analyst” mapped to QP: “LFS/Q3904, V3.0” with minimum accepted score of 80%. Recommended that the Trainer is certified for the Job Role: “Master Trainer (VET and Skills)”, mapped to the Qualification Pack: “MEP/Q2602, v3.0” with minimum score of 80%.
3.	Tools and Equipment Required for Training	☐Yes ☐No <i>(If “Yes”, details to be provided in Annexure)</i>

4.	In Case of Revised Qualification, Details of Any Upskilling Required for Trainer	Upskilling is required as per the modification
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Section 4: Assessment Related

1.	Assessor's Qualification and experience in relevant sector (in years) (as per NCVET guidelines)	Graduate (B.Tech in Biotechnology / Computer Science) with 6 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology and 1 years of experience on the job assessment/ Training experience/ Vocational assessment/ Academic assessment Or Postgraduate (M.Sc. in Biotechnology / Biology) with 6 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology and 1 years of experience on the job assessment/ Training experience/ Vocational assessment/ Academic assessment Or Postgraduate (Any Science Discipline) with 6 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology and 1 years of experience on the job assessment/ Training experience/ Vocational assessment/ Academic assessment And Certified for Job Role -"Bioinformatics Associate/ Analyst" mapped to QP: "LFS/Q3904, V3.0" with minimum accepted score of 80%. Recommended that the Assessor is certified for the Job Role: "Assessor", mapped to the Qualification Pack: "MEP/Q2701, v3.0" with minimum score of 80%.
2.	Proctor's Qualification and experience in relevant sector (in years) (as per NCVET guidelines)	Graduate (B.Tech in Biotechnology / Computer Science) with 6 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology and 1 years of experience on the job assessment/ Training experience/ Vocational assessment/ Academic assessment Or Postgraduate (M.Sc. in Biotechnology / Biology) with 6 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology and 1 years of experience on the job assessment/ Training experience/ Vocational assessment/ Academic assessment Or Postgraduate (Any Science Discipline) with 6 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology and 1 years of experience on the job assessment/ Training experience/ Vocational assessment/ Academic assessment And Certified for Job Role -"Bioinformatics Associate/ Analyst" mapped to QP: "LFS/Q3904, V3.0" with minimum accepted score of 80%.

3.	Lead Assessor's/Proctor's Qualification and experience in relevant sector (in years) <i>(as per NCVET guidelines)</i>	Graduate (B.Tech in Biotechnology / Computer Science) with 6 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology and 4 years of experience on the job assessment/ Training experience/ Vocational assessment/ Academic assessment Or Postgraduate (M.Sc. in Biotechnology / Biology) with 6 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology and 4 years of experience on the job assessment/ Training experience/ Vocational assessment/ Academic assessment Or Postgraduate (Any Science Discipline) with 6 years of Relevant Industry Experience with specialization in Bioinformatics / Computational Biology and 4 years of experience on the job assessment/ Training experience/ Vocational assessment/ Academic assessment And Certified for Job Role -"Bioinformatics Associate/ Analyst" mapped to QP: "LFS/Q3904, V3.0" with minimum accepted score of 80%. Recommended that the Assessor is certified for the Job Role: "Master Assessor", mapped to the Qualification Pack: "MEP/Q2702, v3.0" with minimum score of 80%.
4.	Assessment Mode <i>(Specify the assessment mode)</i>	Online and offline
5.	Tools and Equipment Required for Assessment	☒ Same as for training ☐ Yes ☐ No <i>(details to be provided in Annexure-if it is different for Assessment)</i>

Section 5: Evidence of the need for the Qualification

Provide Annexure/Supporting documents name.

1.	Latest Skill Gap Study (not older than 2 years) (Yes/No): yes
2.	Latest Market Research Reports or any other source (not older than 2 years) (Yes/No): No
3.	Government /Industry initiatives/ requirement (Yes/No): No
4.	Number of Industry validation provided: 14
5.	Estimated nos. of persons to be trained and employed: 500
6.	Evidence of Concurrence/Consultation with Line Ministry/State Departments: If "No", why:

Section 6: Annexure & Supporting Documents Check List

Specify Annexure Name / Supporting document file name

1.	Annexure: NCrf/NSQF level justification based on NCrf level/NSQF descriptors <i>(Mandatory)</i>	Yes
2.	Annexure: List of tools and equipment relevant for qualification <i>(Mandatory, except in case of online course)</i>	Yes
3.	Annexure: Detailed Assessment Criteria <i>(Mandatory)</i>	Yes
4.	Annexure: Assessment Strategy <i>(Mandatory)</i>	Yes
5.	Annexure: Blended Learning <i>(Mandatory, in case selected Mode of delivery is "Blended Learning")</i>	Yes
6.	Annexure: Multiple Entry-Exit Details <i>(Mandatory, in case qualification has multiple Entry-Exit)</i>	NA
7.	Annexure: Acronym and Glossary <i>(Optional)</i>	Yes
8.	Supporting Document: Model Curriculum <i>(Mandatory – Public view)</i>	Yes
9.	Supporting Document: Career Progression <i>(Mandatory - Public view)</i>	Yes
10.	Supporting Document: Occupational Map <i>(Mandatory)</i>	Yes
11.	Supporting Document: Assessment SOP <i>(Mandatory)</i>	Yes
12.	Any other document you wish to submit:	Yes

Annexure: Evidence of Level

NCrf/NSQF Level Descriptors	Key requirements of the job role/ outcome of the qualification	How the job role/ outcomes relate to the NCrf/NSQF level descriptor	NCrf/NSQF Level
Professional Theoretical Knowledge/Process	Few of the job elements, expected to be performed by Bioinformatics Associate/ Analyst are: ● Implement algorithm ● construct and curate databases ● Extract data and Prepare Data	Bioinformatics Associate/ Analyst follows standard operating procedures while working on algorithm implementation, construction and curation of databases, extracting data/ data mining and preparing data for analysis. Also, he/she gets the defined formats in which they are expected to organize and report the analysis outcomes. All the above performance	Level- 5

	• Data mining analysis • Organize and report analysis	outcomes are routine and common in all the projects assigned to bioinformatics associate, hence are categorized as familiar and predictable processes where the bioinformatics associate has situation of clear choice.	
Professional and Technical Skills/ Expertise/ Professional Knowledge	Few of the job elements, expected to be performed by Bioinformatics Associate/ Analyst are: • Implement algorithm • construct and curate databases • Extract data and Prepare Data • Data mining analysis • Organize and report analysis • Ensure compliance	To perform the tasks given in the left-hand side box, a bioinformatics associate/ analyst needs to have the factual knowledge of omics field, biology science and software tools	Level- 5
Employment Readiness & Entrepreneurship Skills & Mind-set/Professional Skill	Few of the job elements, expected to be performed by Bioinformatics Associate/analyst are: • Implement algorithm • construct and curate databases • Extract data and Prepare Data • Data mining analysis • Organize and report analysis • Ensure compliance • Utilize resources • Coordination with manager • Coordination with team members • Coordination with cross functional teams	To perform the tasks of algorithm implementation, data extraction, mining and data analysis, a bioinformatics associate/analyst utilizes the professional skills like, Analytical Skills, Critical Skills, Problem Solving, Decision Making. To organize and report analysis and utilization of resources, he/ she uses the planning and organizing skills as well as customer centricity The scope of utilization of all above professional skills remains limited to routine and repetitive and for a narrow range of applications	Level- 5
Broad Learning Outcomes/Core Skill	Few of the job elements, expected to be performed by Bioinformatics Associate/analyst are: • Implement algorithm • construct and curate databases • Extract data and Prepare Data • Data mining analysis • Organize and report analysis • Ensure compliance • Utilize resources • Coordination with manager • Coordination with team members • Coordination with cross functional teams	To perform the tasks written on the left-hand side box, bioinformatics associate/analyst uses mostly English language for communication in written or oral mode. For implementation of algorithm and database related tasks, he/she applies basics of arithmetic and algebraic principles. For the purpose of coordination related tasks and ensuring compliance to organizational SOPs and client requirements, he/she is expected to have the basic understanding of social political and natural environment at the place of work/ organization he/she is working for.	Level- 5

Responsibility	Bioinformatics associate/analyst has the own responsibility of following: ● Implement algorithm ● construct and curate databases ● Extract data and Prepare Data ● Data mining analysis ● Organize and report analysis ● Ensure compliance Also, he/she has a core job function as Manage your work to meet requirements	Bioinformatics associate/analyst has responsibility for his/her own work and learning and doesn't has to supervise the team. And in case of scenario / situation of no clear choice he is expected to take guidance from supervisor.	Level- 5
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Annexure: Tools and Equipment (Lab Set-Up)

List of Tools and Equipment

Batch Size:

S. No.	Tool / Equipment Name	Specification	Quantity for specified Batch size
1.	Work bench		2
2.	demonstration panels/racks		2
3.	Sitting bench		4
4.	Weighing balance		1
5.	Analytical Weighing Balance		1
6.	PH Meter		2
7.	Co2 cylinder		2
8.	ABC type cylinder		2
9.	Colour coded waster disposable bins		1 each
10.	Chart of Various Valves		1
11.	Laptop	For Class room Instructor : INTEL CORE I3 and above ; RAM 4 GB; HARDDISK (500GB) ; GRAPHICS CARD 2GB; SCREEN 15"	1
12.	LED Screen	55 inch	1

Classroom Aids

The aids required to conduct sessions in the classroom are:

1. Whiteboard
2. Marker Pen
3. Computer or Laptop attached to LCD projector.
4. Computer speaker
5. Pencil

Annexure: Industry Validations Summary

Provide the summary information of all the industry validations in table. This is not required for OEM qualifications.

S. No	Organization Name	Representative Name	Designation	Contact Address	Contact Phone No	E-mail ID	LinkedIn Profile (if available)
1.	Shelcel Biozeen Technologies PVT. LTD	Mr. Jacob Rajan George	Dy. Manager- BPE & Business Development		9036621512	jacob.r@biozeen.com	
2.	Siemens Healthneers	Manohar Kollegal Gopalaswamy	VP R&D and Head of Innovation Cell, Center for Innovation in Diagnostics, Siemens Healthineers, India		9731312758	Manohar.kollegal@siemens-healthineers.com	
3.	Strand Lifesciences	Vamsi Veeramachaneni	Chief Scientific Officer		98456-60296	vamsi@strandls.com	
4.	Institute of Bioinformatics and Applied Biotechnology (IBAB)	Dr.M.Vijayalakshmi	Dean- Academic Affairs, Institute of Bioinformatics and Applied Biotechnology (IBAB)			mviji@ibab.ac.in	
5.	Molecular Solutions	Dr.Raghu.R	CEO		9900090011	rraghu@molecularsolutions.co.in	
6.	Tata Consultancy Services Ltd	Aditya Rao	Principal Scientist		9686246386	adityar.rao@tcs.com	
7.	Bristol Myers Squibb	Debarati Mazumder Tagore	Scientific Director, Bristol Myers Squibb		9945870940	debs.mazumder@gmail.com	
8.	Zydus Lifesciences Limited	Harsh Raj purohit	Deputy Manager	Zydus corporate park , Ahmedabad	7041309081	harsh.rajpurohit@zyduslife.com	
9.	Dr. Reddys Laboratories Ltd.	Y Nagender	Technical Capabilities Expert	8-2-337, Road No. 3, Banjara Hills, Hyderabad,	98449282791	nagendery@srreddys.com	

				Telangana, India 500034			
10.	Emcure Pharmaceutic als Limited	Rajesh Nair	President HR	Plot No. P-1 & P-2, IT- BT Park, Phase- II, MIDC, Hinjawadi, Pune- 411057 Maharashtra	9373314937	Prakash.Khandare @emcure.com	
11.	MAJUSHREE TECHNOPACK LIMITED	KISHORE	HR MANAGER	Near fire station, Vadlapudi village, Kurmannapalem, Visakhapatnam, Andhra Pradesh 530046.	9581199200	Kishore.karrimanju shreeindia.com	
12.	CMS Laboratories India Private Limted	Guntuku Jagadeeswara Rao	Managing Director	47-10-50, Dwaraka Nagar, 4th Lane, 3rd Floor, Above Union Bank, Visakhapatnam- 530016	8919168131	jdguntuku@gmail.c om	
13.	Synaptics Labs Pvt Ltd	M BHARATH	SENIOR MANAGER	Plot No:28-B,APIIC, Lalamkoduru Vill, Rambill(MD),Visakh apatnam, Andhra Pradesh-531011	7569279497	hr@synapticslabs.c om	
14.	VLR FACILITATORS PRIVATE LIMITED	JAYASHREE	HR	Hoty Child School, near dundigal police station, Gandhi Maisamma, Hyderabad, Telangana 500043.	8247212205	jayashreem@gmail. com	

Annexure: Training & Employment Details

Training and Employment Projections:

Year	Total Candidates		Women		People with Disability	
	Estimated Training #	Estimated Employment Opportunities	Estimated Training #	Estimated Employment Opportunities	Estimated Training #	Estimated Employment Opportunities
2025 - 2026	150					
2026-2027	150					
2027-2028	200					

Data to be provided year-wise for next 3 years

Training, Assessment, Certification, and Placement Data for previous versions of qualifications:

Qualification Version	Year	Total Candidates				Women				People with Disability			
		Trained	Assessed	Certified	Placed	Trained	Assessed	Certified	Placed	Trained	Assessed	Certified	Placed
Version 1	2020-2021	87	85	80									
Version 1	2021-2022	52	52	48									
Version 2	2022-2023	24	16	16									
Ver 2	2023-2024	4	1	1									
Ver 2	2024- 2025	2002	1479	1422									

Applicable for revised qualifications only, data to be provided year-wise for past 3 years.

List Schemes in which the previous version of Qualification was implemented:

Content availability for previous versions of qualifications:

☒ Participant Handbook ☒ Facilitator Guide ☐ Digital Content ☐ Qualification Handbook ☐ Any Other:

Languages in which Content is available: English and Hindi

Annexure: Blended Learning

Blended Learning Estimated Ratio & Recommended Tools:

Refer NCVET "Guidelines for Blended Learning for Vocational Education, Training & Skilling" available on:

<https://ncvet.gov.in/sites/default/files/Guidelines%20for%20Blended%20Learning%20for%20Vocational%20Education,%20Training%20&%20Skilling.pdf>

S. No.	Select the Components of the Qualification	List Recommended Tools – for all Selected Components	Offline : Online Ratio
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1	☐ Theory/ Lectures - Imparting theoretical and conceptual knowledge	LMS Portal- LSSSDC Daksh Portal will be utilized with online content/virtual lectures	50:50
2	☐ Imparting Soft Skills, Life Skills, and Employability Skills /Mentorship to Learners	LMS Portal- LSSSDC Daksh Portal will be utilized with online content/virtual lectures	50:50
3	☐ Showing Practical Demonstrations to the learners	LMS Portal- LSSSDC Daksh Portal will be utilized with online content/virtual lectures / Skill labs	100:00
4	☐ Imparting Practical Hands-on Skills/ Lab Work/ workshop/ shop floor training	Skill Labs	100:00
5	☐ Tutorials/ Assignments/ Drill/ Practice	LMS Portal- LSSSDC Daksh Portal will be utilized with online content/virtual lectures / Field Visits	50:50
6	☐ Proctored Monitoring/ Assessment/ Evaluation/ Examinations	Parakh	00:100
7	☐ On the Job Training (OJT)/ Project Work Internship/ Apprenticeship Training	Offline	00:100

Annexure: Detailed Assessment Criteria

Detailed assessment criteria for each NOS/Module are as follows:

NOS/Module Name	Assessment Criteria for Performance Criteria/Learning Outcomes	Theory Marks	Practical Marks	Project Marks	Viva Marks
1. LFS/N3916, v1.0: Discuss about life sciences sector and basics of Bioinformatics Occupation	Life Sciences Sector and Bioinformatics	10	10	5	5
	PC1. Identify the key sub-sectors within the life sciences industry, such as pharmaceuticals, biotechnology, medical devices, and bioinformatics.				
	PC2. Describe major job roles and career pathways in the bioinformatics field across research, diagnostics, and data science.				
	PC3. explain the organizational structure and functional teams typically found in life sciences companies.				
	PC4. Illustrate employment structures, career progression opportunities, and typical employee benefits in the life sciences domain.				
	PC5. Define bioinformatics and describe its interdisciplinary nature and growing importance in healthcare and research.				
	Concepts in Omics and Sequencing Technologies	10	20	5	5
	PC6. Explain the principles and applications of genomics, transcriptomics, and proteomics in life sciences research.				
	PC7. Describe the role of proteomics in studying disease mechanisms and dynamic protein biology.				
	PC8. Define molecular markers and explain their role in gene expression and transcriptomics research.				

	PC9. Explain the concept and workflow of whole genome sequencing and annotation.				
	PC10. Differentiate between traditional sequencing and next-generation sequencing (NGS) technologies.				
	PC11. Identify key sequencing platforms such as Sanger, Illumina, and PacBio, along with their applications.				
	PC12. Explain the process of genomic analysis and accurately differentiate between human, plant, microbial, and metagenomic datasets based on their structure, complexity, and application.				
	Basic Skills in Bioinformatics Tools and Data Analysis	10	10	5	5
	PC13. Demonstrate the workflow of genome sequencing using open-source software or simulation tools.				
	PC14. Prepare and manage sample datasets for bioinformatics analysis.				
	PC15. Perform initial analysis and annotation of genomic sequences using basic bioinformatics tools.				
	PC16. Identify molecular markers from transcriptomic data using publicly available databases and tools.				
	PC17. Present sequencing data output using standardized data visualization and reporting formats.				
	PC18. Apply data safety, confidentiality, and ethical practices while working with biological datasets.				
	Total	30	40	15	15
2. LFS/N3917, v1.0: Utilize Bioinformatics Databases for Data Retrieval and Biological Interpretation	Bioinformatics databases	10	10	4	5
	PC1. Classify major bioinformatics databases into nucleotide, protein, structural, and literature categories				
	PC2. Recognize the purpose and scope of NCBI, UCSC Genome Browser, Ensembl, and related repositories				
	PC3. Identify curated data in ClinVar and PubMed relevant to clinical genomics and biomedical literature				
	PC4. Determine the use of KEGG for pathway analysis and UniProt/PDB for protein research				
	PC5. Compare databases for similarities, strengths, and limitations in application				
	Retrieve and interpret information from databases	15	15	4	2
	PC6. Navigate NCBI to retrieve gene-specific data using accession numbers or keywords				
	PC7. Use UCSC Genome Browser to visualize genomic regions and annotation tracks				

	PC8. Retrieve information on gene/protein variants from ClinVar and dbSNP				
	PC9. Extract protein domain/function details using UniProt and PDB resources				
	PC10. Access biomedical literature on PubMed and filter by relevance, date, or source				
	Analyze biological function through cross-database interpretation	15	15	2	3
	PC11. Perform gene-to-pathway mapping using KEGG				
	PC12. Correlate sequence data from UCSC/NCBI with functional annotation in KEGG				
	PC13. Integrate transcriptomic and proteomic data across multiple databases				
	PC14. Build gene/protein profiles by linking literature, pathway, and structure data				
	PC15. Document bioinformatics findings using standard templates and citation formats				
	Total	40	40	10	10
3. LFS/N3918. V1.0: Apply Computational Bioinformatics Tools for Sequence and Structural Analysis	Sequence Similarity Searches	10	10	3	2
	PC1. Accurately articulate the purpose and functionality of BLAST in sequence similarity searches.				
	PC2. Discriminate between the advantages and disadvantages of standalone BLAST tools versus online tools.				
	PC3. Identify and differentiate between various types of BLAST (e.g., BLASTn, BLASTp, BLASTx, tBLASTn, tBLASTx) and their specific applications in genome and gene-level analysis.				
	PC4. Conduct efficient sequence similarity searches using NCBI Online BLAST for given query sequences.				
	PC5. Interpret and critically evaluate the results of NCBI Online BLAST outputs, including E-value, bit score, and alignment statistics.				
	PC6. Successfully install and configure a basic Standalone BLAST environment on a designated system.				
	PC7. Execute sequence analysis using local datasets with the installed Standalone BLAST.				
	PC8. Apply advanced BLAST options, such as filtering, scoring matrices, and gap penalties, to optimize searches for specific genome/gene analysis tasks.				
	Design Primers and Perform Multiple Sequence Alignment	10	10	3	2

	PC9. Discuss the fundamental principles and parameters involved in effective primer design using tools like Primer3 and NCBI Primer-BLAST.				
	PC10. Design suitable primers for a given nucleotide sequence, adhering to specified criteria using Primer3.				
	PC11. Utilize NCBI Primer-BLAST to validate primer specificity and identify potential off-target binding sites.				
	PC12. Explain the critical importance of multiple sequence alignment (MSA) in evolutionary and functional studies.				
	PC13. Conduct accurate multiple sequence alignment using MEGA software for a given set of sequences.				
	PC14. Interpret and analyze alignment outputs from MEGA, including phylogenetic trees and conservation patterns.				
	Visualize Molecular Structures	12	12	2	3
	PC15. Describe the crucial role of molecular visualization tools, specifically PyMOL, in comprehending protein structure and function.				
	PC16. Load diverse molecular structure files (e.g., PDB, CIF) into PyMOL.				
	PC17. Manipulate molecular structures within PyMOL, including rotation, translation, and scaling.				
	PC18. Identify and highlight key features within molecular structures in PyMOL, such as active sites, binding domains, and secondary structures.				
	PC19. Generate and interpret publication-ready images from PyMOL for basic molecular representations, adhering to scientific presentation standards.				
	PC20. Compare and contrast the outputs and functionalities of different sequence alignment and visualization tools used in structural bioinformatics.				
	Manage Operating Systems and Automate Tasks using Linux	8	8	2	3
	PC21. Demonstrate how to perform a basic installation of a Linux OS (e.g., using bootable media or virtual machine).				
	PC22. Execute essential Linux commands to navigate directories, create/remove files, and manage permissions.				
	PC23. Utilize advanced command-line techniques such as piping, redirection, and grep to manipulate and filter data.				
	PC24. Write and execute simple bash scripts for automating routine bioinformatics tasks (e.g., file backup, log filtering).				
	Total	40	40	10	10
	Data extraction and preparation	20	21	5	6

4. LFS/N3910 V3.0: Use statistical tool and programming scripts for data mining and transforming data	PC1. extract biological data from databases or datasets	-	-	-	-
	PC2. perform screening and identification using bioinformatics tools	-	-	-	-
	PC3. explain different data sources and how to access information from data sources	-	-	-	-
	PC4. develop scripts (short programs) for scanning or transforming large amount of data				
	PC5. match and manipulate strings through the use of regular expressions by changing file formats from one to another				
	PC6. extract sequence, parameters, and annotation from flat files by using Perl, Python or R script				
	PC7. convert raw data to platform compatible format				
	PC8. generalize FASTA format for storing biological (DNA or protein) sequences				
	PC9. utilize web applications based on appropriate program scripts like Perl on cross Operating System (OS) platform (Linux etc.)				
	PC10. check Quality Check (QC) parameters to qualify the data quality				
	PC11. check metadata of samples				
	PC12. correlate deliverables and biological inputs				
	PC13. communicate with appropriate stakeholder for any gap				
	Data mining and analysis	15	24	5	4
	PC14. analyze data from databases or datasets using computational tools to derive biological or medical knowledge and insight from them	-	-	-	-
	PC15. implement bioinformatics tools to predict structure and function of genes, proteins, drug ingredients and metabolic pathways	-	-	-	-
	PC16. manage and organize biological data and results using databases	-	-	-	-
	PC17. recall bioinformatics packages for R, Bio python, Bio perl, Bioconductor for variety of biological data sets, for examples array data, sequences data, graphs, protein structure data, clinical data	-	-	-	-
	PC18. apply Big data tool to enable parallel computing and distributed programming	-	-	-	-
	PC19. perform primary analysis for confirmatory check and pipeline qualification	-	-	-	-
	PC20. perform secondary analysis for ascertaining biological meaning of data				
	PC21. assist Bioinformatics Data Scientist in Biological Correlation with the predefined outcome				
	PC22. assist Bioinformatics Data Scientist in publications				
	Total Marks	35	45	10	10
5. LFS/N0107 v9.0: Coordinate with Supervisors and Other Cross-functional team members	Coordination with manager	10	20	5	5
	PC1. receive work instructions from reporting manager and understand work output requirements	-	-	-	-
	PC2. seek advice and opinion from manager on the approach taken for carrying out work	-	-	-	-
	PC3. report any challenges, obstacles in completing the work as per specifications and timelines	-	-	-	-
	PC4. assist the manager with his/her responsibilities	-	-	-	-
	Coordination with team members	10	10	5	5

	PC5. work as a team with colleagues and share workload	-	-	-	-
	PC6. put team over individual goals	-	-	-	-
	PC7. work to resolve conflicts within the team	-	-	-	-
	Coordination with cross functional teams	10	10	5	5
	PC8. articulate support/ inputs/data needed from cross-functional teams	-	-	-	-
	PC9. interact with the necessary cross-functional teams to gather the required data	-	-	-	-
	PC10. provide proactive support/ inputs/data requested by other teams	-	-	-	-
	PC11. participate in cross-functional team meetings and share relevant information				
	Total Marks	30	40	15	15
6. DGT/VSQ/N0102 : Employability Skills (60 Hours)	Introduction to Employability Skills	1	1	-	-
	PC1. Identify employability skills required for jobs in various industries	-	-	-	-
	PC2. identify and explore learning and employability portals	-	-	-	-
	Constitutional values – Citizenship	1	1	-	-
	PC3. recognize the significance of constitutional values, including civic rights and duties, citizenship, responsibility towards society etc. and personal values and ethics such as honesty, integrity, caring and respecting others, etc.	-	-	-	-
	PC4. follow environmentally sustainable practices	-	-	-	-
	Becoming a Professional in the 21st Century	2	4	-	-
	PC5. recognize the significance of 21st Century Skills for employment	-	-	-	-
	PC6. practice the 21st Century Skills such as Self-Awareness, Behavior Skills, time management, critical and adaptive thinking, problem-solving, creative thinking, social and cultural awareness, emotional awareness, learning to learn for continuous learning etc. in personal and professional life	-	-	-	-
	Basic English Skills	2	3	-	-
	PC7. use basic English for everyday conversation in different contexts, in person and over the telephone	-	-	-	-
	PC8. read and understand routine information, notes, instructions, mails, letters etc. written in English	-	-	-	-
	PC9. write short messages, notes, letters, e-mails etc. in English	-	-	-	-
	Career Development & Goal Setting	1	2	-	-
	PC10. understand the difference between job and career	-	-	-	-
	PC11. prepare a career development plan with short- and long-term goals, based on aptitude	-	-	-	-
	Communication Skills	2	2	-	-
	PC12. follow verbal and non-verbal communication etiquette and active listening techniques in various settings	-	-	-	-
	PC13. work collaboratively with others in a team	-	-	-	-
	Diversity & Inclusion	1	2	-	-

	PC14. communicate and behave appropriately with all genders and PwD	-	-	-	-
	PC15. escalate any issues related to sexual harassment at workplace according to POSH Act	-	-	-	-
	Financial and Legal Literacy	2	3	-	-
	PC16. select financial institutions, products and services as per requirement	-	-	-	-
	PC17. carry out offline and online financial transactions, safely and securely	-	-	-	-
	PC18. identify common components of salary and compute income, expenses, taxes, investments etc	-	-	-	-
	PC19. identify relevant rights and laws and use legal aids to fight against legal exploitation	-	-	-	-
	Essential Digital Skills	3	4	-	-
	PC20. operate digital devices and carry out basic internet operations securely and safely	-	-	-	-
	PC21. use e- mail and social media platforms and virtual collaboration tools to work effectively	-	-	-	-
	PC22. use basic features of word processor, spreadsheets, and presentations	-	-	-	-
	Entrepreneurship	2	3	-	-
	PC23. identify different types of Entrepreneurship and Enterprises and assess opportunities for potential business through research	-	-	-	-
	PC24. develop a business plan and a work model, considering the 4Ps of Marketing Product, Price, Place and Promotion	-	-	-	-
	PC25. identify sources of funding, anticipate, and mitigate any financial/ legal hurdles for the potential business opportunity	-	-	-	-
	Customer Service	1	2	-	-
	PC26. identify different types of customers	-	-	-	-
	PC27. identify and respond to customer requests and needs in a professional manner.	-	-	-	-
	PC28. follow appropriate hygiene and grooming standards	-	-	-	-
	Getting ready for apprenticeship & Jobs	2	3	-	-
	PC29. create a professional Curriculum vitae (Résumé	-	-	-	-
	PC30. search for suitable jobs using reliable offline and online sources such as Employment exchange, recruitment agencies, newspapers etc. and job portals, respectively	-	-	-	-
	PC31. apply to identified job openings using offline /online methods as per requirement	-	-	-	-
	PC32. answer questions politely, with clarity and confidence, during recruitment and selection	-	-	-	-
	PC33. identify apprenticeship opportunities and register for it as per guidelines and requirements	-	-	-	-
	Total Marks	20	30	-	-
	Program with Python and R for Biological Data Analysis	20	25	5	5

7. LFS/N3919, v1.0: Computational Programming and Cloud Infrastructure for Bioinformatics	PC1. Install and configure a bioinformatics programming environment using Python and relevant libraries (e.g., Biopython, Pandas).				
	PC2. Create, manipulate, and process biological sequences and data using Python string operations and control structures.				
	PC3. Implement data structures (e.g., lists, sets, dictionaries) and functions for organizing and processing bioinformatics data in Python.				
	PC4. Apply Biopython tools to parse biological files and perform basic sequence analysis and 3D structure handling.				
	PC5. Install and set up the R environment and RStudio for bioinformatics work.				
	PC6. Create, manipulate, and import/export biological data using R's fundamental data types and functions.				
	PC7. Utilize Bioconductor and other R packages (e.g., ggplot2) for sequence analysis and data manipulation.				
	PC8. Generate publication-quality visualizations for biological data using R programming.				
	Manage Databases and Leverage Cloud Computing for Bioinformatics	10	25	5	5
	PC9. Write basic SQL queries using SELECT, FROM, WHERE, ORDER BY, and JOIN statements to retrieve biological data.				
	PC10. Create and manipulate tables, defining appropriate data types for genomic and proteomic datasets in SQL.				
	PC11. Import and export data using SQL commands (e.g., LOAD DATA INFILE, INSERT INTO, EXPORT TO CSV).				
	PC12. Manipulate bioinformatics data using SQL operations such as UPDATE, DELETE, GROUP BY, and HAVING.				
	PC13. Set up a basic cloud account and effectively navigate the cloud computing Management Console.				
	PC14. Launch and configure EC2 instances with appropriate specifications for compute tasks in bioinformatics.				
	PC15. Create and manage storage buckets using Amazon S3 and upload/download large-scale datasets.				
	PC16. Deploy a sample bioinformatics application or script using cloud computing EC2 or Lambda.				
		30	50	10	10
8. LFS/N3920, v1.0: Perform DNA-Sequence Data Analysis for Variant Calling in Bioinformatics	NGS Fundamentals and Data Sourcing	10	10	3	2
	PC1. Describe the fundamental concepts of Next-Generation Sequencing (NGS) and its application in DNA sequencing.				
	PC2. Explain key terminologies commonly used in NGS workflows (e.g., reads, depth, coverage, paired-end, base quality).				

PC3. Articulate the purpose and utility of the Sequence Read Archive (SRA) database for retrieving publicly available sequencing data.				
PC4. Efficiently search and download DNA sequencing datasets from the SRA database for analytical purposes.				
PC5. Identify the critical steps in a typical DNA-Seq analysis pipeline from raw reads to variant calls.				
Quality Control and Read Processing	10	10	3	2
PC6. Install and configure essential Linux command-line tools required for DNA sequencing quality control and preprocessing (e.g., FastQC, Trimmomatic).				
PC7. Perform comprehensive quality control analysis of raw sequencing reads using appropriate software to assess data quality metrics.				
PC8. Interpret quality control reports to identify common sequencing artifacts and biases.				
PC9. Execute trimming and filtering operations on raw sequencing reads to remove low-quality bases, adapter sequences, and contamination.				
PC10. Evaluate the effectiveness of trimming and filtering steps by re-assessing read quality.				
Align Reads and Perform Variant Calling	10	10	2	3
PC11. Prepare reference genomes by performing genome indexing using standard alignment tools (e.g., BWA).				
PC12. Execute read alignment of processed DNA sequencing reads to a reference genome using appropriate aligners.				
PC13. Interpret alignment outputs (e.g., BAM/SAM files) to assess mapping quality and coverage.				
PC14. Install and configure the Genome Analysis Toolkit (GATK) and its dependencies on a Linux system.				
PC15. Apply GATK best practices pipeline steps (e.g., base recalibration, indel realignment) for accurate variant calling.				
PC16. Perform variant calling using GATK tools (e.g., HaplotypeCaller) to identify single nucleotide polymorphisms (SNPs) and insertions/deletions (indels).				
Predict Variant Effects and Visualize Data	10	10	2	3
PC17. Predict the functional effects of identified genetic variants (e.g., synonymous, non-synonymous, stop-gain) using annotation tools.				
PC18. Utilize variant annotation databases to gather relevant biological information for identified variants.				
PC19. Prepare variant call format (VCF) files for visualization in genomic browsers.				

	PC20. Visualize genetic variations and their associated read alignments using genomic visualization tools like Integrative Genomics Viewer (IGV) for comprehensive interpretation.				
		40	40	10	10
9. LFS/N3921, v1.0: Perform bulk and single cell transcriptomics Data Analysis for Transcriptomic Interpretation in Bioinformatics	RNA-Seq Fundamentals and Data Preparation	10	20	5	5
	PC1. Explain the fundamental concepts of RNA-seq and its applications in gene expression and transcriptome analysis.				
	PC2. Articulate key terminologies commonly used in RNA-seq workflows (e.g., reads, transcripts, isoforms, FPKM, TPM).				
	PC3. Install and configure essential Linux command-line tools required for RNA-seq data processing and quality control.				
	PC4. Collect RNA-seq datasets from public repositories (e.g., SRA) for subsequent analysis.				
	PC5. Perform comprehensive quality control analysis of raw RNA-seq reads using appropriate software (e.g., FastQC).				
	PC6. Execute read trimming and filtering operations to remove low-quality bases, adapter sequences, and ensure data reliability.				
	Reference-Based RNA-Seq Analysis	10	10	5	5
	PC7. Perform genome indexing for reference genomes to enable efficient RNA-seq read alignment.				
	PC8. Execute RNA-seq read alignment to a reference genome using suitable aligners (e.g., STAR, HISAT2).				
	PC9. Apply appropriate data normalization methods (e.g., using Cufflinks, DESeq2, edgeR) to account for sequencing depth and library size variations.				
	PC10. Merge data from multiple RNA-seq samples and identify differentially expressed genes (DEGs) between experimental conditions.				
	PC11. Interpret the results of differentially expressed gene analysis, including fold changes, p-values, and statistical significance.				
	PC12. Perform functional annotation of differentially expressed genes using relevant databases (e.g., GO, KEGG).				
	PC13. Conduct pathway enrichment analysis and network analysis to explore gene interactions and biological significance of DEGs.				
	De Novo RNA-Seq Analysis and Interpretation	10	10	5	5
	PC14. Set up and configure specialized tools for de novo RNA-seq analysis, such as Trinity, RSEM, edgeR, or Assembly-stats.				
	PC15. Execute transcriptome assembly from raw RNA-seq reads using de novo assemblers (e.g., Trinity).				

	PC16. Estimate transcript or gene abundance counts from de novo assembled				
	PC17. Generate count matrices and identify differentially expressed genes in de novo assembled transcriptomes.				
	PC18. Perform BLAST analysis of de novo assembled transcripts to identify homologous sequences and provide initial annotation.				
	PC19. Interpret the results of de novo DEG analysis and evaluate transcriptome assembly statistics (e.g., N50, contig counts).				
	PC20. Perform functional enrichment analysis of differentially expressed genes derived from de novo transcriptome assemblies.				
		30	40	15	15
10. LFS/N3922, v1.0: Perform Spatial Transcriptomics Analysis for Tissue-Specific Gene Expression Mapping and Visualization	Understand Spatial Transcriptomic Data and Preprocessing Workflows	10	20	5	5
	PC1. Accurately describe the data structures and output formats generated by common spatial transcriptomics platforms, including FASTQ files, spatial barcodes, and associated image files.				
	PC2. Clearly explain the sequential workflow for spatial transcriptomic data preprocessing using industry-standard tools like SpaceRanger.				
	PC3. Discuss the critical purpose and effective methodologies for integrating histological images with gene expression matrices in spatial transcriptomics analysis.				
	Perform Data Acquisition, Preprocessing, and Initial Visualization	10	10	5	5
	PC4. Download and extract publicly available spatial transcriptomics datasets efficiently and accurately.				
	PC5. Utilize SpaceRanger to align sequencing data to a reference genome with high precision.				
	PC6. Generate accurate count matrices and spatial feature outputs using SpaceRanger.				
	PC7. Employ Loupe Browser to effectively visualize spatial gene expression across tissue sections.				
	PC8. Perform basic interactive exploration of spatial domains within Loupe Browser.				
	Conduct Advanced Spatial Data Analysis and Interpretation	10	10	5	5
	PC9. Load spatial data matrices and image files into Seurat (R) or Scanpy (Python) correctly.				
	PC10. Perform data normalization, dimensionality reduction (PCA, UMAP), and clustering on spatial transcriptomic data using Seurat or Scanpy.				
	PC11. Identify spatially variable genes using appropriate spatial statistics methods in Seurat or Scanpy.				

	PC12. Overlay gene expression data accurately onto tissue images for contextual interpretation.				
	PC13. Generate and interpret spatial heatmaps, cluster plots, and gene expression overlays to derive biological insights.				
	Total	30	40	15	15
11. LFS/N3923, v1.0: Perform Targeted Microbiome Profiling Using Metagenomic Analysis and Phylogenetic Visualization Tools	Conduct Metagenomic Analysis for Microbial Profiling	30	40	15	15
	PC1. Explain the fundamental concepts and applications of metagenomics analysis for microbial community profiling.				
	PC2. Set up and configure necessary bioinformatics tools for metagenomic sequencing data analysis (e.g., QIIME2, DADA2, MEGA).				
	PC3. Download and preprocess raw metagenomic sequencing data from public repositories				
	PC4. Perform quality control and read trimming on metagenomic reads to ensure high data quality.				
	PC5. Import preprocessed metagenomic data into QIIME2 for downstream analysis.				
	PC6. Conduct quality assessment and denoising of amplicon sequences using DADA2 within QIIME2.				
	PC7. Analyze phylogenetic diversity (alpha and beta diversity) of microbial communities using appropriate metrics.				
	PC8. Perform taxonomic classification of sequences to identify microbial genera and species present in samples.				
	PC9. Visualize taxonomic profiles of microbial communities using tools like Krona Plot.				
	PC10. Construct phylogenetic trees of microbial sequences or taxa using software such as MEGA for evolutionary relationships.				
	Total	30	40	15	15
12. LFS/N3924, v1.0: Perform Microarray-Based Gene Expression Profiling and Bioinformatics Analysis for Differential Gene Interpretation	Conduct Microarray- Based Gene Expression Analysis				
	PC1. Describe the principles and methodologies of microarray technology for gene expression profiling.				
	PC2. Download raw microarray data from public repositories (e.g., GEO) and perform initial preprocessing steps.				
	PC3. Execute the microarray processing pipeline, including background correction and data normalization.				
	PC4. Identify differentially expressed genes (DEGs) from normalized microarray data using statistical methods.				

	PC5. Annotate differentially expressed genes with relevant biological information (e.g., gene names, functions, pathways).				
	PC6. Conduct functional enrichment analysis of DEGs to identify enriched biological processes, molecular functions, and cellular components.				
	PC7. Perform network analysis of gene interactions to explore relationships among differentially expressed genes.				
	PC8. Visualize differential gene expression results using volcano plots for quick interpretation of significance and fold change.				
	PC9. Generate heatmaps to represent patterns of gene expression across different samples or conditions.				
	PC10. Interpret the biological significance of findings from both metagenomic and microarray analyses.				
	Total	30	40	15	15
13. LFS/N3925, v1.0: Development and application of Algorithm for AI and ML	Algorithm Development for AI and ML	20	25	5	5
	PC1. Describe the fundamental concepts of algorithm				
	PC2. Make use of object-oriented approaches and structured programming rules in algorithm development and implementation				
	PC3. Apply logical and algorithmic thinking while programming for AI and ML				
	PC4. Verify correctness of algorithm				
	Customization of Algorithm for application of AI and ML	10	25	5	5
	PC5. Select appropriate Machine Learning algorithm based on problem type				
	PC6. Apply greedy algorithms to different cases				
	PC7. Refine and implement a well-structured algorithm for data processing and analysis.				
	PC8. Use algorithm in the collective data processing.				
	PC9. Deploy the perfected Model for real world use				
		30	50	10	10
14. LFS/N3926, v1.0: Apply Machine Learning and Computational Strategies for Big Data interpretation	Apply Machine Learning for Genomic Data Analysis	7	14	5	6
	PC1. Describe the fundamental concepts of machine learning, including supervised and unsupervised learning, and their specific applications in genomic data analysis.				
	PC2. Explain linear models and nearest neighbor algorithms for pattern recognition and classification in biological datasets.				
	PC3. Apply Support Vector Machines (SVM) for classification tasks on genomic and other high-dimensional biological data.				
	PC4. Implement Naïve Bayes Classifiers for specific bioinformatics use cases, such as sequence classification or variant prioritization.				

	PC5. Utilize decision trees and random forests to build interpretable machine learning models from biological features.				
	PC6. Apply logistic regression for predictive analysis of biological outcomes (e.g., disease risk, drug response).				
	PC7. Employ clustering algorithms (e.g., K-means, hierarchical) for unsupervised pattern discovery and dimensionality reduction in complex biological data.				
	Perform Statistical Analysis for Biological Data Interpretation	11	14	5	5
	PC8. Explain essential statistical methods for bioinformatics, including descriptive statistics (mean, median, mode, variance, standard deviation) and data structures.				
	PC9. Perform correlation and regression analysis to identify relationships and build predictive models from genomic data.				
	PC10. Understand and apply probability concepts, including Bayes Theorem, in bioinformatics for predictive and diagnostic scenarios.				
	PC11. Select and apply appropriate sampling techniques and understand distribution theory (e.g., normal, binomial) for biological datasets.				
	PC12. Formulate and execute hypothesis testing for statistical significance in biological data analysis (e.g., t-tests, ANOVA, chi-square).				
	PC13. Apply inferential statistics to draw robust conclusions and generalize findings from biological experiments.				
	PC14. Utilize statistical tools and libraries (e.g., in Python, R) for effective data management, analysis, and visualization of biological data.				
	Develop Basic Algorithms for Bioinformatics	12	12	5	4
	PC15. Understand fundamental principles and methods of program design for bioinformatics applications.				
	PC16. Develop algorithms using basic programming structures such as loops, conditionals, and functions to solve bioinformatics problems.				
	PC17. Differentiate between efficient and naïve algorithmic approaches based on their computational complexity and performance characteristics.				
	PC18. Apply structured programming techniques for organizing and solving computational problems in bioinformatics.				
	PC19. Explain object-oriented programming (OOP) concepts (e.g., classes, objects, inheritance) and their relevance in bioinformatics software development.				
	PC20. Apply greedy algorithms for optimization problems in bioinformatics (e.g., sequence alignment, gene order).				
		30	40	15	15

Grand Total	445	575	165	165
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Annexure: Assessment Strategy

This section includes the processes involved in identifying, gathering, and interpreting information to evaluate the Candidate on the required competencies of the program.

1. Assessment System Overview:

The assessment for the Training will be conducted toward the end of the training duration. The assessment of the qualification shall be carried out by NCVET approved assessment agencies empanelled by LSSSDC after a defined evaluation process. For Execution of the assessment for training for the qualification, LSSSDC will be engaging more than one NCVET approved assessment agency/ body.

1.1 Criteria of selection of assessment body/agency:

The assessment body/agency is selected based on:

- Prior experience and understanding of Life Sciences or similar sector.
- Experience in conducting assessments for similar job roles.
- Manpower and Technical capabilities.
- Geographical reach
- Existing Network in the Life Sciences Sector
- Agencies internal policies to maintain standards, quality & professional Integrity
- Agencies policy and practices in assessor management
- NCVET approval

1.2 Assessment tool development for assessment of Training:

For the Training assessment, the assessment instrument development is done by the selected assessment body with close monitoring and support of LSSSDC at every stage.

1.2.1 Digital Written test for knowledge assessment:

Scope – Is used to test the knowledge component of the Qualification/ Micro Credential/ NOS.

Tools –computer or tab based online or offline.

Method – objective type questions, match the columns, fill in the blanks, tick the odd man out, choose the correct option, choose the best answer, True or false, Identify the object, tool or machinery, arrange in proper sequence, case study, scenario-based responses.

Analysis – Question paper is divided into sections. Each Section intends to assess a particular knowledge field of the trainee. Thus, section-wise calculation of marks gives a clear idea of the areas of improvement or expertise of the trainee. While a consolidated mark gives the overall rating of the trainee.

1.2.2 Digital Written test for skill assessment:

Scope – Is used to test primarily the Skill component of the Qualification/ Micro Credential/ NOS. Trainee's expertise in handling and managing the situation is tested.

Tools – computer or tab based online or offline questions

Method – A situation is narrated or created in the question posed to the trainee and he is asked objective type questions to select the correct reaction to the situation. The selected situations are based on real situations.

Analysis – Question paper is divided into sections. Each Section intends to assess a particular skill field of the trainee. Thus, section-wise calculation of marks gives a clear idea of the areas of improvement or expertise of the trainee. While a consolidated mark gives the overall rating of the trainee.

1.3 Steps for assessment tool development:

- The selection of assessment tool(s) is done as per the assessment criteria prescribed in Qualification/ Micro Credential/ NOS.
- For Bioinformatics Associate/Analyst assessment, a blueprint of the question paper is part of the assessment tool for training in Bioinformatics.
- Development of layout of Question paper is such that the entire PCs (Performance Criteria) of that Qualification/ Micro Credential/ NOS are covered.
- Score per question maps with the weightage given to that PC, in the assessment criteria, and the level of difficulty of the question.
- An expert from industry is selected who is called "Subject Matter Expert" (SME). This SME must have over 13-15 years of experience in the industry in manufacturing occupation.
- SME is screened and approved by LSSSDC. He/she is oriented by both LSSSDC and Assessment agency on – creating question Bank, level of questions, end the desired outcome of the assessment.

1.4 Execution of Training Assessment/ RPL Assessment:

- Once the assessment date for training is decided with common agreement of Industry/ Vocational Training Centre and LSSSDC, LSSSDC allocates the batch to an NCVET approved and LSSSDC empanelled assessment body/agency.
- Assessment agency ensures
 - the availability of required infrastructure
 - the availability of validated assessment tools for the assessment of training for the assigned qualification
 - the availability of assessor as per assessor eligibility criteria of the qualification
- Assessment agencies send the assessment confirmation to VTP/TC looping SSC
- Assessment agency deploys LSSSDC certified assessor for executing the assessment
- LSSSDC monitors the assessment process & records
- The assessment is executed in two possible ways depending on the choice of the industry:

1.4.1 Tab based assessment using physical proctoring

1.4.2 Smartphone-based assessment using e-proctoring

1.4.1 Tab-based assessment using physical proctoring

- A representative from the Assessment agency is present on the day of assessment to executing the assessment at the venue in case of physical proctoring.
- The assessment agency representative carries an identity card and letter from the council authorizing to conduct the assessment.
- Assessment agency representative ensures the authenticity of Trainee's identity by verifying the documents (any document issued by GOI, such as Ration card, Aadhaar Card, Driving License, Passport, Election card, etc)
- The assessment agency representative maintains the records of attendance, verified documents, and tablet instruments used in the assessment.
- Assessment agency representative collects evidence of the assessment in the best possible way (videos, pictures, voice recordings, etc)
- Assessment agency representative transfers the assessment scores from tab to assessment agency server, using a secure, encrypted web-based program.
- The assessment agency after processing the results and putting them in standard format hands over to LSSSDC within 7 days of assessment.

1.4.2 Smartphone-based assessment using e-proctoring

- All trainees enrolled in the batch due for assessment, are registered on an assessment tool application using their unique mobile number and e-mail ID along with a Govt. ID issued proof.
- An assessment link is sent to the mail ID of each trainee with a defined expiry date of the link.
- Trainee at any location can click on the link using his/her smartphone or a web camera-enabled computer system
- Using the unique credentials and Govt ID number, the trainee logs in for the start of assessment and completes the assessment.
- The authenticity of Trainee's identity is done by assessment application by verifying the documents (any document issued by GOI, such as Ration card, Aadhaar Card, Driving License, Passport, election card, etc.) and a live photo capture
- A live video of the candidate during the assessment is captured to collect the evidence of the assessment
- Once the assessment is complete, the assessment application automatically assessment scores to the assessment agency server, using a secure, encrypted web-based program.
- The assessment agency after processing the results and putting them in standard format hands over to LSSSDC within 7 days of assessment.

2. Testing Environment:

- The Centre/ location of the assessment is pre decided and geo tagged in case of physical assessment
- The assessment of LSSSDC qualifications is 99% done in digital environment while 1% pen and paper is used ONLY in business exigencies
- Based on the size of batch the assessment duration/ no. of required assessors is decided to ensure detailed assessment without any negative impact on quality of assessment
- The system driven automated assessment management system ensures uniform time allocation to each student, unique logins for each student and automated randomization of questions for developing multiple sets of question paper for single batch.
- Identity check of the student is mandated

3. Assessment Quality Assurance levels/Framework:

- Question bank is created by the Subject Matter Experts (SME) of Assessment Agency are verified by the other SME of LSSSDC
- All Questions are mapped to the specified assessment criteria
- Assessor eligibility criteria are structured to ensure quality and knowledge credentials of an assessor like-wise the trainer's quality and knowledge credentials.
- Eligible Assessor must be certified by LSSSDC for the respective and relevant qualification
- The tools used for assessment are validated for relevance and feasibility for skill assessment of the qualification in consideration

4. Types of evidence or evidence-gathering protocol:

- Time-stamped & geotagged reporting of the assessor from assessment location
- ID Proof of the students
- Educational qualification of students
- Certificate of Trainer
- In case of Physical assessment, geotagged photographs of the students undergoing assessment
- While students are undergoing assessment on the digital assessment platform the system captures random photos of the student which is audited by LSSSDC

5. Method of verification or validation:

- Surprise visit to the assessment location
- ID Proof of the students for identity verification
- Educational qualification verification of students for validation of entry level criteria
- Certificate of Trainer to verify the credential of vocational educator
- Random photos taken by the digital system are verified during audit by the assessment team

6. Method for assessment documentation, archiving, and access

- Hard copies and digital copies (whichever is applicable) of the assessment evidences are stored with assessment agency team for 5 years
- Assessment transcripts are stored in the server space of assessment agency for 5 years
- Assessment question banks and validation records are stored with assessment agency and LSSSDC digitally
- Assessment records are archived with assessment agency archive server after 5 years for another 5 years
- Access of assessment records are controlled with restricted access to concerned department and stakeholders and is shared on demand after due approval of Head of Assessment and Certification-LSSSDC

7. On the Job Training Assessment (applicable for OJT/ Apprenticeship):

1. Each module/ NOS will be assessed separately.
2. The candidate must score minimum percentage as per assessment criteria laid out in qualification in each module to successfully complete the OJT exam.
3. Tools of OJT Assessment that will be used for assessing whether the candidate is having desired skills and competence, including Soft Skills effectively:
 - Videos of Trainees during OJT (wherever possible)
 - Observation based mark sheet from Supervisor or OJT examiner
 - Simulated question paper
 - XR practice module analytics wherever possible
4. Assessment of each Module will ensure that the candidate is able to:
 - Meet minimum performance criteria of the expected outcome/ skill set for each module/ NOS
 - Understand and know the required concepts and its application at workplace
 - Has gained the required employability skills

Annexure: Acronym and Glossary

Acronym

Acronym	Description
AA	Assessment Agency
AB	Awarding Body
ISCO	International Standard Classification of Occupations
NCO	National Classification of Occupations
NCrF	National Credit Framework
NOS	National Occupational Standard(s)
NQR	National Qualification Register
NSQF	National Skills Qualifications Framework
OJT	On the Job Training

Glossary

Term	Description
National Occupational Standards (NOS)	NOS define the measurable performance outcomes required from an individual engaged in a particular task. They list down what an individual performing that task should know and also do.
Qualification	A formal outcome of an assessment and validation process which is obtained when a competent body determines that an individual has achieved learning outcomes to given standards

Qualification File	A Qualification File is a template designed to capture necessary information of a Qualification from the perspective of NSQF compliance. The Qualification File will be normally submitted by the awarding body for the qualification.
Sector	A grouping of professional activities on the basis of their main economic function, product, service or technology.
Long Term Training	Long-term skilling means any vocational training program undertaken for a year and above. https://ncvet.gov.in/sites/default/files/NCVET.pdf

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