

परीक्षार्थी का पूरा नाम Vaishali Sharma

हस्ताक्षर

कक्ष निरीक्षक का नाम परीक्षार्थी हारा सम्पूर्ण चिपरण भर दिया

प्रश्नों की क्रम संख्या	a/I	b/II	c/III	d/IV	e/V	f/VI	g/VII	h/VIII	i/IX	j/X	चेता
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प्राप्तांक

(शब्दों में) *Vaishali* अंकों में



R

2018-

भाग-2

M.Sc. Internal

चौधरी चरण सिंह विश्वविद्यालय, मेरठ  
Ch. Charan Singh University, Meerut

निम्नलिखित विवरण परीक्षार्थी द्वारा स्वयं भरा जाए (To be filled by the Examinee)

All  
07/05/19परीक्षा का नाम M.Sc. Zoology वर्ष 20 2019 भाग/सेमेस्टर II  
(Name of Exam) (Year 20.....) (Part / Semester)विषय Zoology प्रश्न-पत्र/पाठ्यक्रम पेपर कोड नं. H-2062  
(Subject) (Paper/Course) (Paper Code No.)परीक्षा का दिन Wednesday दिनांक 1/5/19  
(Day of Examination) (Date)

## प्राप्तांक एवं पूर्णांक परीक्षकों द्वारा भरे जायें

पूर्णांक... (Max. Marks)



2018-

भाग-3

चौधरी चरण सिंह विश्वविद्यालय, मेरठ

अधिकारी विरेन्द्र देव पुष्ट भाग देवे

Date Stamp to be affixed here

मार्च 2019

(परीक्षार्थी द्वारा भरा जाए)

परीक्षा का नाम M.Sc-Zoology भाग/सेमेस्टर II  
विषय Biostatistic & Bioinformatics  
प्रयोग पत्र 1/5/19

परीक्षार्थी का अनुक्रमांक (Roll Number)

उत्तर-पुस्तक क्रमांक  
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(परीक्षार्थी की श्रेणी)

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नामांकन संख्या (Enrollment Number)

M 15541386

पेपर कोड  
H 20 62

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परीक्षार्थी का पूरा नाम  
Vaishali

Sharma

कक्ष निरीक्षक का नाम

Vaishali  
Sharma

Rajm

# Section 'A'

## Q-1 Hypothesis

introduced by Pearson's & Pearson's by Ronald Fisher, Karl-son.

→ Hypothesis testing is a statistical method that is used to define anatomy of statistical method!

→ Hypothesis is in various types.

### ① Null hypothesis

alternative hypothesis → Null hypothesis is the

→ Null hypothesis is denoted by  $H_0$ :  
 $\mu_1 = \mu_2$  that is show that  
there is no difference between the  
two hypotheses.

## ② Alternative hypothesis

Alternative hypothesis shows that the result  
is the real value of testing.

Q-2.

## Genetic Disorders

→ Genetic Disorders  
are the errors in Genes -  
As a result Genetic Disease  
arises due to called Genetic  
Disorders.

→ Genetic Disease are passed  
by the Genes next one generation.

① ~~Harmophelia~~

② ~~Colour Blindness.~~

→ Harmophelid & Colour Blindness  
In the Genetic Disorders.

→ In Colour Blindness - Red  
& Green Colour not identified.

~~G3~~ Gene Bank → Gene Bank Defined  
as the Collection Sequence Database  
of DNA & RNA.  
→ In Bioinformatics Sequence Data  
Bank is the Biological Collection  
of genetic material!  
→ So Sequence Database Work  
with the Bank, Collaboration  
of Gene Bank, DNA Data  
Bank, Tcupan, EMBL.

→ Gene Bank Collection is also Biological Data.

→ Gene Bank Collect the Data & Information to  
Defined & give like EMBL,  
other Laboratory

DBJ ch.

By

http : →  
-protocol.

Hyper text transfer

→ When we log in any site at the  
it come in website.

→ http is the transfer protocol.

Q's

DDBJ

→ DNA Data Bank of Japan.

→ It Collect the DNA Sequences.

→ DDBJ is the Biological Collection of Data in formatters.

→ DDBJ works with the Molecular Biology Laboratory of EMBL (European Molecular Biology Laboratory).

## Section 'B'

9

Ans

Swiss Port

Swiss Post  
Collaboration of  
Bank

Work with the  
EMBL & Data  
of Bioinformatics.

→ If provide the higher level  
of manipulation with the  
Collaboration of Data.

→ It work with the Top EMBL  
is the Computed annotated Work

- Similar format to EMBL.<sup>10</sup>
- Swiss Port is the ~~Collect~~ of protein Sequence -
- Different types of protein Sequence are collected by the Swiss Port & identified the ~~Sequence~~.
- ie it is also called the Library of Protein Sequence.

→ by Swiss port received files<sup>11</sup>  
by the SRS.

⇒ SRS is the Software  
that helps to assign port  
to received different protein  
sequences.

Features of Swiss Port

① Annotation

② Minimal Redundancy.

③

Integration with other  
Database

④

Documentation

⑤

Q7.

Computer → A Device that  
Computers, especially a program  
the electronic machine that  
Performs mathematical & logical high-speed Math-  
or that Operation  
Data etc. ~~assemblies~~, storage

Different types of Computers—

- ① Super Computer.
- ② Micro Computer.
- ③ Personal Computer.

Parts of Computer. → 2 types  
of Components are found -

- ① Computer Hardware
- ② Computer Software.

# Computer Hardware

Hardware is the physical part of the computer that

- Can we touch with our fingers.
- Computer Hardware is the 3 types →

①

Input Device

②

Output Device

③

Storage Device.

# Input Device

that get information from the Computer

Input Device in the Input Device

① Keyboard

if is used to type files. Different keys are present at Keyboard. Number Key 1-10 present.

Q

Mouse

Smallest  
Components

part  
on

Mouse is the  
that move the  
monitor screen.

Output Device

that  
the  
get  
Computer.

Output  
information  
Device  
out of

1

Speaker

Output

Speaker is the  
Device.

(2)

Pointers →  
Output Device → Pointers is the  
Information Out of the Computer

Storage Device

→ it is the.

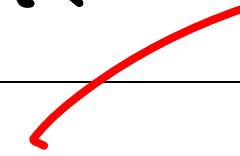
Output & Input are both.  
If it stores the Data so  
if is also known Storage Device

①

Hard Disk

②

CD

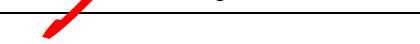


③

DVD ( Digital video Disk )

④

Pen drive.



→ Computer Software is the part  
of the computer that say,  
what to do.

See on Monitor

Screen

- ① MS Word ② MS Power Point etc.

## Section C

Q 10.

Sequence Databases

Sequence Database

is the Collection of DNA & RNA Sequence. ~~it is the collection of Data to Detect & analyzing Bioinformatics.~~

→ In other word like Define the Sequence Database is Collection of Bioinformatics.

→ European BLAST, Molecular Biology Gen Bank, DDBJ are all the collect Data.

→ Sequence with the Database is Collaboration Work of NIG. (National Institute of Genetics).

→ When We thought the Sequences Database the 2 main function were cruise in our mind. Data & firstly than collection of sequences. Second function of DNA.

→ Types of Sequence Database,

- ① Generalised Database.
- ② Specialised Database.

# Sequence Database

Generalised Database

① EBTs

② STSS

③

Specialised Database

① Protein Database ② Nucleotide Database.

(i) Swiss Prot

① EMBL

② PIR

(Protein information Resource)

② GenBank

# Generalized Database

① EBTs → Expressed Sequence  
text.  
i.e Define the Sequence of  
DNA & RNA fragments.

② STSS → Sequence tagged  
sites.

# Specialised Database

①

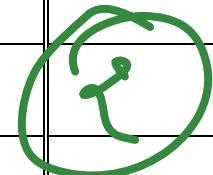
## Protein Database:

that Define  
about the Protein Sequence  
of DNA fragment. this  
are the 2 types —

①

## Swiss Prot

Define in  
Section - B, Question - 8  
Page No - 9.

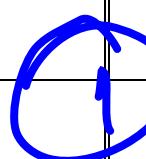


PIR

Protein Information  
Resource and Define the  
Sequencer Database.

Nucleotide Database

~~are the 2 types~~ these



EMBL

Biology

European Molecular  
Laboratory

③ Gene Bank → Define in Section  
A → Question N. - 3.

BLAST  
Search tool. Basic Local alignment  
algorithm for Blast is an  
Sequence Database. Destine

~~O<sub>2</sub>~~ Test Significance  
of test. of Signification 3 types

① chi-square test  $(\chi^2)^2 / n^2$

② mainly t test → if it is the  
two types.

(i) Paired + test

(ii) Unpaired t-test

(3)

## ANOVA

(Analysis of Variance)

Chi-square test

test used for Chi-square single  
Data.

→ When Data of We have Single  
significance they  
We check by the chi-square  
test.

→ chi square test is denoted by the  $(\chi^2)$  test.

→ the formula for testing the chi-square test is the

$$\chi^2 = \sum \frac{(O - E)^2}{E}$$

(O-E)  
2/E

O = Observed Value.

E = Expected Value.

In this process in result  
two Value - tabulated Value  
& observed Value.

is if T.V. > O.V. - Tabulated  
Value more than the observed  
Value We accept the  
hypothesis testing.

→ if T.V.  $<$  O.U. . Tabulated  
Value less than observed Value  
We reject the hypothesis  
testing.

→ Pearson's published the  
chi - square test.

→ In the standard application<sup>33</sup> of this test the observations are classified into mutually exclusive classes.

→ A common chi-square test is constructed from a square error.

→ Test Square test that follow chi-square test.

→ if chi - square test used  
from the assumption reject  
or accept the null  
hypothesis.

→ Null hypothesis ~~is rejected by~~ 3  
 $H_0: \mu_1 = \mu_2$  flat show  
 that there is no difference  
 $H_0$  the two populations.

Explains  
not  
Explains  
not









