

“HSMD: HUMAN SKIN MICROBIOME DATABASE”

Project report submitted in partial fulfilment of the requirement for
the degree of Bachelor of Technology

In

Bioinformatics

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To



BONAFIDE CERTIFICATE

This is to certify that this project report entitled “**HSMD: Human Skin Microbiome Database**”, submitted to Jaypee University of Information Technology, Waknaghat, is a bonafide record of work done by “**Jatin Sharma, Namrata Thakur and Diksha Sharma**” for the degree of B.Tech Bioinformatics has been carried out under my supervision.

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Declaration by Authors

This is to affirm that this report title “**HSMD: Human Skin Microbiome Database**” has been written by us i.e. Jatin Sharma, Namrata Thakur and Diksha Sharma under the supervision of Dr. Jayashree Ramana. No part of the report has been plagiarized from other sources. All information included from other sources have been duly acknowledged. I aver that if any part of the report is found to be plagiarized, I shall take full responsibility for it.

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Acknowledgement

We would like to express our special thanks of gratitude to our project guide **Dr. Jayashree Ramana**, Assistant Professor, Department of Biotechnology and Bioinformatics Jaypee University of Information Technology, Waknaghat who helped us in conceptualizing the project and actual building of procedures used to complete the project.

We would also like to thank **Dr. Sudhir Kumar**, our Head of department for providing us with this opportunity to work on a project like this, which helped us in doing a lot of research and came to know about so many things.

Lastly we would like to thank our family and friends who supported us throughout the project and willingly extended their help every time we required.

Thanking you,

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LIST OF ABBREVIATION

HTML	Hypertext Markup Language
CSS	Cascading Style Sheet
JS	Java Script
PHP	Hypertext Preprocessor

ABSTRACT

HSMD (Human Skin Microbiome Database): It is the web site created such that it will provide data about microorganisms that are responsible for causing various disorders of human skin.

Microbiome is the combined genetic material of the microorganisms in a particular environment.

Chapter 01.

INTRODUCTION

Human skin that is known to be the largest organ has a diverse environment of microorganisms (that are harmful or even may be beneficial to us). These microorganisms colonize the human skin. Colonization is dependent on several factors such as topographical location, endogenous host and exogenous ecological factors and thus biome of our skin's surface directs their colonization. Skin microbiota is controlled by the immune responses (innate and adaptive). As human skin is diverse and vary from person to person, several molecular methods are being raised so as to view the bacteria that are residing on the human skin. Microbiome's study is augmented and it's even necessary to understand microbial involvement in diseases related to skin. This will assist in antimicrobial and pro- microbial ways and treatment.

Skin's environment consists of diverse habitats. The main role of the human skin is to act as physical barrier, regulate the body temperature, protect from harmful effects of various radiations and eliminate toxic substances in form of sweat. Our skin is also an edge to the outside surroundings. Microorganisms in the form of bacteria, viruses and fungi colonizes the skin though harmful in nature, plays a major role such as Symbiotic bacteria take up a huge range of skin niches. These defend from attack by more pathogenic or harmful organisms. These microorganisms even have a role to play in our cell mediated immunity as they train T cells to react to identical microbes.

The diverse habitat of skin environment is a collection of living biological and physical components. The balance between host organism and microorganism needs to be understood. If the balance in either way is destroyed, it can result in various skin infections and diseases. Amongst their balance reasons of distress can be either exogenous or endogenous.

Microbiome, the colony of vast microorganisms (bacteria, viruses and fungi) possess specific environment and also the collection of microorganisms that are present on the human body. This collated environment of genomes of microorganisms specifically found on the human body form one colony that makes up the Microbiome.

Or simply we can say that microbiome is generally referred to all microbes belonging to a community. While sometimes it even is referred to as collection of microbes' genes in a community.

CHAPTER 02.

OBJECTIVE

To develop a web server that:

- Archives all the data about the skin microbiome available in literature.
- Provide the scientific community with information on prokaryotic species that are present on the human skin in various diseases.

CHAPTER 03.

LITERATURE REVIEW

As we know, psoriasis is a condition where building up of skin cells occur and scaly, itchy and dry patches get formed.

Yan D et al. in their paper “The Role of the Skin and Gut Microbiome in Psoriatic Disease” reported about changes observed in the psoriatic disease.

For this a number of studies were conducted by them on skin and gut micobiota in psoriatic patients and non-diseased individuals. Gut microbiome was collected from stool and skin microbiome through biopsy, or skin swabs with or without culturing. The study showed a trend towards an increased relative abundance of Streptococcus , along with decreased level of Propionibacterium in psoriasis patients compared to healthy individuals. In the gut microbiome, the ratio of Firmicutes and Bacteroidetes was ruffled in psoriatic individuals compared to healthy controls. Actinobacteria was also relatively underrepresented.

From this study, a large composition of microbiomes was observed in psoriatic patients. These microbiomes are even responsible for additional diseases along with psoriasis. Propionibacterium which are known for various functions in a human body, like modulating the immune system, their loss can therefore lead to decreased immune tolerance and increased propensity for psoriatic inflammation. Likewise increase in Streptococcus may play a pathogenic role in psoriasis as streptococcal infections have been associated with the later development of guttate psoriasis and the worsening of chronic plaque psoriasis. Changes in the abundance of Staphylococcus in psoriatic skin are less consistent.

It remains unclear whether the observed differences in the microbiota have a causal role in psoriasis or are a consequence of alterations in the environmental milieu from psoriasis.

CHAPTER 04.

MATERIAL A ND METHODS

4.1 PROTOCOL

Data collection (organisms involved in skin microbiota)



Taxonomic study (classification and complete hierarchical data)



Collection of 16s rRNA



Linking organism data to other databases like strain info, ncbi etc.



Preparing a database for skin Microbiome

4.2 STEPS FOLLOWED

1. Research papers are collected from PubMed using keywords such as “skin diseases”, “human skin AND Microbiome” ,”skin AND Microbiome”, “[disease name] AND Microbiome”, “skin microbiota” etc.
2. After reading these papers, PMID are collected from these.
3. Then in NCBI this ID is used by selecting ‘BioProject’ in the drop down menu.
4. Then biosample is selected.
5. Click on first link.
6. SRA link is clicked and then click on ‘Run’.
7. Out of certain options given go to “analysis”.
8. Then a table containing names of microorganisms appear. This data is maintained in a form of excel sheet.
9. For each microorganism their taxonomical data is collected.
10. Database is prepared.
11. Using HTML, PHP and CSS, a home page of website is created where certain pages are linked.

4.3 Use of computational languages:

4.3.1 HTML – (Hyper Text Markup Language)

The back-end language that is used for developing web page.

For Home Page :

```
1 <!DOCTYPE html>
2 <html>
3 <head>
4 <meta http-equiv="Content-Type" content="text/html; charset=utf-8" />
5 <link href="images/logo.jpg" rel="shortcut icon">
6 <link rel="stylesheet" type="text/css" href="css/style.css" />
7 <script type="text/javascript" src="js/jquery.min.js"></script>
8 <script type="text/javascript" src="js/jquery.easing.min.js"></script>
9 <script type="text/javascript" src="js/jquery.nivo.slider.pack.js"></script>
10 <script type="text/javascript">
11     $(window).load(function() {
12         $('#slider').nivoSlider();
13     });
14 </script>
15 <title>HSMD-home page</title>
16 <meta name="keywords" content="" />
17 <meta name="description" content="" />
18 <link href="http://fonts.googleapis.com/css?family=Source+Sans+Pro:200,300,400,600,700,900" rel="stylesheet" />
19 <link href="default.css" rel="stylesheet" type="text/css" media="all" />
20 <link href="fonts.css" rel="stylesheet" type="text/css" media="all" />
21
22 </head>
23 <body>
24 <div id="header-wrapper">
25 <div id="header" class="container">
26 <div id="logo">
27     <font size="6" face="Arial"><a href="#"><strong>HSMD</strong></a></font>
28 </div>
29 <br>
30 <div id="menu">
31 <ul><font size="3" face="Arial">
32     <li class="current page item"><a href="#" accesskey="1" title="">Homepage</a></li>
```

Figure 4. 1 HTML file for Home Page


```

33     <li><a href="database.html" title="">Database</a></li>
34     <li><a href="contact.html" accesskey="4" title="">Contact Us</a></li>
35
36     </font>
37 </ul>
38 </div>
39 </div>
40 </div>
41 <div id="page" class="container">
42 <div id="site content">
43 <div id="content">
44 <div class="title">
45 <h2>Welcome to our website</h2>
46 <div id="banner_image">
47 <div id="slider-wrapper">
48 <div id="slider" class="nivoSlider">
49 
50 
51 
52 
53
54 </div><!--close slider-->
55 </div><!--close slider_wrapper-->
56 </div><!--close banner_image-->
57 <font size="4" face="Arial">
58 <p>This website is dedicated to <strong> database</strong> for<strong> human skin microbiome</strong>
59 which will present a provisional naming scheme for the currently unnamed species so that strain,
60 clone, and probe data from any laboratory can be directly linked to a stably named reference scheme.</p>
61 <p>To discuss more about the information, the links are given on the sidebar.</p>
62 </font>
63 </div>

```

Figure 4.2 HTML file for Home Page

```

64 | </div>
65 | <div id="sidebar">
66 |   <ul class="style1">
67 |     <li class="first">
68 |       <h2><I><font color = "purple">About the Human Skin Microbiome : </font></I></h2>
69 |       <div style="clear: both;">&nbsp;</div>
70 |       <h3></h3>
71 |       <p><font size="4">The skin is the human body's largest organ,
72 |         colonized by a diverse milieu of microorganisms, most of which are harmless
73 |         or even beneficial to their host.
74 |       </p>
75 |
76 |     </li>
77 |     <li>
78 |       <p><font size="4"> Colonization is driven by the ecology of the skin surface,
79 |         which is highly variable depending on topographical location, endogenous host factors and exogenous
80 |         environmental factors. The cutaneous innate and adaptive immune responses can modulate the skin microbiota
81 |         , but the microbiota also functions in educating the immune system. The development of molecular methods
82 |         to identify microorganisms has led to an emerging view of the resident skin bacteria as highly diverse
83 |         and variable. An enhanced understanding of the skin microbiome is necessary to gain insight into microbial
84 |         involvement in human skin disorders and to enable novel promicrobial and antimicrobial therapeutic
85 |         approaches for their treatment.
86 |       <a href="https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3535073/"><font color="blue"><b>See more...</b></font></a>
87 |     </li>
88 |   </ul>
89 | </div>
90 | </div>
91 | </div>
92 | <div id="footer-wrapper">
93 |   <div id="footer" class="container">

```

Figure 4.3 HTML file for Home Page

```

94 |   <div class="col-md-12 text-center">
95 |     <div style="clear: both;">&nbsp;</div>
96 |     <p><font color="white">Copyright &copy; 2017 | Human Skin Microbiome Database</font></p>
97 |     <div style="clear: both;">&nbsp;</div>
98 |   </div>
99 | </div>
100 | </body>
101 | </html>
102 |

```

Figure 4.4 HTML file for Home Page

4.3.2 PHP (Hypertext Pre-processor)

This is a server side scripting language that is usually designed for the web development and is even used generally as a programming language. Here we used this language for our database page.

For Database Page:

```
1 <!DOCTYPE html>
2 <html>
3 <head>
4 <meta http-equiv="Content-Type" content="text/html; charset=utf-8" />
5 <link href="images/logo.jpg" rel="shortcut icon">
6 <link rel="stylesheet" type="text/css" href="css/style.css" />
7 <title>Search page</title>
8 <meta name="keywords" content="" />
9 <meta name="description" content="" />
10 <link href="http://fonts.googleapis.com/css?family=Source+Sans+Pro:200,300,400,600,700,900" rel="stylesheet" />
11 <link href="default.css" rel="stylesheet" type="text/css" media="all" />
12 <link href="fonts.css" rel="stylesheet" type="text/css" media="all" />
13
14 <!--[if IE 6]><link href="default_ie6.css" rel="stylesheet" type="text/css" /><![endif]-->
15 <?php
16
17     session_start();
18     require('dbconfig.php');
19     $conn = mysqli_connect($servername, $username, $password, $dbname);
20
21     if (!$conn) {
22         die("Connection failed: " . mysqli_connect_error());
23     }
24
25     $userTable = "taxon_description";
26
27     $sql = "SELECT * FROM $userTable";
28     $result = mysqli_query($conn, $sql);
29
30
31 ?>
```

Figure 4.5 Code for .php file

```
32 </head>
33 <body>
34 <div id="header-wrapper">
35 <div id="header" class="container">
36 <div id="logo">
37 <font size="6" face="Arial"><a href="#"><strong>HSMD</strong></a></font>
38 </div>
39 <div id="menu">
40 <ul><font size="3" face="Arial">
41 <li><a href="index.html" accesskey="1" title="">Homepage</a></li>
42 <li><a href="database.php" title="">Database</a></li>
43 <li><a href="contact.html" accesskey="4" title="">Contact Us</a></li>
44 </font>
45 </ul>
46 </div>
47 </div>
48 </div>
49 <div id="page" class="container">
50 <div id="site_content">
51 <div class="content">
52 <br><br><br>
53
54
55
56 <div class="post">
57 <p></p>
58 <font size="4" color="red"><U>TAXON DESCRIPTION:</U></font></h3><br>
59 <div style="clear: both;">&nbsp;</div>
60 <div style="clear: both;">&nbsp;</div>
61 <div class="entry">
```

Figure 4.6 Code for .php file

...contd.

```
62
63
64     <table border="1" cellpadding="10">
65
66         <tr>
67
68             <th width="200" align="left"><b><font color="black">ID</font></b></th>
69             <th width="200" align="left"> <b><font color="black">SuperKingdom</b></font></th>
70             <th width="200" align="center"><b><font color="black">Organism</b></font></th>
71             <th width="150" align="center"><font color="black">Rank</font></th>
72             <th width="200" align="center"> <b> <font color="black">Description</b></font></th>
73
74         </tr>
75
76     <?php
77
78     if(mysqli_num_rows($result) > 0){
79
80     while($row = mysqli_fetch_assoc($result)) {
81         $unique = $row['ID'];
82         echo '
83
84         <tr>
85         <td width="100" align=" left">'. $row['ID']. '</td>
86         <td width="100" align="left">'. $row['SuperKingdom']. '</td>
87         <td width="100" align="center"><i>'. $row['Organism']. '<i></td>
88         <td width="100" align="center">'. $row['Rank']. '</td>
89         <td width="100" align="center"><a href="one.php?unique=' . $unique. '">
90         <input type="submit" value="Click here!"></a></td>
91
```

Figure 4.7 Code for .php file

```
92
93
94     }
95
96     }
97     ?>
98
99
100
101     </table>
102     </div>
103
104
105
106     <div style="clear: both;">&nbsp;</div>
107     <div style="clear: both;">&nbsp;</div>
108 </div>
109 </div>
110 </div>
111 <div id="footer-wrapper">
112 <div id="footer" class="container">
113 <div class="col-md-12 text-center">
114 <div style="clear: both;">&nbsp;</div>
115 <p><font color="white">Copyright &copy; 2017 | Human Skin Microbiome Database</font></p>
116 <div style="clear: both;">&nbsp;</div>
117 </div>
118 </div>
119 </body>
120 </html>
```

Figure 4.8 Code for .php file

4.3.3 CSS - (Cascading Style Sheets)

It is used to describe how HTML elements are to be displayed on screen. It is used for saving a lot of work.

```
8  body {
9      margin: 0;
10     padding: 0;
11     background: #C5DA99 url(images/img01.jpg) repeat;
12     font-family: Arial, Helvetica, sans-serif;
13     font-size: 14px;
14     color: #787878;
15 }
16
17  h1, h2, h3 {
18     margin: 0;
19     padding: 0;
20     font-weight: normal;
21     font-family: 'Abel', sans-serif;
22     color: #3DA29B;
23 }
24
25  h1 {
26     font-size: 2em;
27 }
28
29  h2 {
30     font-size: 2.8em;
31 }
32
33  h3 {
34     font-size: 1.6em;
35 }
36
37  p, ul, ol {
38     margin-top: 0;
39     line-height: 180%;
```

Figure 4.9 Code for .css file

...contd.

```
40  | }
41
42  | ul, ol {
43  | }
44
45  | a {
46  |     text-decoration: none;
47  |     color: #5E5E5E;
48  | }
49
50  | a:hover {
51  | }
52
53  | #wrapper {
54  |     padding-top: 50px;
55  | }
56
57  | .container {
58  |     width: 1000px;
59  |     margin: 0px auto;
60  | }
61
62  | /* Header */
63
64  | #header-wrapper {
65  |     overflow: hidden;
66  |     height: 140px;
67  | }
68
69  | #header {
70  |     width: 900px;
```

Figure 4.10 Code for .css file

...contd.

```
71     height: 100px;
72     margin: 0 auto;
73     padding: 0px 50px;
74     background: url(images/img02.jpg) repeat;
75 }
76
77 /* Logo */
78
79 #logo {
80     float: left;
81     width: 300px;
82     margin: 0;
83     padding: 0;
84     color: #FFFFFF;
85 }
86
87 #logo h1, #logo p {
88 }
89
90 #logo h1 {
91     line-height: 100px;
92     letter-spacing: -2px;
93     text-transform: lowercase;
94     font-size: 3.8em;
95 }
96
97 #logo h1 a {
98     color: #FFFFFF;
99     text-shadow: 1px 1px 0px rgba(0,0,0,.2);
100 }
101
```

Figure 4.11 Code for .css file

```
438 /* Footer */
439
440 #footer {
441     height: 100px;
442     margin: 0 auto;
443     padding: 0px 0 15px 0;
444     font-family: 'Abel', sans-serif;
445 }
446
447 #footer p {
448     margin: 0;
449     padding-top: 10px;
450     letter-spacing: 1px;
451     line-height: normal;
452     font-size: 14px;
453     text-transform: uppercase;
454     text-align: center;
455     color: #527800;
456 }
457
458 #footer a {
459     color: #527800;
460 }
```

Figure 4.12 Code for .css file

4.3.4 JavaScript

It is used for making web pages interactive and provides online programs.

```
2  (function() {
3      var method;
4      var noop = function () {};
5      var methods = [
6          'assert', 'clear', 'count', 'debug', 'dir', 'dirxml', 'error',
7          'exception', 'group', 'groupCollapsed', 'groupEnd', 'info', 'log',
8          'markTimeline', 'profile', 'profileEnd', 'table', 'time', 'timeEnd',
9          'timeStamp', 'trace', 'warn'
10     ];
11     var length = methods.length;
12     var console = (window.console = window.console || {});
13
14     while (length--) {
15         method = methods[length];
16
17         if (!console[method]) {
18             console[method] = noop;
19         }
20     }
21 }());
22
23
24 if (typeof Object.create !== 'function') {
25     Object.create = function(obj) {
26         function F() {}
27         F.prototype = obj;
28         return new F();
29     };
30 }
31
32 (function($, window, document, undefined) {
33     "use strict";
```

Figure 4.13 Code for .js file

...contd.

```
171         return section || this.$links[0].hash;
172     }
173 };
174
175 $.fn.singlePageNav = function(options) {
176     return this.each(function() {
177         var singlePageNav = Object.create(SinglePageNav);
178         singlePageNav.init(options, this);
179     });
180 };
181
182 $.fn.singlePageNav.defaults = {
183     offset: 0,
184     threshold: 120,
185     speed: 400,
186     currentClass: 'current',
187     easing: 'swing',
188     updateHash: false,
189     filter: '',
190     onComplete: false,
191     beforeStart: false
192 };
193
194 })(jQuery, window, document);
195
```

Figure 4.14 Code for .js file

CHAPTER 05.

RESULTS

After collection of data from several papers and resources on human skin Microbiome, we collected the data and assembled them into one common excel file and then worked on site where we created three pages (i.e. home page, database page where collection of data is represented and further links are given in it regarding taxonomy , and lastly the contact page).

Home page:

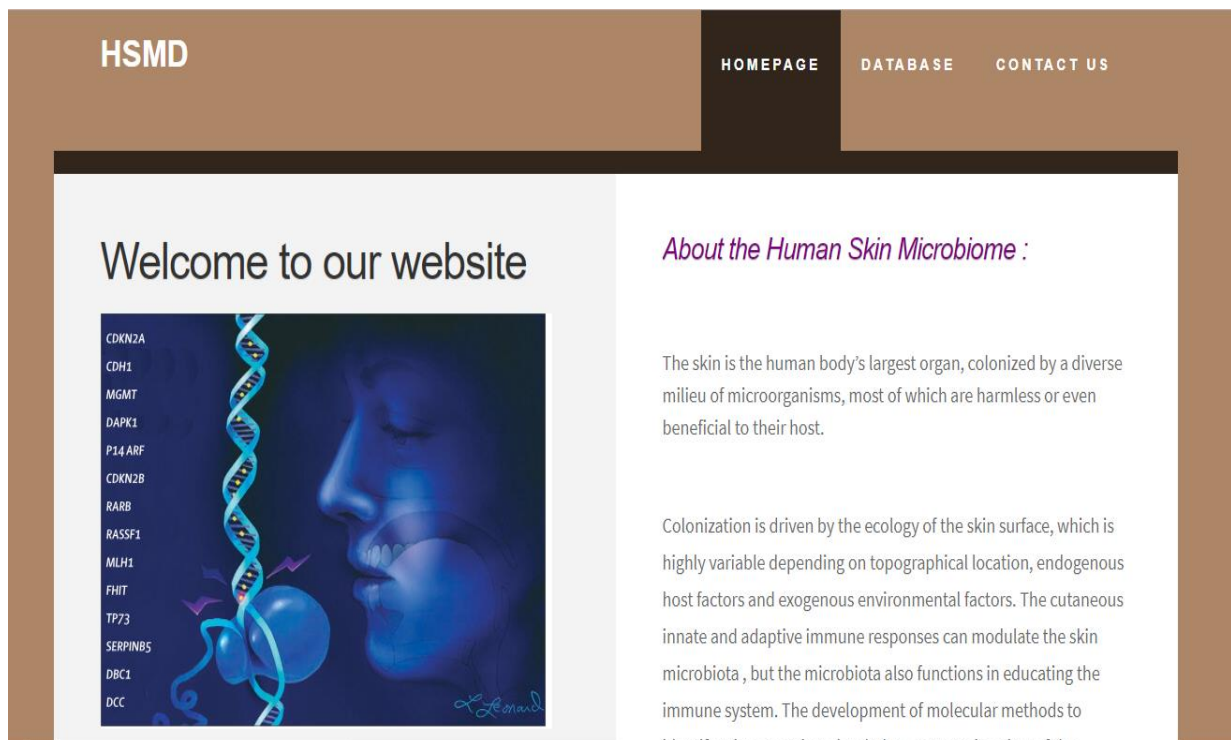


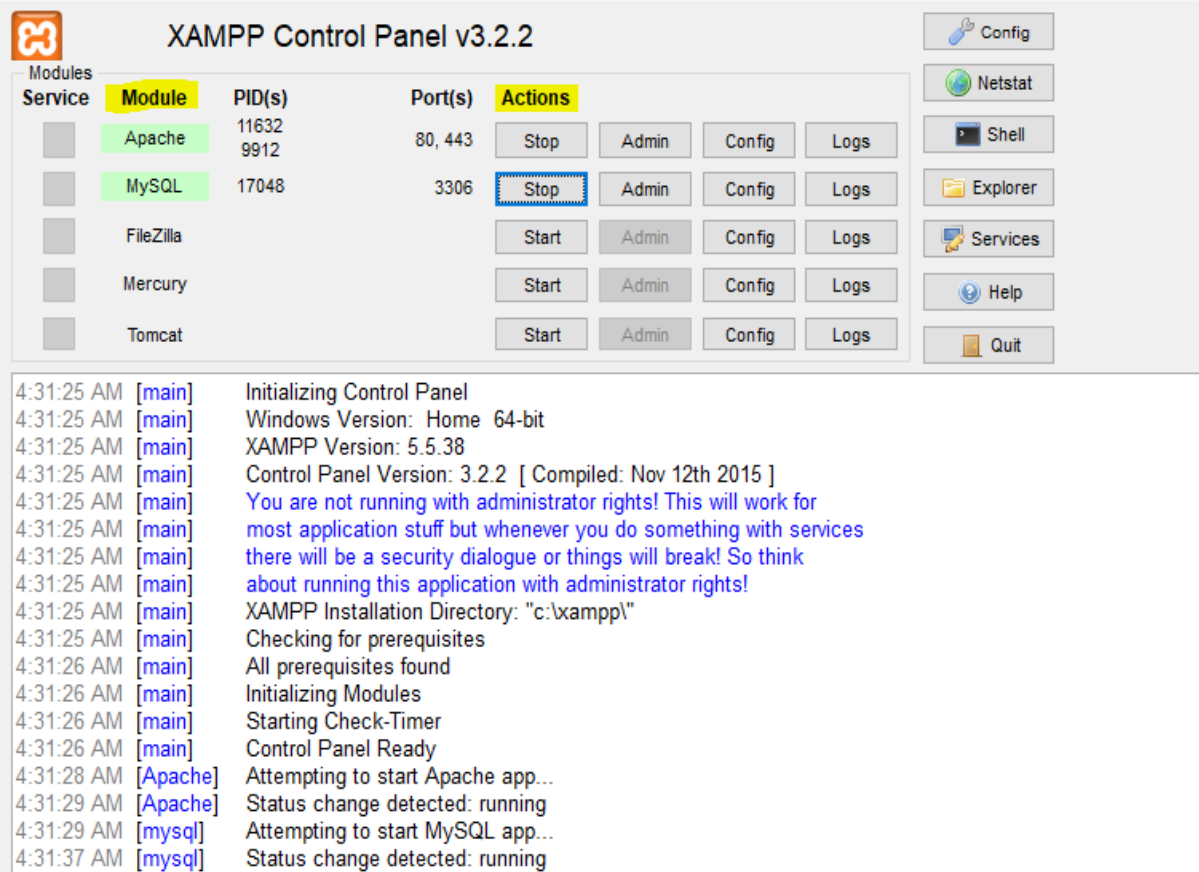
Figure 5.1 View of the homepage

Database page:

For this page, certain steps were performed:

1. Install xampp in the system. Then in the folder named xampp we have another folder 'htdocs'. Here create your folder (name given as 'hsmd'). In this store your all files like html files, sql file, css file, js file and others.
2. Excel sheet containing the data was converted into .csv file.
3. Then xampp control panel was run. Actions for module (apache and MySQL) were started.

XAMPP Control Panel v3.2.2 [Compiled: Nov 12th 2015]



Service	Module	PID(s)	Port(s)	Actions
<input type="checkbox"/>	Apache	11632 9912	80, 443	Stop Admin Config Logs
<input type="checkbox"/>	MySQL	17048	3306	Stop Admin Config Logs
<input type="checkbox"/>	FileZilla			Start Admin Config Logs
<input type="checkbox"/>	Mercury			Start Admin Config Logs
<input type="checkbox"/>	Tomcat			Start Admin Config Logs

4:31:25 AM [main] Initializing Control Panel
4:31:25 AM [main] Windows Version: Home 64-bit
4:31:25 AM [main] XAMPP Version: 5.5.38
4:31:25 AM [main] Control Panel Version: 3.2.2 [Compiled: Nov 12th 2015]
4:31:25 AM [main] You are not running with administrator rights! This will work for most application stuff but whenever you do something with services there will be a security dialogue or things will break! So think about running this application with administrator rights!
4:31:25 AM [main] XAMPP Installation Directory: "c:\xampp\
4:31:25 AM [main] Checking for prerequisites
4:31:26 AM [main] All prerequisites found
4:31:26 AM [main] Initializing Modules
4:31:26 AM [main] Starting Check-Timer
4:31:26 AM [main] Control Panel Ready
4:31:28 AM [Apache] Attempting to start Apache app...
4:31:29 AM [Apache] Status change detected: running
4:31:29 AM [mysql] Attempting to start MySQL app...
4:31:37 AM [mysql] Status change detected: running

Figure 5.2 While XAMPP Control Panel is made to run

- In the chrome we open localhost/phpmyadmin. Here we create database.
- Then .csv file is imported using load data.

#	Name	Type	Collation	Attributes	Null	Default	Extra	Action
1	Pri_ID	int(3)			No	None	AUTO_INCREMENT	Change Drop Primary Unique Index Spatial More
2	ID	int(3)			Yes	NULL		Change Drop Primary Unique Index Spatial More
3	SuperKingdom	varchar(8)			Yes	NULL		Change Drop Primary Unique Index Spatial More
4	Organism	varchar(45)			Yes	NULL		Change Drop Primary Unique Index Spatial More
5	Rank	varchar(13)			Yes	NULL		Change Drop Primary Unique Index Spatial More
6	Description	varchar(10)			Yes	NULL		Change Drop Primary Unique Index Spatial More

Figure 5.3 Image showing structure of 'taxon_description' table

#	Name	Type	Collation	Attributes	Null	Default	Extra	Action
1	Pri_ID	int(3)			No	None	AUTO_INCREMENT	Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
2	ID	int(3)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
3	Organism	varchar(45)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
4	NCBI_Taxonomy_id	varchar(8)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
5	NCBI_Taxonomy_ID_Link	varchar(114)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
6	Type_Strain	varchar(14)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
7	Straininfo_Link	varchar(97)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
8	SuperKingdom	varchar(8)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
9	Class_Domain	varchar(8)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
10	Class_Phylum	varchar(19)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
11	Class_Class	varchar(21)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
12	Class_Order	varchar(19)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
13	Class_Family	varchar(20)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
14	Class_Genus	varchar(17)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
15	Class_Species	varchar(31)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
16	16sRNA_Sequence	varchar(90)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
17	PubmedID	varchar(11)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
18	Pubmed_Search	varchar(14)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
19	Pubmed_Search_Link	varchar(75)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
20	Nucleotide_search	varchar(14)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
21	Nucleotide_Search_Link	varchar(76)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
22	Protein_Search	varchar(14)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
23	Protein_Search_link	varchar(76)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
24	ACCESSION	varchar(14)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns
25	Disease	varchar(21)			Yes	NULL		Change Drop Primary Unique Index Spatial Fulltext Distinct values Add to central columns

Figure 5.4 Image showing the structure for 'description' table linked to table 'taxon_description'

6. Database created is then exported and stored in the folder created in htdocs of xampp folder in C drive.

In the database page in order to see the taxon description, under the description column click on the “click here” button .

Then,

You will obtain a “taxon description” page like this :

Porphyromonas sp. KLE 1280

HSMD ID : 80
Organism : Porphyromonas sp. KLE 1280
Disease : atopic dermatitis
Accession ID : LT801206
NCBI Taxonomy ID : [1496](#)
Type Strain : CCUG 14451
(more info at [StrainInfo](#))

Classification :

Superkingdom	Bacteria
Domain	Bacteria
Phylum	Bacteroidetes
Class	Bacteroidetes
Order	Bacteroidales
Family	Porphyromonadaceae
Genus	Porphyromonas
Species	sp. KLE 1280

16sRNA sequence: [Click here!](#)

Pubmed ID: 1421670
Pubmed Search: [244](#)
Nucleotide Search: [3070](#)
Protein Search: [39868](#)

Figure 5.5 Image showing Human skin microbiome description for *Porphyromonas species*

In this page we will obtain taxon description of the microorganism found on the human skin , responsible for diseases . This will contain information about:

1. HSMD ID
2. Organism Name
3. Disease Caused By the Oragnism
4. Accession ID
5. NCBI Taxonomy ID
6. Type Strain
7. Hierarchical Classification
8. 16sRNA sequence
9. Pubmed ID
10. Nucleotide Search ID
11. Protein Search ID

Here in this description page you can view the above mentioned by clicking on the links .

For example, in the shown image if we click on “click here”, a page will be displayed showing 16s RNA sequence.

16sRNA sequence:	Click here!
Pubmed ID:	1421670
Pubmed Search:	<u>244</u>
Nucleotide Search:	<u>3070</u>
Protein Search:	<u>39868</u>



Figure 5.6 example showing where one can get more information through

Porphyromonas sp. partial 16S rRNA gene, isolate Otu000261

GenBank: LT801206.1

[FASTA](#) [Graphics](#)

Go to: 

```
LOCUS       LT801206                426 bp    DNA     linear   ENV 20-NOV-2017
DEFINITION Porphyromonas sp. partial 16S rRNA gene, isolate Otu000261.
ACCESSION  LT801206
VERSION    LT801206.1
DBLINK     BioProject: PRJEB19934
KEYWORDS   ENV.
SOURCE     Porphyromonas sp.
  ORGANISM Porphyromonas sp.
            Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales;
            Porphyromonadaceae; Porphyromonas.
REFERENCE  1
AUTHORS    Vanlancker,E.
TITLE      Direct Submission
JOURNAL    Submitted (10-MAR-2017) GHENT UNIVERSITY, Center for Microbial
            Ecology and Technology (CMET), Coupure Links 653, 9000 Ghent,
            Belgium
FEATURES   Location/Qualifiers
   source   1..426
            /organism="Porphyromonas sp."
            /mol_type="genomic DNA"
            /isolate="Otu000261"
            /isolation_source="Human gut in vitro model"
            /db_xref="taxon:1924944"
            /environmental_sample
   gene     <1..>426
            /gene="16S rRNA"
   rRNA     <1..>426
            /gene="16S rRNA"
            /product="16S ribosomal RNA"
```

Figure 5.7 Image shows data for 16s RNA sequence on click

And similarly if we click on another link as follows:

Pubmed ID:	1421670
Pubmed Search:	<u>244</u>
Nucleotide Search:	<u>3070</u>
Protein Search:	<u>39868</u>




Figure 5.8 example showing where one can get more information about pubmed

Article types

Clinical Trial
Review
Customize ...

Text availability

Abstract
Free full text
Full text

Publication dates

5 years
10 years
Custom range...

Species

Humans
Other Animals

[Clear all](#)

[Show additional filters](#)

Format: Summary Sort by: Most Recent Per page: 20

Send to

Best matches for **Porphyromonas sp**:

[Porphyromonas bronchialis sp. nov.](#) Isolated from Intraoperative Bronchial Fluids of a Patient with Non-Small Cell Lung Cancer.

Sato T et al. Tohoku J Exp Med. (2015)

[Porphyromonas pasteri sp. nov.](#), isolated from human saliva.

Sakamoto M et al. Int J Syst Evol Microbiol. (2015)

[Porphyromonas pogonae sp. nov.](#), an anaerobic but low concentration oxygen adapted coccobacillus isolated from lizards (*Pogona vitticeps*) or human clinical specimens, and emended description of the genus **Porphyromonas** Shah and Collins 1988.

Kawamura Y et al. Syst Appl Microbiol. (2015)

[Switch to our new best match sort order](#)

Search results

Items: 1 to 20 of 244

<< First < Prev Page 1 of 13 Next > Last >>

[Linking Antimicrobial Potential of Natural Products Derived from Aquatic Organisms and Microbes](#)

1. [Involved in Alzheimer's Disease - A Review.](#)

Stojkovic D, Kostic M, Smiljkovic M, Aleksic M, Vasiljevic P, Nikolic M, Sokovic M.
Curr Med Chem. 2018 Mar 8. doi: 10.2174/0929867325666180309103645. [Epub ahead of print]
PMID: 29521212

Figure 5.9 Image shows pubmed data

Contact Page:

Through this page, information can be obtained regarding the skin Microbiome from the authors.

The screenshot shows a contact page with a light gray background. On the left, there is a form titled "Send a Message". Below the title, it says "Here you can contact us for more information and the database we've created!!". The form has three input fields: "Name", "Email Address", and "Message". Below the "Message" field is a "Send" button. On the right, under the heading "Our Contact:", the authors are listed as "Jatin Sharma, Namrata Thakur, Diksha Sharma" with the role "Web Designer & Data collector". Below this, three email addresses are listed: "jatins925@gmail.com", "thakurnamrata07@gmail.com", and "sharmadiksha236@gmail.com". At the bottom right, the department and university are listed: "Department of Biotechnology and Bioinformatics", "Jaypee University of Information Technology", "Waknaghat, Solan", and "Himachal Pradesh (INDIA)".

Figure 5.10 Contact page of database

CHAPTER 06.

CONCLUSION

This HSMD site provides biological entries for each species and an extensive catalogue of genes that these microbes express along with the entire genome of species, protein information, strain information, taxonomical classification, sequence of 16srRNA and a few more information.

REFERENCES

1. Emma Barnard, Baochen Shi, Dezhi Kang, Noah Craft and Huiying Li. The balance of metagenomic elements shapes the skin microbiome in acne and health.
2. Yan D, Issa N, Afifi L, Jeon C, Chang HW, Liao W. The Role of the Skin and Gut Microbiome in Psoriatic Disease. Available from: doi: 10.1007/s13671-017-0178-5
3. Akemi TAKEMOTO, Otomi CHO, Yuka MOROHOSHI, Takashi SUGITA, Masahiko MUTO. Molecular characterization of the skin fungal microbiome in Patients with psoriasis.
4. Yanhan Wang, Sherwin Kuo, Muya Shu, Jinghua Yu, Stephen Huang, Ashley Dai, Aimee Two, Richard L. Gallo, Chun-Ming Huang. Staphylococcus epidermidis in the human skin Microbiome mediates fermentation to inhibit the growth of Propionibacterium acnes: implications of probiotics in acne vulgaris.
5. Di Yan, Naiem Issa, Ladan Afifi, Caleb Jeon, Hsin-Wen Chang & Wilson Liao. The Role of the Skin and Gut Microbiome in Psoriatic Disease.
6. Patrick L.J.M. Zeeuwen, Michiel Kleerebezem, Harro M. Timmerman, and Joost Schalkwijk. Microbiome and skin diseases.
7. Richard L. Gallo. Human Skin Is the Largest Epithelial Surface for Interaction with Microbes.
8. Brigitte Dreno, Richard Martin, Dominique Moyal, Jessica B. Henley, Amir Khammari and Sophie Seit . Skin Microbiome and acne vulgaris : STAPHYLOCOCCUS, a new vector in acne.

9. Julia Oh, Allyson L. Byrd, Morgan Park, NISC Comparative Sequencing Program, Heidi H. Kong, Julia A. Segre. Temporal Stability of the Human Skin Microbiome.
10. Lauren Seale, Leah A. Cardwell & Steven R. Feldman (2018): Adherence to biologics in patients with psoriasis, Expert Review of Clinical Immunology, DOI: 10.1080/1744666X.2018.1427065
11. <http://www.straininfo.net/>
12. <https://www.ncbi.nlm.nih.gov/>
13. Neto JF, Tchornobay AM . Como o clipping pode auxiliar o dermatologista. An Bras Dermatol. 2009;84:173-176.
14. Werner B, Antunes A. Microscopic examination of normal nail clippings. Dermatol Pract Concept. 2013;3:9-14.
15. Stephen S, Tosti A, Rubin AI. Diagnostic applications of nail clippings. Dermatol Clin. 2015; 33:289-301.
16. Wilsmann-Theis D, Sareika F, Bieber T, et al. New reasons for histo- pathological nail-clipping examination in the diagnosis of onychomycosis. J Eur Acad Dermatol Venereol. 2011;25:235-237.
17. Werner B, Fonseca GP, Seidel G. Microscopic nail clipping findings in patients with psoriasis. Am J Dermatopathol. 2015;37:429-439.
18. Van Der Velden HMJ, Klaassen KMG, Van De Kerkhof PCM, et al. Fingernail psoriasis reconsidered: a case-control study. J Am Acad Dermatol. 2013;69:245-252.
19. Garzitto A, Ricceri F, Tripo L, et al. Possible reconsideration of the Nail Psoriasis Severity Index (NAPSI) score. J Am Acad Dermatol.

20. Mukai MM, Werner B, Filho J, et al. NAPSÍ utilization as an evaluation method of nail psoriasis. *An Bras Dermatol.* 2012;87:256-262.