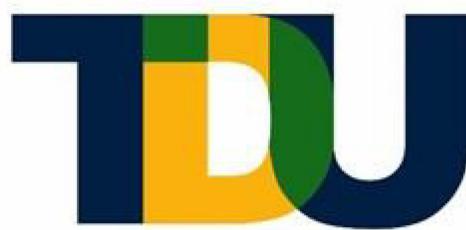


**Analysis of hospital based Ayurvedic clinical practice to gain
Real World data knowledge**

**A THESIS TO BE SUBMITTED TO
THE UNIVERSITY OF TRANS-DISCIPLINARY
HEALTH SCIENCES AND TECHNOLOGY**



**THE UNIVERSITY OF TRANS-DISCIPLINARY
HEALTH SCIENCES & TECHNOLOGY**

**FOR THE AWARD OF THE DEGREE OF
DOCTOR OF PHILOSOPHY
BY
Vinay Mahajan
UNDER THE GUIDANCE OF
Dr. Ashwini Godbole**

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THE UNIVERSITY OF TRANS-DISCIPLINARY HEALTH
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DECLARATION BY THE CANDIDATE

I declare that this thesis entitled “Analysis of hospital based Ayurvedic clinical practice to gain Real World data knowledge” submitted for the award of Doctor of Philosophy to THE UNIVERSITY OF TRANS-DISCIPLINARY HEALTH SCIENCES AND TECHNOLOGY, Bengaluru, is my original work, conducted under the supervision of my guide Dr. Ashwini Godbole. I also wish to inform that no part of the research has been submitted for a degree or examination at any university. References, help and material obtained from other sources have been duly acknowledged.

I hereby confirm the originality of the work and that there is no plagiarism in any part of the dissertation.

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CERTIFICATE

This is to certify that the work in this thesis “Analysis of hospital based Ayurvedic clinical practice to gain Real World data knowledge” submitted by Vinay Mahajan was carried out under my supervision. No part of this thesis has been submitted for a degree or examination at any university. References, help and material obtained from other sources have been duly acknowledged. I hereby confirm the originality of the work and that there is no plagiarism in any part of the dissertation.



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Acronyms

- ACD: Ayurvedic Classification Dictionary
A-HMIS: Ayurveda Hospital Management Information System
AYUSH: Ayurveda, Yoga and Naturopathy, Unani, Siddha and Homeopathy
CCRAS: Central Council for Research in Ayurvedic Sciences
CDISC: Clinical Data Interchange Standards Consortium
COPD: Chronic Obstructive Pulmonary Disease
COSTART: Coding Symbols for Thesaurus of Adverse Reaction Terms
CTC: Clinical Toxicity Grade
DARWIN EU: Data Analysis and Real-World Interrogation Network
EHR: Electronic Health Record
EMA: European Medicinal Agency
EMR: Electronic Medical Record
EU: European Union
GCP: Good Clinical Practice
GCRP: Good Clinical Research Practice
GDP: Gross Domestic Product
HM: Hospital Management
I-AIM: Institute of Ayurveda and Integrative medicines
ICD: International Classification of Diseases
ICH: International Council for Harmonization of Technical Requirements for Pharmaceuticals for Human Use
IDC: International Data Corporation
IDC: International Data Corporation
IP visit: In-Patient visit
ISO: International Organization for Standardization
LOINC: Logical Observation Identifiers Names and Codes
MedDRA: Medical Dictionary for Regulatory Activities
NCI: National Cancer Institute, USA
NEJM: New England Journal of Medicine
OP visit: Out-Patient visit
PMDA: Pharmaceuticals and Medical Devices Agency (Health Authority Japan)
RCT: Randomized Controlled Trial
RMSD: Rheumatic and Musculoskeletal disease
RWD: Real World Data
RWE: Real World Evidence
SQL: Structured Query Language
TDU: The University of Trans-Disciplinary Health Sciences & Technology
THERAN: THE Research Application Nexus
TKDL: Traditional Knowledge Digital Library
UHC: Universal Health Coverage
US FDA: US Food and Drug Administration

WHO: World Health Organization

WHO-ART: World Health Organization Adverse Reactions Terminology

WHO-DDE: World Health Organization Drug Dictionary Enhanced

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Abstract

Various electronic equipment like computers, mobile devices, wearables, and other sensors collect and store huge amounts of health-related data. This explosion of data carries potential to better design and conduct clinical studies to answer questions previously thought infeasible. Advancement of cutting-edge analytical capabilities is allowing researchers to analyze and comprehend this data at greater depths, permitting medical product development and approval at an accelerated speed [1]. Real world data (RWD) is the information relating to patient health status and/or the delivery of health care routinely collected from a variety of sources like epidemiological studies, clinical practice, already published articles to answer questions previously thought infeasible.

Approval of Ibrance by US FDA for male breast cancer, a drug already approved for females and French health authorities allowing a Real World Evidence (RWE) study of 600+ patients, over a period of 18 months, for a conditional re-imbursement scheme in COPD, are a couple of recent examples of approvals using RWD data. A study carried out by Clarivate Analytics, USA, reports 27 (non-exhaustive list), <5% of all approved drugs, examples of drug approvals by US FDA, EMA, Japan's PMDA and Health Canada, across broad spectrum of medicines between years 1998 and 2019 using RWD from Electronic Health Records and registries. These data were used either as primary data, when non-comparative data were available to demonstrate tolerability and efficacy, or as a supportive data when validating findings. This provides increasing usage of "naturally reported data" in drug approvals in modern biomedicine. These examples provide evidence of novel use of data, which may have otherwise gone unused. The power available to society would have never been unearthed if not for this way of use of RWD [2].

Is Ayurvedic area dealing with the same type of challenge of not realizing the potential of available data? Just to give a glimpse of enormity of data: more than 10 crore number of patients have been reported on AYUSH website (As of May 2020). More than 140+ countries have population of less than 10 crores [3].

It is safe to assume that the conceptual developments in Ayurvedic knowledge base have taken place through everyday observations and basic laws of nature. These fundamentals have been adjusted to the relevant times as per the passage of time based on observations and experiences, where there are no artificial restrictions on usage of medicines, duration of treatment or type of patients to treat, which is next to impossible in a protocol driven clinical trial setting [4] [5].

Taking inspiration from respected Prof Patwardhan's quote, "Charaka would not have ignored modern technologies if they had been available during his time" [6], this study attempts to discover hidden wealth of Ayurveda related information in EHRs created at TDU hospital using modern methods of data sciences and statistical programming. Since 2011 to October 2017, the hospital database contained data for approximately 51,000 patients, more than 1,50,000 visits, close to 900 disease types and more than 3,000 variations of medical procedures [7]. The proposed study "Analysis of hospital based Ayurvedic clinical practice to gain Real World data knowledge"

targets the methodological and learning framework as well as creation of many tools based on free softwares for various stakeholders in following categories:

- Hospital managements, clinicians, and patients
- Universities and learning institutes – clinical communication, researchers to build vital evidence-base
- Policy makers – AYUSH and relevant ministries
- Healthcare providers - Ayurveda Healthcare systems, General healthcare systems

1 Introduction

1.1 Origins of Pharmaceutical Industry

The origins of the pharmaceutical industry go back to the apothecaries and pharmacies that gave traditional therapies going back to the Middle Ages. The modern medicines regulation began only after revolutionary development in the 19th century life sciences, in chemistry, physiology and pharmacology, which put a robust foundation for the modern drug research and development [8]. In year 1947, one of the first international standards was established due to the ethical and medical misconduct of the Nazis in World War II. The Nuremberg Code created 10 standards that include voluntary informed consent, risk to subject must be weighed against benefits, actions that injure human subjects must be avoided, and the subject has the right to end the experiment at any time [9]. Unfortunate events like deaths due to diethylene glycol poisoning in the US in 1930s, the thalidomide disaster in late 1950s, catalyzed the development of medicines regulation. By the year 1964 World Medical Assembly developed the Declaration of Helsinki. It became a key international document describing the ethical principles that underlie GCP. These principles provide guidance in medical research involving human subjects. The document has been amended on a regular basis, with its most recent update done in October 2013, in Brazil [10]. The World Health Organization (WHO) and the United Nations Educational, Scientific and Cultural Organization (UNESCO) in 1949 jointly established The Council for International Organizations of Medical Sciences (CIOMS) [11]. The use of statistics as a scientific field to support R&D of new medicines grew multifold since the Kefauver-Harris Amendments (1962) and continues to grow [12]. These clearly stated that the Food and Drug Administration (FDA) would require “substantial evidence” of the impact of a drug in a clinical trial setting and proof of safety will not be sufficient for new drug approvals as had been required in the initial regulatory requirements. It issued a document titled “Proposed International Guidelines for Biomedical Research Involving Human Subjects” to help apply the principles of the Declaration of Helsinki and the Nuremberg Code, in 1982. These guidelines were revised in 1992, which resulted in the “International Ethical Guidelines for Biomedical Research Involving Human Subjects.” Due to the increasing global footprint of clinical research, the International Conference on Harmonisation (ICH) was established in 1990 [13]. In 2016, the name was changed to International Council for Harmonisation of Technical Requirements for Pharmaceuticals for Human Use (ICH). ICH created guidelines based on 4 pillars of quality, safety, efficacy, and regulatory obligations to protect public health. These guidelines get updated on a regular basis [13]. These efforts have shown that, in the USA and all over world, since 1970s, the value of medicine has been clearly demonstrated. Human population have exhibited a longer life expectancy, a lower infant mortality rate, and the higher quality of life.

1.2 Elaboration of Clinical Trials: Origin of RCT Blinded Trials

Randomized Controlled Trial (RCT) is a classical research design of randomly allocating participants to one or the other treatments under investigation. Randomization is the fundamental characteristic of an RCT, and it describes the random distribution of participants to the study arms. RCTs aim towards supporting a conclusion that the difference in the outcomes among participants

in study arms was exclusively caused by the intervention, as randomization equalizes the study group in all other factors. Thus, RCTs set the standard of excellence in health sciences research.

Although, randomization reduces the bias of participant assignment to the intervention and control group, it does not rule out the chance of bias, for example, due to investigator/caregiver or the patients themselves or bias generated during subjective adjudication of an outcome variable. However, RCTs do help in reliable description of causality between the intervention and outcome.

Blinding as a procedure, assists in monitoring and controlling several types of biases that might unintentionally creep into the study. Two major biases, namely performance bias and ascertainment bias can be controlled using blinding. Blinding deals with four groups of people associated with a trial: the study participants, the investigator(s), the outcome assessor(s), and the data analyst(s). Depending upon the groups of people blinded, trials are categorized as open label, single blinded, double blinded, triple blinded, and quadruple blinded trials [14].

Physicians and clinical researchers have remained confident that RCTs deliver the most rigorous test of preventive, diagnostic, and therapeutic interventions. They are universally denoted as the “gold standard” of experimental medical analysis, as an undisputable starting point in preventive, diagnostic or therapeutic evaluation. An article written by Alvan Feinstein and Ralph Horwitz in The New England Journal of Medicine (NEJM) in December 1982, is the first instance of RCTs being referred to as “gold standard” [15]. 1982 appears to be late date for the first usage of the “gold standard” terminology. The authors say that they were eager to be proven wrong on this 1982 date. But despite massive searches across many textbooks, conference materials, journals, and archival collections have not thrown up any earlier date [15].

While probing details regarding RCTs on the ClinTrial.gov website the following data was seen on 24th April 2020 [16], [Link](#). Total trials in the ClinTrial.gov database was 3,36,905. The estimated % of RCTs ranged between 3% and 20%. Remaining 80% to 97% of the registered trials are not RCTs (Figure 1-1). As of April 2020, Clintrial.gov database had 19% RCTs of all the studies registered in the database. This provides us with enough evidence that a lot of research work is carried outside of the RCT framework.

Figure 1-1: RCTs on ClinTrials.gov

Terms	Search Results*	Entire Database**
Synonyms		
Randomized control trial	1,862 studies	1,862 studies
trial	56,745 studies	117,642 studies
Clinical Trials	21,302 studies	42,784 studies
CLINTRIAL	17 studies	67 studies
control	50,668 studies	188,230 studies
Comparator	37,863 studies	123,329 studies
Controlled	31,962 studies	66,966 studies
Control Group	7,483 studies	24,005 studies
controlling	390 studies	1,772 studies
Randomized	56,945 studies	178,454 studies
Randomization	6,723 studies	12,452 studies
RANDOM	1,267 studies	3,526 studies
randomized clinical trial	6,234 studies	6,234 studies
clinical randomized trials	35 studies	35 studies
clinical trial	56,945 studies	118,708 studies
trial	56,743 studies	117,627 studies
Intervention Study	551 studies	1,599 studies
CLINTRIAL	17 studies	67 studies
clinical	32,693 studies	138,751 studies

This is a screenshot taken from the ClinTrial.gov website showing number of Randomized Clinical Trials. Estimates of RCT range between 3% considering “Randomized control trial (1,862)” and “randomized clinical trial (6,234)” and 20%: considering “Randomized control trial (1,862)”, “Randomized (56,945)” and “randomized clinical trial (6,234)”

1.3 Modern Hospitals, Everyday Clinical Practice and Healthcare Environment

Health information provided by hospitals is vital for public health administrators. Such data, accumulated from all the relevant hospitals, are essential in formulating health policy planning for the district / state / country, by matching this data with population statistics and other demographic data, and the health resources of the district / state / country. This medical information, containing not only data about the patient's illness but also the success or failure of therapy, could be a precious source of clinical training for medical students, nurses, and related health care work force. This could also be basis of new medicines and therapies. The development of new therapeutic drugs is built upon careful observations of experienced physicians, and the comparison and analyses of administered drugs, gathered from the patient's data. This in turn leads to continuous medical progress in uncovering new entity of a disease or a new method of diagnosis [17].

One trend all modern hospitals have in common is that the amount of processed information generated per patient is constantly increasing e.g., Electronic Medical Record (EMR), patient charts, CT scans, X-rays, ECGs, pathology reports, wearable devices, sensor data, etc. When such

information is properly compiled and aggregated, it could provide data for efficient hospital administration. How each patient is treated can yield important medical data, while the number of patients handled and treated, grouped by sex, age, and diagnosis, provides basic information that could be useful for administrators [18].

This information is processed manually or partially automatically in many instances. This inefficient method results in delays in reaching crucial treatment decisions, for instance when test results fail to get back to the physicians in time, or in delayed action by administrations when a prompt response might be needed.

1.4 Real world evidence and observational studies

Real-world data are data captured in an observational manner, in a natural setting. Ordinary clinical practice, producing a never-ending flow of results from everyday practice, can be viewed as infinite sequence of unsystematic observational studies. There must be rational use of this outcome data from patients collected from everyday clinical practice as it is far more representative of the general population and medical practice than those data coming from formal clinical trials [19]. Practice-based medicine is an important way to advance science [20]. For this to happen, the treating doctor should be a “clinician researcher investigator”. Doctors even in their busy practice, can see patterns, then formulate a research hypothesis, and then proceed to test it. Hence, a doctor can be good at good clinical practice (GCP) and good clinical research practice (GCRP). One can support the other and vice versa, and this way medicine advances [21].

Investigation of literature across time points from year 2000 to year 2020 shows that well designed observational studies produced treatment effects comparable to RCTs:

Year 2000: 99 reports across 5 clinical topics covering observational studies provided comparable results like those of the randomized, controlled trials. There was no systematic over estimation of treatment effects seen [22].

Year 2007: RCTs provides one kind of knowledge but could prevent us from understanding other properties of a drug. When observational epidemiological studies are carried out correctly, they can be both more conceptually complex and more powerful than an average RCT, especially in assessing drug safety. Both kinds of research if done with rigor and with scientific humility, can be supplementary / complementary to each other [23].

Year 2014: There was little evidence found for significant effect estimate differences between observational studies and RCTs regardless of specific observational study design, heterogeneity, or inclusion of studies of pharmacological interventions. The results highlight that level of heterogeneity in meta-analysis of RCTs or observational studies is an important factor [24].

Year 2020: Cumulative evidence suggests that appropriately conducted RWD studies have the potential to support regulatory decisions in the absence of RCT data. Further work may be needed to better show the settings in which RWD analyses can robustly and consistently match the results of RCTs and the situations in which they cannot match. After careful consideration of the potential for bias, regulators can then determine when they would accept RWD in place of an RCT [25].

The data from RWE studies and Observational studies have a wealth of information which if processed accurately and summarized in a structured manner can lead us to numerous assertions and confirmations. There have been many attempts to generate clinical evidence from primary health care by systematic utilization of patient records. But this has not been easily possible due to the deficient clinical data, in-accurate input “garbage in” leading to “garbage out”, insufficient follow-up, and very few fully completed case records with risk factors, co-morbidities, etc.

Both clinical practice and research based on the principles of primary care could contribute substantially as follows:

Clinical practice (1) uses medical knowledge and supports confirmation of research findings, (2) focuses on individual patients but still generates data, (3) has a short action span and immediate reward, (4) it regards authority, follows custom, earns income, and encourages research. Clinical research complimentarily (1) creates knowledge by focusing on future clinical practice, (2) focuses on groups of patients to generate data, (3) has a long action span and delayed reward of discovery, (4) questions authority, challenges custom, earns reputation, and enriches practice.

1.5 EHR across the globe

In early 2000s countries like Canada, UK, New Zealand, Estonia, etc. started collecting clinical practice data at a national level. The key challenges experienced while implementing Electronic Medical Records (EMR) faced by them were: infrastructure creation, policy & regulations, standards & interoperability, and research, development & education [26].

Resource shortages, amplified by various socio-economic problems pose substantial difficulties for development of workable healthcare solutions which are global in nature. Healthcare development is one of most important aspects for the progress of both social and economic development of the world. More than 1/4th of the world’s population has unmet healthcare needs. On World Health Day 2018, WHO introduced the concept of Universal Health Coverage (UHC): healthcare for everyone and everywhere. However, this has not been completely effective due to the financial limitations within systems and factors like aged-population-related chronic diseases influence the availability, accessibility, and quality of care [27].

However, EMR data has been widely used for analysis and many papers have been published. These have generated supportive data for a variety of clinical outcomes, evaluation methods, and implementation of new technology or interventions along with awareness of unintended consequences and thus supporting the clinical practice decisions and aiding to improve the healthcare process or clinical outcomes for the patients.

1.6 Role of Statistics, Analyst, Programmer

Statistics emerged as an extended stream from mathematics, operational research, and economics. Application of statistics in various fields of research like genomics, epidemiology, nutrition, biological science, biomedical research connoted the word “biostatistics”. Apart from biological sciences, statistics is applied in variety of other fields like market research, insurance, trades and stocks, banking etc. The 1990s presented explosive increase in applications of computationally

demanding methods. These methods were naturally based on statistical principles, due to the emphasis on exploratory nature of the problem and the importance of data. Statistical modeling has become more complex due to the volume of data, computational requirements, and varied data sources. These developments led to creation of new roles like statistical programmer - statistical analyst, clinical programmer - clinical analyst [28]. Clinical data analysts (or clinical informatics analyst) are healthcare professionals responsible for confirming the validity of scientific experiments and data gathered. They apply their knowledge of data acquisition, data management, data analysis, and data interpretation to healthcare data, providing actionable insights that doctors, clinical scientists, and others can use. They may be responsible for automating internal and external reports, creating executive-level dashboards, and presenting information to help various stakeholders understand the operational impact of the data. Data analysts ensure that processes and protocols associated with clinical research are followed, thus improving overall care [29], [30], [31]. They provide data insights that drive clinical process improvement, such as reducing readmissions and hospital-acquired conditions [32]. Clinical data analysts generate and provide the results of clinical business intelligence to management and all stakeholders. They coordinate with other researchers (e.g., clinical strategy, clinical operations) to determine the questions to be answered as well as the appropriate measures that should be taken to ensure data analysis proves to be useful. These roles combine strengths from multiple areas to build a powerful storyline on six dimensions of quality care: safe, effective, patient centered, timely, efficient, and equitable [33].

1.7 Traditional Chinese Medicine history and philosophy

Traditional Chinese Medicine (TCM) has been in practice for more 3000 thousand years [34] through Shang Dynasty (1600-1046 BC), Han Dynasty (206 BC–220 AD), and Zhou dynasty (1100-221 BC) of China [35]. Classic of Changes (Yi Jing) and Classic of poetry (Shi Jing) are considered the oldest medical writings available for TCM [34]. Subsequent foundation of TCM are based on the four classics across different era are Inner Canon of the Yellow Emperor (Huang Di Nei Jing, ~26 BCE), Yellow Emperor's Canon of Eighty-One Difficult Issues (Nan Jing, ~106 CE), Treatise on Cold Damage Disorders (Shang Han Lun, ~206 CE), and Shennong's Materia Medica (Shen Nong Ben Cao Jing, ~220 CE) [34]. Acupuncture, herbal medicine, diet, movement, and manual therapy are considered the five main branches of TCM [36]. TCM is based on the Five Elements theory, Wood, Fire, Earth, Metal, and Water which describes the human body. A blend of Chinese philosophy, culture, ritual, and medical practices, TCM and herbal medicine demand a broad understanding which is not limited to science [37]. Zheng (syndrome), a basic unit in TCM, decides the therapeutic methods. The process of how to get the outcome is called differentiation of Zheng, which is based on the physiology and pathology of TCM helps in determining the course of treatment [36]. This narrative practice, either in the form of classics or passed down orally, retains the medical knowledge of ancient Chinese people. Until the 20th century, most Chinese could only use TCM as a medical service. After the modern medicine breakthroughs TCM has been going re-assessment efforts based on modern scientific methods [34], [38], [39], [40], [41], [42]. One such example is of Artemisinin and its derivative dihydroartemisinin which was referred to in a medical classic by Ge Hong (284–346 CE). This drug was tested by Tu and her colleagues

using modern methods. It has saved millions of lives threatened by malaria throughout the world [43], [44]. For this phenomenal work, Tu was awarded the 2011 Lasker Award for clinical research and the 2015 Nobel Prize in Physiology or Medicine [45], [46].

Researchers have found use of “case record” in advancing traditional knowledge through the history of TCM in various phases of maturity. First phase defined by the creation and development of the discipline of TCM medical records; second phase covers the standardization of writing structure of TCM medical records; third phase outlined by books written by veteran TCM doctors on recording and studying TCM medical records. Most recent stages of development account for the explosion of TCM case reports published in journals; the establishment of TCM medical records databases and application platforms integrating computer programs and artificial intelligence; and the last but not the least, many reporting guidelines have been developed in order to improve the reporting quality of case report in TCM [35].

A short review of the available databases:

Post year 2000, many researchers have developed many web-based freely available databases covering topics like molecular properties, substructures, TCM ingredients, and TCM classification, based on intended drug actions. TCM Database@Taiwan database contains more than 20,000 pure compounds isolated from 453 TCM ingredients [47]. SymMap is a symptom mapping database integrating TCM with modern medicine in common aspects at both the phenotypic and molecular levels [48]. TCMSP: traditional Chinese medicine systems pharmacology database and analysis platform. It consists of all the 499 Chinese herbs registered in the Chinese pharmacopoeia with 29,384 ingredients, 3,311 targets and 837 associated diseases. It contains tools for visualization and analysis of TCM results on the network level for chemists, biologists, and pharmacologists [49]. TCMIO: Traditional Chinese Medicine on Immuno-Oncology database covering the mechanisms of TCM in cancer immunity and TCM-inspired identification of novel drug leads for cancer immunotherapy [50]. TCMID: traditional Chinese medicine integrative database for herb molecular mechanism analysis [51]. YaTCM: Yet another Traditional Chinese Medicine Database for Drug Discovery [52].

A short review of the clinical trials and registries for TCM:

There are not many registries for TCM yet, but some are getting developed. The China Stroke Registry for Patients with Traditional Chinese Medicine (CASES-TCM) study is a prospective, multicenter, observational disease registry aiming to register 20,000 hospitalized patients [53]. The China Amyotrophic Lateral Sclerosis Registry of Patients with Traditional Chinese Medicine (CARE-TCM) provides an opportunity to better understand which TCM interventions patients with ALS are receiving, what the characteristics of patients with ALS are, and how these interventions impact clinical measures. This registry was initiated in March 2021. This study includes a voluntary nationwide registry. Detailed data collection will be performed every 3 months for 5 years. Baseline characteristics and 5-year survival will be collected [54].

A review of TCM trials on Clintrials.gov till Sept 2015 shows 1270 TCM trials listed on the website. Most of these trials were carried out either in China or in the USA. More than 50% of the

trials were for acupuncture and 35% for herbal medicines. 55.7% that were studies with less than 100 enrolled subjects. 8.7% of completed studies had reported results of trials. Even though there are issues, it is good to see these studies getting registered on Clintrials.gov [55]. Text data extraction using deep learning models has been tried out in TCM on literature, but online search did not filter up many such examples on patient data [56]. My search could not filter Real world evidence studies within TCM area. Since early 2000s there have been some efforts put in at the national level on outcomes research and big data. In year 2010 officially RWE concept was rolled out for TCM, and 2016 onwards this has been spread across the country. Chinese Drug administration has started using RWE in pre-approval process for Supporting evidence for investigational new drug. Chinese national authority NMPA has issued a guidance for “Clinical development of traditional Chinese medicine hospital preparations” under the overall guidance for “Key Considerations in Using Real-World Evidence to Support Drug Development” Center for Drug Evaluation, NMPA May, 2019 [57], [58].

This data shows that within TCM area there is an opportunity to carry out work based on naturally reported patient level data.

1.8 The Indian context

India has a mixed system of healthcare consisting of government hospitals, private hospitals, family doctors and private medical practices. We see this trend reflected in the actual health seeking behavior of communities where people tend to combine medicine systems like Allopathy, Ayurveda, Siddha, Sowa Rigpa, Unani, Homeopathy and Yoga depending on the nature of the disease [59]. India, having one of the largest rural populations in the world, it becomes imperative to be both inclusive and optimal in the use of available resources from any stream of healthcare. Along with global healthcare challenges, Indian healthcare faces specific issues like inadequate healthcare resources, insufficient funding, poor healthcare infrastructure and rural–urban disparity. The national healthcare budget is a lowly single digit percentage of the Gross Domestic Product (GDP). The number of doctors, nurses and health workers are small in comparison to high population in certain regions. The availability and utilization of technology is also at the lower end of the usage [60].

Integrating modern medicine and AYUSH systems, acronym for Ayurveda, Yoga and Naturopathy, Unani, Siddha and Homeopathy, folk medicines as well as technological advances into the India healthcare system can generate new opportunities for healthcare. These efforts will be noteworthy where healthcare systems have limitations in terms of infrastructure, expertise, and human resources. This integration will not only allow utilization of the positives of each of the medical streams but will generate new data-based evidence due to integration possible using technology. Ongoing monitoring and updating patient’s data together with consistent updates to physicians can help in identifying disease and treatment patterns. Through this analysis, authorities or the government can employ specific precautions, or even start necessary facilities to avoid healthcare issues before the situation gets out of hand [61].

The application of such assessed and analyzed data are substantial as the information brings out more and more knowledge about an area or a person. In under-resourced countries such as India,

the resultant benefits are expanded further, suffering is reduced, hospital resources are saved and socio-economic improvements that lift a nation's wellbeing are recognized. Moreover, India could achieve improved healthcare delivery, care audit, epidemiological study and quick response to epidemics and bring economic benefits to individuals by reducing the healthcare cost.

1.9 National level efforts AYUSH

This section covers efforts put in by the Government of India at the National level. The Ministry of AYUSH is a part of Government of India to promote and expand use of AYUSH systems of health care and medicine in India. To administer the different medicine systems encompassed by the Ministry of AYUSH, it has five research councils or departments, affiliated courses, and affiliated national institutes [3]. One of AYUSH affiliates, CCRAS has developed National AYUSH Morbidities and Standardized Terminologies E-Portal NAMASTE portal. It provides information about Standardized terminologies and Morbidity codes along with dedicated data entry module for updating morbidity statistics in consolidated form as well as on real time basis [62]. To publicize the merits of AYUSH systems across the globe, a web-based portal for Research publications was launched in 2011, which is being maintained by NIIMH Hyderabad [63]. Ayurveda Hospital Management Information System (A-HMIS) is a complete IT platform for all functions of health care delivery systems and patient care in AYUSH centers. THERAN (THE Research Application Nexus): HMIS is developed by Siddha Central Research Institute, Chennai under Central Council for Research in Siddha. These are 2 additional examples of ongoing work under Ministry of AYUSH [64]. Ministry of AYUSH has created AYUSH GRID to cohesively implement projects under Digital India Movement. It is an amalgamation of IT projects planned for advancement of AYUSH pan India [65]. The dashboard available on AYUSH homepage (accessed on 25th May 2020), reveals the following facts: the screenshot shows almost 10 crore patients treated at some or the other point (Figure 1-2, Figure 1-3). There are approximately 140+ countries with less than 10 crore population, which provides a perspective on the size of data available at the AYUSH level. It remains to be seen how to convert "data into information, information into knowledge and knowledge into wisdom" [66].

Figure 1-2: Screenshot of a dashboard from AYUSH website



Dashboard from AYUSH website covering: AYUSH institutes, Infrastructure projects, National medicinal plants board, Health infrastructure, Education and communication, Research, Practitioners and patients, Drug Industry, Budget, and Schemes

Figure 1-3: Ayurvedic practitioners and patients from AYUSH dashboard

Practitioners & Patients									
Practitioners									
#	Facility	Ayurveda	Unani	Siddha	Yoga	Naturopathy	Homoeopathy	Sowa-Rigpa	Total
1	Registered Practitioner(IQ & NIQ)	443704	51110	9125	0	2485	293455	0	799879
2	Institutional Qualified Registered Practitioner	294162	38672	5685	0	2349	246792	0	587660

Patients							
#	System	IPD	OPD			Total	
		CHC	CHC	Dispensaries	PHCs	IPD	OPD
1	Ayurveda	1390950	16557395	71486719	8455545	1390950	96499659
2	Unani	102884	2220231	8109909	1504284	102884	11834424
3	Siddha	210016	10617115	1634022	16858888	210016	29110025
4	Yoga	15741	1564861	50150	1282064	15741	2897075
5	Naturopathy	18636	138187	210634	72176	18636	420997
6	Sowa Rigpa	0	0	7050	0	0	7050

Close

Screenshot from AYUSH website covering: Approximately 4.5 lakhs Ayurvedic practitioners and more than 10 crore treated patients. Data regarding different medical systems within AYUSH has been presented. Ayurvedic practitioners and patients treated by ayurvedic interventions are considerably more than by any other traditional medical practice.

1.10 Science of ayurveda

There are some models proposed by various authors to handle complex and tricky situations arising in defining and understanding the action mechanism of Ayurvedic intervention. As described by Dr. Girish Tillu in his talk at TDU, huge observational data for Ayurvedic medicines covers large number of books and manuscripts, 57 authentic books (Drug and cosmetic act 1940, page 47) [67], more than 4500 diseases including subtypes and conditions (Ayusoft database) [68], more than 81,000 formulations (TKDL database) [69], more than 4,00,000 Practitioners in India [66], infinite documents, references, experiential data, living tradition and knowledge in public domain [7]. Dravyaguna (Pharmacology), Bhaisajya Kalpana (Pharmaceutics), Nidana (Diagnosis) and Chikitsa (Management principles). This data points to a validated knowledge base.

Dr. D. B. Vaidya has explained the concept of reverse pharmacology to understand the action mechanism of Ayurvedic intervention. He says that there is huge amount of observational data available, showing relatively low side effects that have been reported. This existing data should be used as basis to carry out large interventional Ayurvedic trials to assess safety, efficacy, and pharmacokinetic information. This approach will be economical and could be less time consuming compared to the sequential drug development or the hierarchical model used in western medicine. He further talks about integrating meticulously documented experiential and experimental observations [70].

Prof R. H. Singh has opined that lab-based research experiments within Ayurvedic area during the last 50 years have not been rewarding. On the other hand, literary experiments to make a few of the classical Ayurvedic texts accessible to masses have been extremely useful. This situation warrants newer strategies of scientific research without compromising on the fundamental principles of Ayurveda [4].

Prof. Bhushan Patwardhan writes that there are substantial similarities between the traditional systems like Ayurveda and modern medicines. Ayurveda emphasizes on health promotion, disease prevention, early diagnosis, and personalized treatment. The modern medicine system approach uses predictive, preventive, and personalized medicine (PPPM). In case of Ayurveda, the evidence can be drawn from two main sources: (1) Evidence based on historical and classical nature of clinical practice supported by credible and accepted documentation. (2) Evidence based on ongoing scientific research to support various theories, medicines and procedures used in Ayurvedic medicine [71] [72].

Dr. Ram Manohar has expressed that Ayurveda is based on 5000 years of clinical practice. Hence, practice-based clinical trials should complement natural ways to gain insights [73].

Dr. Baghel's interpretation is that one should think of Ayurveda being in the developmental phase like any other medical systems. Like many other scholars he thinks that Ayurveda is a pure science based on logical explanation, which is called *Darshana*. Ongoing research in Ayurveda should impact academics, pharmacy, and practice in a profound way to convert data into information, information into knowledge and knowledge into wisdom [74].

As per Prof. Darshan Shankar's analysis as of 2015, at the national level, Ayurveda receives a meagre 3% of the Central health Budget and at the State level, making it difficult to fund any meaningful research projects. Despite Ayurveda's strengths, it has some limitations in current scenario. To advance the science there is a need to embrace tools of information technology to organize its vast multifaceted data, in searchable formats. Meticulously documented clinical experiences interpreted through Ayurveda-biology will expand rejuvenation of healthcare in India [59].

All the thought leaders cited here point to the strengths of Ayurveda as well as the immediate needs. They have pointed out that the research must be of high quality, and it must be impactful. They have indicated the need for experimental as well as experiential research. They have already provided a few new solutions and have urged to the research community to find new ways of tackling problems [75].

1.11 Potential opportunities for Real World Data analysis within Ayurveda

The western medicines are developed using a method called as hierarchical method where it tries answering questions with limited scope e.g., what is the efficacy of a particular drug, what is the safety profile of a drug? This method assumes a step wise approach and deals with the problem in successively conducted clinical trials of various types in a specific sequence. The pharmacology of the molecule is ascertained first at the very beginning. These studies are followed by cohort studies including open-label randomized studies but in general the clinical trial testing usually concludes with a blinded, randomized controlled trial (RCT). As already pointed out, RCTs are the “gold standard” of evidence generation as they offer most internal validity and minimal bias [76]. These studies could be complemented by using case studies, case series. This “one step at a time” approach has worked very well in the western medicine framework.

Ayurveda has been practiced for more than a millennium and is widely accepted in India as a worthy medical system. Over the last few decades' people across the world have gained knowledge and realized the importance of the age-old medical system and are constantly driven towards it. Although, having been in practice for ages Ayurveda still does not enjoy the recognition which the Western medicine does. Hence there needs to be a structured approach towards making this possible. The untapped potential of Ayurveda needs to be scientifically communicated globally for a wider reach for it to be utilized as a public health tool for promotion of health and prevention of diseases [76].

Ayurvedic vaidya usually use paper-based case report to record a patient's Ayurvedic parameters along with other details of medical consultation. These are typically not exchanged with other vaidyas. There is a huge amount of data available on paper and if digitized could be a big revolutionary step. Increased use and interoperability with electronic medical records of digital Ayurvedic patient management systems are required. Based on a report published by AYUSH [66], there are 4.5 lakh registered Ayurvedic practitioners. Even if 5% of doctors start using EMRs, i.e., 22,500 doctors and if data for 2 new patients is entered every day (~225 working days) for the whole year, 50 lakh unique patients' data can be generated in a single year. Currently, this gold mine of data has not been built yet.

1.12 What this study aims to contribute to

This study aims to contribute to interests of multiple stakeholders involved in clinical research. Based on arguments given above about availability of observational data, availability of technology, the Indian context and the specific case about Ayurveda and need to understand the science behind it, the study would highlight multiple use cases. The study would highlight tools and information generated through these tools and this could be interchangeably used by interested stakeholders including:

1.12.1 Hospital management

To keep any hospital functioning smoothly, operational insights from routine hospital data are important to improve management and efficiency of day-to-day activities. How many patients are present in the database? What are the characteristics of these patients? What is the gender distribution and age group distribution? Which countries, states, cities do they come from? How many times do they visit the hospital? What is the number of In-Patients & Out-Patients? What kind of assessments are done at each visit? What is the duration of visits for a patient? Which diseases are getting treated? Are the patients benefiting? How do you measure benefit?

Regular analysis of data would give insights which will allow for operational proficiencies, cost savings and eventually profitability. Finally, patients' satisfaction would improve if a hospital functions efficiently.

1.12.2 Clinicians or treating doctors

Let us understand what kind of benefits the clinicians can have from this study. Traditionally many clinicians in their own practice use paper CRF to capture patient data. The hospital has electronic data capture system, which is essentially doing the same job, but data capture is electronically done. Are they ready to adopt to a new way of working? Does onboarding training at hospital cover this part of the job? Do they see this as an additional burden or an integral part of day-to-day work? How can experience of clinicians using the Health Information system be viewed? Do doctors like data entry part of job? Do the doctors have time for real data entry while consulting patients?

Answers to some of these questions can be generated indirectly by understanding the quality of the database and data contents. Does hospital management take any feedback from the clinicians who are the primary "end users" of the data capture system? This timely feedback loop should provide great inputs into evolution of the system both operationally as well as scientifically.

The electronic data capture provides unique opportunities to clinicians such as they have access to the data from other practicing clinicians. This gives indirect learning opportunities of understanding treatment protocols, treatment variations employed, rare diseases treated at the hospital. Retrospective analysis of disease and treatment should provide ideas about disease variations, appropriateness of documentation, disease – disease combinations, disease – treatment combinations. These documented combinations could be clinically meaningful, could be season wise, gender wise, age wise varying. Retrospective analysis of treatments should provide tendencies of treatment prescription such as use of classical treatments, herbo mineral treatments.

Data review and analysis tools developed for this thesis can enhance patient and doctor interactions.

1.12.3 Universities and students

Teaching material for students: Over the years, teaching methodology has not transformed even though there are quite a lot of advances in modern methodology. Can learning objectives of different kinds be tackled by making insights generated from this data available to the students. For example, can complex disease-treatment relationships be made easily visually available. Can interesting ways of explaining text and advice from Ayurveda which have contemporary relevance be created? For example, occurrence of certain diseases in certain geographic areas or season. Very few large-scale studies like this have taken place in Ayurveda, so this study with large amounts of observational data can provide exploratory opportunities to describe findings, textually as well as diagrammatically. Tools developed here can be used as a supplementary material for any MD / PhD student.

Scientific literature generation by researchers: Most hospitals in India or any part of the world mainly focus on treatment and not on research publications. Can a research team be put together for medical communication who publish papers as their primary job? If there is no known profile of patients visiting an Ayurvedic hospital and if this data can be generated and represented in the right form, it will provide novel information. How can we measure the strengths and weaknesses of an Ayurvedic practice? How should researchers evaluate changes in results of a practice over time? Is it possible to build new hypothesis? Is prescribed treatment truly personalized? Is it possible to trace back the treatment regimen followed and compare it to classical fundamentals? Is there a way to compare the demographics and patient characteristics from a Ayurvedic hospital against a mainstream western hospital? Which are rare diseases identified in the database? Can a clinically meaningful document be written, like a case series about this rare disease?

How can anyone use these data as “secondary use”? Can this data be used by insurance companies? Do the approved labels of medicines and prescriptions in the database match each other? Metal based formulations are questioned by non Ayurvedic community, what insights can be drawn about the rasa-aushadhis? Which are these medicines? For what diseases are they given and for what duration? Before providing the metal-based treatment and after providing the metal-based treatment, is there any difference in duration seen in treatments? What is the percentage of patients that are prescribed these medicines and what is the percentage of duration of all the duration of treatment given to these patients?

1.12.4 Policy makers – AYUSH and relevant ministries, insurance sector:

Policy makers and insurance companies can use insights from this data to decide on which treatments to cover for insurance. Government agencies can use this data to promote Ayurveda as a medical system throughout the world. They can make policies similar to policies that govern western medicine.

1.13 Introduction to real life data

As presented above, the potential benefits of gathering and analyzing such data are huge. A quick history of how this ability to collect data has come about is given below. This history also

highlights the challenges of collecting and analyzing data in general on top of challenges associated with clinical research and Ayurveda specifically. With the passage of time, revolutions in technology have continually increased the creation of information and its exchange. With the advancement for communication from spoken to written, it became simpler to create texts, books thereby documentation; thus aiding transfer of knowledge from one person to another as well as from generation to generation without losing any data in translation. With increased and improved writing, compilation of articles, tables and records, there came a time where storing them became important, thus came in the libraries. The ability to effortlessly widen accumulated data had to wait until the 15th century. Around 1439, Johannes Gutenberg developed the printing press, causing an astonishing growth in the sharing of information at an economical cost.

The 20th century generated a remarkable growth in the publication of scientific journals and monographs, most of which were not critically reviewed, as most physicians had no way to access to the existing medical information. Towards the late 20th century, the spread of computers and the internet providing immediate virtual access to diverse information has entirely changed the way knowledge is collected, stored, and circulated. The flow of information has been increasing at almost exponential levels. Today, data sets are measured in zettabytes (10^{21} bytes). Cost-effectively collected and stored data allows researchers across the world to successfully advance understanding of science and medicine [77].

International Data Corporation (IDC) is one of the premier global providers of market intelligence, information technology, and a host of other areas. They predicted in a report issued in Dec 2018 that the world's cumulative data will grow from 33 zettabytes to a 175ZB by 2025, for a compounded annual growth rate of 61%. A zettabyte is a trillion gigabytes multiplied that by 175 times. This growth of data has been seen in every industry, in every corner of the world. The relentless increase in the quantity and flood of information denotes an important professional opportunity, but a challenge simultaneously for those in medicine and science [78].

As indicated by Toby Cosgrove MD, from Cleveland, medical information doubles every 73 days, in the year 2020, as compared to approximately 3.5 years in 2010. An estimated 8,00,000 papers were published in 5,600 medical journals every year. It is projected that 12,000 new articles and 300 randomized controlled trials will be added to Medline each week, and that new medical articles will appear at a rate of one every 26 seconds [79]. To be able to generate any kind of analysis and make accurate predictions, there is a need to access, connect various sources, collate, and consume all the data. Data is being produced, obtained, and stored in numerous number of structures [80].

During an appointment at a hospital, diverse types of data are collected. Raw data are observations about individual patients created by the treating doctor at a hospital. These data may be in the form of measurements of patient's characteristics such as age, gender, height, weight, blood pressure, heart rate, etc. Raw data may also include description of the medical history, physical exam information, clinical laboratory results (e.g., serum lipid values, hemoglobin levels), whole exome or genome sequences, imaging results, ECGs, questionnaire data, or self-reported data (e.g., symptoms, quality of life).

Raw data, unprocessed source data, like unrefined gold buried deep in a mine is a precious resource. It is often: (1) Inconsistent, containing both relevant and irrelevant data, (2) Imprecise, containing incorrectly entered information or missing values, (3) Repetitive, containing duplicate data. To utilize the raw data to its fullest potential, it needs to be extracted, filtered through, understood, and transformed into analyzable format. One of the surveys carried out by Forbes estimates that data cleaning accounts for up to 80% of the development time and cost in data warehousing projects. Understanding the scope of data being analyzed and seeing the changes made to the data can accelerate the entire process of going from “information to building wisdom” [81] [82] [83] [84].

1.14 Introduction to clinical data understanding

The health care industry uses either a paper-based record keeping method and/or electronic health record (EHR) system to manage patient data. More and more organizations are using electronic data capture, but the practicing doctors in individual clinics may still be documenting observations on paper. The EHR has become an integral part of medical care, which transforms health care service quality and improves physicians' satisfaction and facilitates patients' decision. Accurate information from EHR enables physicians' decision making and measures clinical validity, which in turn upgrades the quality of patient care. This functionality is crucial during diagnosis and therapy, which benefits medical and legal practices too [80].

Health authorities and top-level journals require the data to be submitted along with research papers. The analyzable data set, is the result of many decisions made by varied people, as explained above. The errors, flaws, or biases in the processing of source data, will not necessarily be identified in the analyzable dataset. After the electronic data entry, new variables are generated to support further analysis. The final cleaned analyzable datasets consist of various components such as participant characteristics and primary outcome, pre-specified secondary and tertiary outcomes, adverse event data and exploratory data [85].

Physicians and other scientists are getting better at producing data. But we must become proficient—with or without the help of technology—at mining and managing the data in ways that will allow us to use it to maximum effect [86]. The full analyzable dataset is generally the most useful set of data to share, with large and likely important benefits to science and society. Secondly, the full analyzable dataset provides scientific validity to the outcome and ensures replication and repeatability. Further, meta-analysis increases the statistical power of detecting effects and maximizes the value of the outcome in the clinical knowledge base. Finally, analyzable data allows for further scientific discovery through additional secondary analyses, as well as the conduct of exploratory research to generate hypotheses for additional studies [87].

1.15 Introduction to study of demographics and patient characteristics

We will proceed with understanding the data contents and see if any of the questions raised earlier can be solved. Demography is the study of the population. It explains the composition, the distribution and the data trends seen in the population. Roles and functions for demography studies can be broadly defined as, (1) population projections, (2) inputs into government budget, (3) evidence-based policy, and (4) communication of vital statistics [88]. There is very little data on

the profile of patients accessing traditional systems of medicine. A comparative study of profile of patients using an Ayurveda clinic and modern medicinal clinic will help in understanding of utilization of services and preference for health seeking behaviour.

1.16 Introduction to study of diagnostics and interventions

Diagnosis is one of the most important aspects in the process of treatment of the disease or condition. It is a patient-centered, cyclic process of gathering information, analyzing information, determining the health condition, and defining the type of intervention and continuously monitoring the progress till the desired state of functions/doshas is arrived at. Ayurvedic treatment involves removal of the causative factors. It assists in getting the functions/doshas into balance. The success of a treatment is possible only by timely and accurate diagnosis, a tailor-made intervention accompanied by an effective collaboration of the physician and the patient [89]. The term comorbidity refers to the coexistence of multiple diseases in relation to a primary disease in a patient. Patients report multiple diseases during their visits to the hospital. Some of these reported disorders are expected and some are unexpected. There are known as well as unknown disease combinations present due to biological linkages. Clinical and epidemiological studies indicate that disease comorbidities have a great impact on health status, selection of appropriate treatments and health system costs. Understanding comorbidities and their etiology is key to identify new preventive and therapeutic strategies.

Finally, all these steps (1) accessing and understanding real life data, (2) converting that data into analyzable format, (3) understanding demographics and patient characteristics, and (4) understanding diagnostics and interventions should help in building transdisciplinary evidence to increase the scientific understanding outside of the community, then increase the confidence and thereby widening the user base.

1.17 Structure of the thesis document

The thesis is structured as follows: Chapter 2 covers study design and numerous methods applied for data analysis. In section 2.7, table (Table 2-2) presents a consolidated view of various analysis, context about different analysis and their possible relationships with each other. Detailed observations of these experiments are documented in chapter 3 Results. Challenges with respect to overall system architecture and data collection are documented in chapter 3. Chapter 4 provides some solutions to these challenges. Supplementary interpretations are further illustrated in chapter 4. Chapter 5 covers several conclusions drawn based on the analysis and key take away message. Chapter 6 appendix provides detailed material generated for this PhD work. Appendix section 6.2 provides details about the master dataset developed for whole of this study. Appendix section 6.3 provides information regarding the source database. Appendix section 6.4 provides a table to track all analysis presented in the thesis. Appendix section 6.5 provides R, SQL, and D3js programs developed to generate different datasets and analysis. Chapter 7 covers the references.

All the tables and figures are cross referenced and clicking on the table number or figure number in the document takes the reader to that table or figure. Column “Figure number and analysis name (linked to the actual figure)” in Table 2-2: Proposed methods and analysis use cases allows a reader

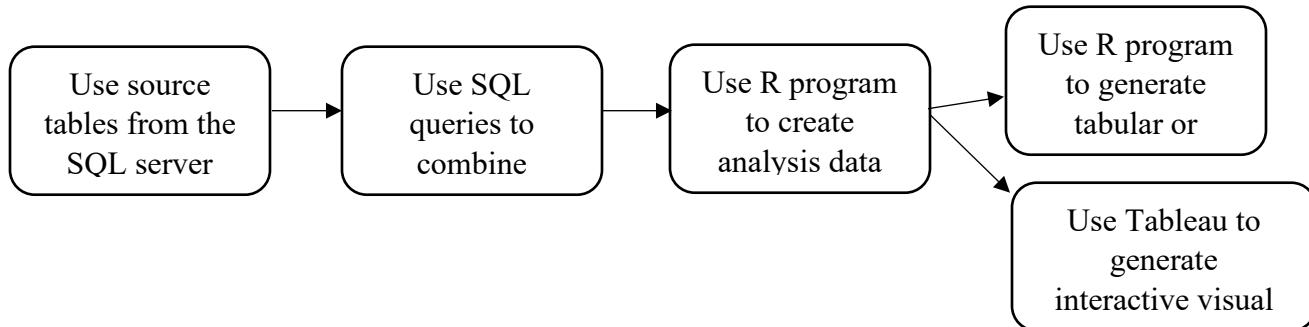
to go the actual link of specific analysis. “Link to analysis” part under any figure or table allows a reader to go to actual link of specific analysis.

2 Methods

2.1 Study design

This was a retrospective study of Electronic Health Records (EHR) at TDU. Electronic Health Records of patients from 2011 to 2017 are used. It contained data for more than 51,000 patients, more than 1,50,000 visits, more than 900 variations of disease types, more than 3,000 variations of medical procedures. The study was approved by the authorities of IAIM and TDU (refer Appendix section 6.1). We explored “naturally reported data” for getting insights into demographics, health-seeking behaviors, and other health parameters. Sensitive information related to patients and doctors was not extracted to maintain confidentiality. Data was analyzed through SQL [90] and R programs [91], python [92], Java [93], D3js [94] and tableau [95] software. A high-level pictorial representation of the technical study is displayed below (Figure 2-1).

Figure 2-1: Pictorial representation of analysis



2.2 Data analysis design

The data analysis was represented using many different methods such as: (1) tabular representation using frequency counts [96], (2) descriptive summary statistics [96], (3) data representation on world / country map [97], (4) boxplot representation [98], (5) barplot [99] and (6) dotplot representation [99], (7) radar plot representation [100], (8) individual patient level data listings – line by line data representation, (9) various types of bubble plots [99], [101], (10) circular data representation [102], (11) collapsible tree diagram [103], (12) treemap / mosaic plot [104], (13) butterfly plot [105], (14) area plot [99], (15) calendar plot [99].

After converting the source data into analyzable format, the next logical step is to generate various descriptive Statistics. This assessment is covered by frequencies, measures of central tendency (also called averages), and measures of variability. Frequency statistics means to count the number of times that each variable occurs. E.g., number of males and females, number of diseases reported, number of treatments prescribed, to name a few. This calculation is displayed by both the absolute or actual number and relative or percentage totals. Measures of central tendency provide a number that represents the entire data for a particular variable, such as mean, median. Measures of variability indicate the degree to which scores differ around the average. It is essential for any end user to have a sound understanding of study data. Initial statistics for all studies should include descriptive statistics [96].

For many centuries humans have used maps for various reasons. Maps are used to display geographically linked data providing a clearer and more intuitive visualizations. Maps allow to see the distribution of data in each area going from district, state, country. Technology has enabled creation of interactive maps. These allow zooming in and out, panning around, identifying certain features, querying data by topic(s) or specific indicator(s), producing reports and visualizing information in the map [97].

Boxplots were invented in the 1970s by American statistician John Wilder Tukey. They are also called as a box and whisker plot. Boxplots display five-number summary of data - the minimum, first quartile, median, third quartile, and maximum. Sometimes, the mean is also indicated by a dot or a cross on the box plot [98].

William Playfair is considered to have designed the bar plot. A bar plot is a graph that represents the category of data with rectangular bars. The length and height are proportionate to the values which they represent. The bar plots can be drawn either horizontally or vertically. One of the axes of the plot shows specific categories being compared. The other axis denotes the measured values corresponding to those categories [99].

A dot plot can be used for any graph that is translating data in a dot or small circle. A dot plot is also known as a strip plot. It is a simple form of data visualization consisting of data points plotted as dots on a graph with an x- and y-axis. These types of charts are used to graphically depict certain data trends or groupings [99].

A radar plot is a 2-dimensional representation of multivariate data as a polygon. Each variable included in the plot is represented as an axis. All axes have the same origin. The position and angle of axes are usually not informative, so any variable can be represented in any order. If different axes represent months or seasons, then the order of representation would be important as there is a certain meaning to ordering. The bars on each axis represented by the variable are called radii. A radar plot looks like an irregular polygon arranged on top of each other, all with the same center. These are used in many fields such as medicines, sports, education, and different businesses. Radar plots are also called spider plots, cobweb plots, star plots, polar plots to name a few [100].

A bubble plot is a plot that displays three dimensions of data. Each entity with its triplet variable 1, variable 2, variable 3 of associated data. 2 of the 3 variables are used on the x and y axis and a numeric variable determining bubble size is used to determine the size [99], [101].

An area plot is a variation of line plot. In this plot data points are connected by a continuous line and the area below the lines is filled with colors or textures. This plot compares two or more quantities with an area chart. Area graphs can be effective for showing the fluctuations of various data series over time [99].

A butterfly plot is a comparative bar plot or a histogram that displays the distribution of a variable for two subpopulations. A butterfly plot could be displayed either vertically or horizontally [105].

A calendar plot is a visualization used to show activity over the course of a long span of time, such as months or years. They are used to illustrate how some variable alters depending on the day of the week, or how it changes over time [99].

The treemap functions as a visualization composed of nested rectangles. This was developed by Prof. Ben Shneiderman, from the University of Maryland. The rectangles represent certain categories within a selected dimension and are ordered in a hierarchy, or “tree.” Quantities and patterns can be compared and displayed in a limited chart space. Treemaps represent part to whole relationships [95], [104].

Tabular listings of data are generated at individual patient level. These are equivalent to displaying source data. They are the basis for all tables, listings, and figures (TLFs). To make the listings readable different components are data are shown in different listings. Patient profile listing covers all data for a patient in one consolidated report. This is used in data review and clinical review.

These various analyses enable data to be reported in different levels of details. Most of these representations are interactive, end user can perform filtering tasks while using the visualizations. Tableau’s drill down facility provides additional ways of analyzing the data. Tooltip functionality allows extra dimension to provide more details [95].

2.3 Converting real life clinical data into analyzable format

2.3.1 Data access

Patient data was stored in the hospital database. “Read only” access was provided to the hospital database, to avoid any accidental updates to the records, thus preventing the risk of source data change or loss. The details for accessing the hospital management system are as follows:

1. Install PostgresSQL locally on the system and then connect to the database as per details below.
2. Install Cygwin terminal locally on the system.
3. Login using the Cygwin terminal (the following command will prompt for password):
`psql -h xx.yy.zz.ww -p ABCD -d iaim -U iaim_ro`
4. Postgress Data Base details are as follows:
 - Hostname: xx.yy.zz.ww
 - port: ABCD
 - user: iaim_ro
 - password: efghijk

The real login and IP details are not presented to keep the confidentiality of secure access.

An independent (not interfering in the day-to-day transactions of the hospital), remote access for the specific version of the database was established.

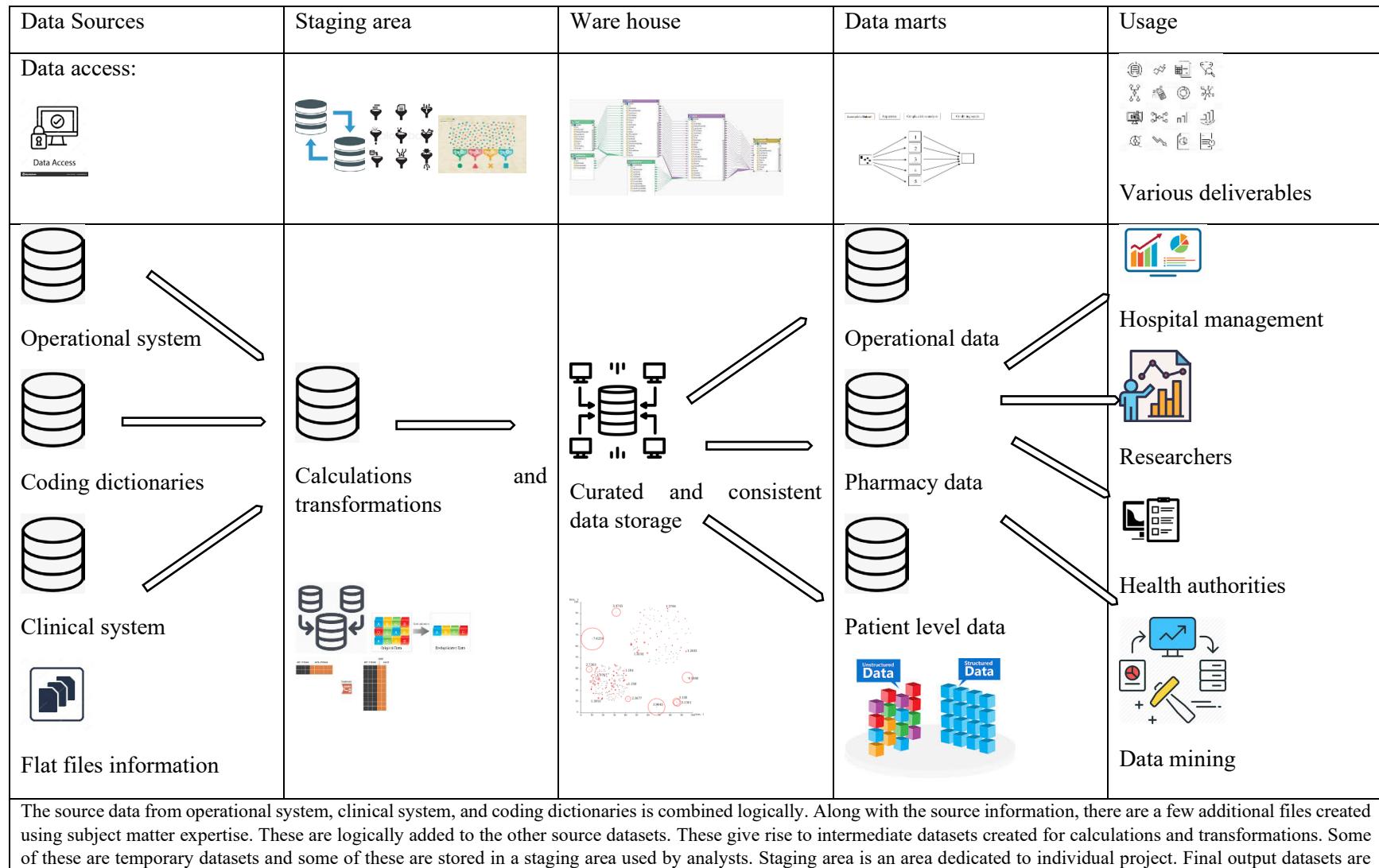
2.3.2 Data preparation

It is very important to think through the data preparation stage about the data holistically. Audience is critical while preparing data. It is important to assess, who will use the data and where and when and for what purpose. The answer to these questions determines how the data should be processed. Data preparation has a lot of different components, from restructuring to reformatting to cleaning, and should not be constrained by a specific order. This data is stored in a central place called as a data warehouse. It is a central repository of data within for an organization. Data flows into a data warehouse from various systems. This data is used to make operational, business, and scientific decisions [106]. This detail influences the data preparation process significantly, determining both the amount of effort and detail [82]. The following steps were followed in data preparation (Figure 2-2). The relevant details can be found in individual R, SQL, python programs (refer Appendix 6.5):

- Merging, joining: Combine relevant data from different datasets into a new dataset. A “join” is an operation that connects two or more datasets by their matching columns. This establishes a relationship between multiple datasets, which merges data together so a query can be made on the combined data [84].
- Appending: Combine two or more similar datasets into a single dataset [84].
- Filtering: Rule-based reduction of a larger dataset into a smaller dataset. The goal of data filtering is to refine a data source to only what the user needs. Data filtering involves the selection of specific rows, columns, or fields to display from the dataset [82] [84].
- Deduping: Remove duplicates based on a defined criterion. Data deduplication is a data compression process to identify and remove repeated copies of information. Deduplication allows storage of one unique copy of data in the database. This process allows for examining incoming data and compares it to data that is already stored in the system [82] [84].
- Transforming: This involves converting data from one structure (or no structure) to another to integrate it with a data warehouse or with different applications [82] [84] [106].
- Format revision: Format revisions fix problems of different data types. Similar data captured in different formats creates problem for analysis. E.g., one dataset may capture treatment information as a coded numeric variable whereas another dataset may capture the same treatment information as a text. This inconsistency results in misrepresentation as well as sometimes loss of information. Along with the data format it is important to ensure the variables have appropriate lengths so that no data is truncated. Standardizing the data formats and lengths ensures correct data joins and appends. This could involve the conversion of male - female, units from one unit to another, datetime, phone number list, etc. to name a few into a consistent format. Format adjustment could involve dividing a comma-separated list into multiple columns [84].
- Categorical variable creation: This transformation is used to change a numeric series into fixed, categorical ranges, say, from {2,5,8...} to {2-5, 6-9, 10-13...}. E.g., the seasonal fluctuations

in diseases using Indian seasons, RMSD and Metabolic disease group creation, treatment groupings into kashaya, asava, arka, etc. [84].

Figure 2-2: Flow diagram from data source to final usage by various usage types



stored in a central place called as a data warehouse. It is a central repository of data within for an organization. These datasets are used to make operational, business, and scientific decisions by various stakeholders by converting them into interactive analysis, dashboards, formal project reports.

2.3.3 Data derivation

The case report form at each visit captures disease and medication data, along with demographic, background data and a few more characteristics (outlined later in the document). This data creates documented complete picture of each patient from various parts of the database including In-Patient visits, Out-Patient visits, Diseases reported as per Ayurvedic Classification dictionary, Medication prescribed and Ayurvedic services prescribed. These components of data were logically arranged in one dataset by using various data transformation steps. In addition, there were new variables derived to create necessary information for the potential analyses. Some of the challenges experienced to assemble the “reference dataset” from the source data and practical explanation of the “data preparation” steps taken are given below.

1. The database was manually explored using various SQL programming commands to check variables and observations from numerous tables (Figure 2-3)
2. Patient information and key variables needed to be understood: unique patient ID is MR_NO, and unique ID for individual visit is PATIENT_NO (many tables containing patients' clinical information have this variable as the key variable)
3. Reference files needed to be used to reformat the coded variables
4. First section of the creation:
 - Extract relevant data tables from the source database (Figure 2-4)
 - Transform the variables, join the tables based on logical link
 - Create “staged data” (Figure 2-5) which can be also called as snapshot of data
 - Reference files (disease categories, Indian seasons) which were needed for calculations were developed using expert's help (Figure 2-6)
5. Second section of the program:
 - Cleanse the tables
 - Transform the tables for combining
 - Join the tables using logical link
 - Derive additional variables as necessary
 - Filter the data using reference files created in the earlier section
6. In this process, we used 13 source datasets (5 reference datasets and 8 patient level datasets) and 72 variables to generate the necessary snapshot of the source data. These were rearranged into 6 datasets and 40 variables. 3 additional reference files were used for further processing. 1 final dataset having 39 variables from source and 33 newly derived variables is built. (Figure 2-7). All these steps were covered in 50 stages of programming.

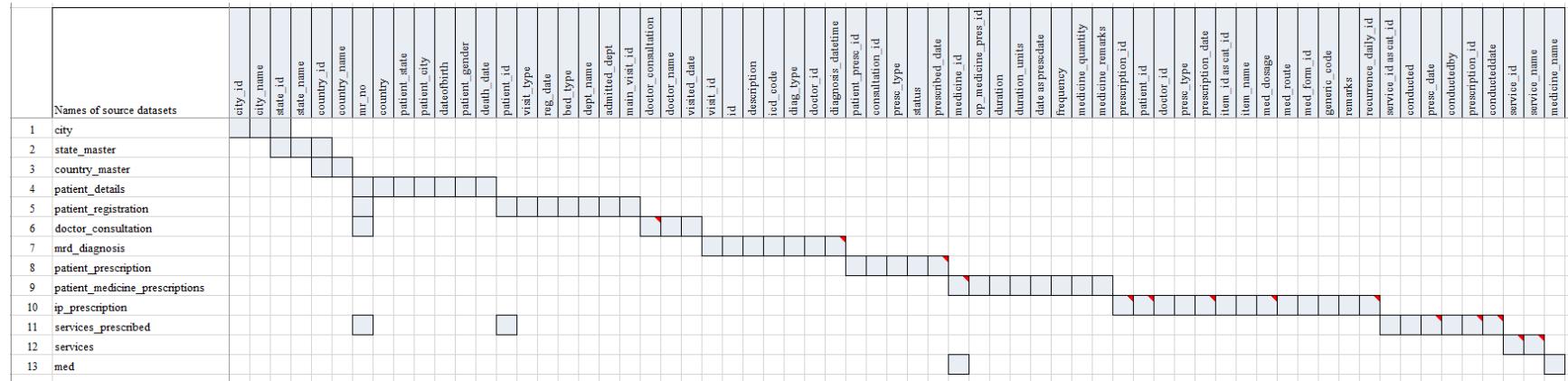
7. The entire workflow is pictorially depicted in (Figure 2-8).
8. Information about the final dataset is detailed in (Table 6-1).

Figure 2-3: A glimpse of data tables used to store source data from the database

action rights	diet prescribed	hospital technical	package componentdetail	patient registration	section field options	store_item_batch_details	test details
admission	discharge format detail	icu bed charges	package item charges	patient section details	service consumable usage	store item details	test org details
anesthesia_type_charges	doctor charges backup	ip bed details	package prescribed	patient_section_details_origin	service documents	store item lot details	test results master
area master	doctor charges op backup	ip prescription	patient activities	patient section forms	service master charges	store patient indent details	test visit report signatures
bed_details	doctor consultation	item supplier prefer supplier	patient consultation field values	patient section image details	service master charges backup	store patient indent main	test visit reports
Bill	doctor_consultation_charge	manf master	patient demographics mod	patient section values	service org details	store po	tests conducted
bill_activity_charge	doctor_medicine_favourites	medicine dosage master	patient deposits	patient service prescriptions	services	store po_main	tests prescribed
bill adjustment	doctor_op_consultation_charge	medicine_id_health_authority unique	patient_deposits_setoff_adjustments	patient test prescriptions	services prescribed	store_reagent_usage_details	theatre charges
bill_charge	doctor_org_details	message_recipient	patient_details	ppfv_form_detail_id	stk_chkpt	store_reagent_usage_main	diet charges
bill_receipts	dyna_package_charges	mrd_codes_doctor_master	patient_discharge	preauth_prescription_activities	stock_issue_main	store_retail_customers	user services depts.
complaintslog	dyna_package_org_details	mrd_codes_master	patient_documents	prescribed_medicines_master	store_adj_details	store_sales_details	visit vitals
consultation_charges	equipement_charges	mrd_diagnosis	patient_general_docs	progress_notes	store_adj_main	store_sales_main	vital reading
consultation_org_details	estimate_bill	mrd_observations	patient_hvf_doc_values	registration_charges	store_checkpoint_details	store_stock_details	section field desc
deposit_setoff_total	estimate_charge	operation_charges	patient_medicine_prescriptions	sample_collection	store_estimate_details	store_transaction_lot_details	section master
diagnostic_charges	favourite_reports	operation_org_details	patient_other_medicine_prescriptions	sch_resource_availability	store_grn_details	store_transfer_details	ha_item_code_type
diagnostic_charges_backup	fixed_asset_master	other_services_prescribed	patient_other_prescriptions	sch_resource_availability_details	store_grn_main	store_transfer_main	package_charges
diagnostic_reagent_usage	follow_up_details	outsource_sample_details	patient_packages	scheduler_appointment_items	store_indent_details	supp_inv_id	patient_prescription
diagnostics	growth_chart_reference_data	pack_org_details	patient_pdf_form_doc_values	scheduler_appointments	store_indent_main	supplier_master	

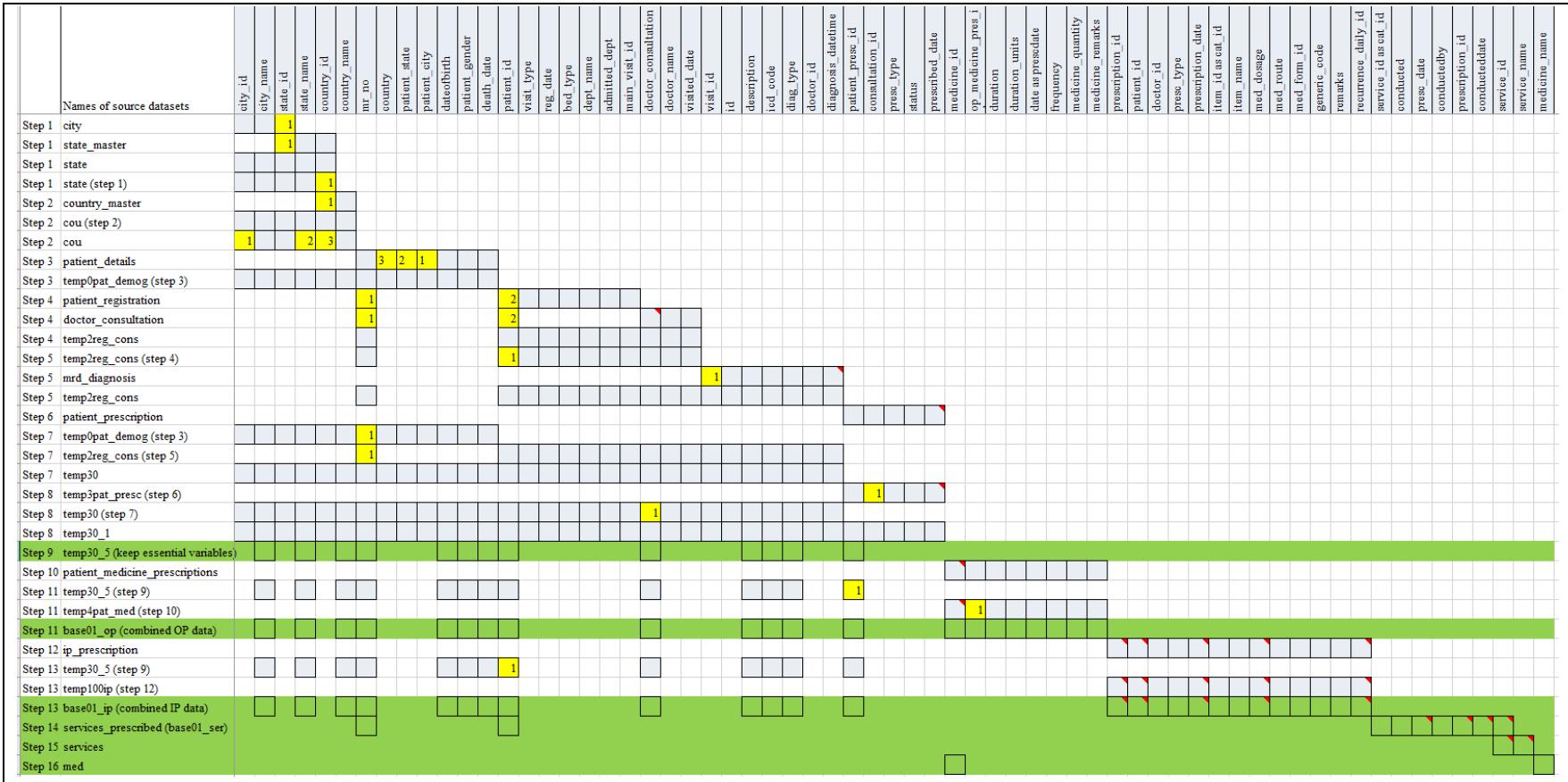
This table presents a glimpse of inventory of data tables in database. The cells marked in yellow are used for the generation of the analysis ready datasets.

Figure 2-4: Extraction of relevant data from Source database



Each row in the above figure is one source dataset. Each column represents a variable. The gray-coloured cell denotes the presence of the variable in the dataset. There are 13 datasets, and 72 variables represented in the above table used to derive analysis datasets

Figure 2-5: Staged data converted into 6 datasets



The source datasets have been merged step by step using the variables marked in yellow colour. The above picture shows 16 steps taken to generate 6 datasets, marked in Green for subsequent processing. The variables marked in numbered yellow squares are the logical links between the datasets and are used for data preparation steps.

Figure 2-6: Staged data

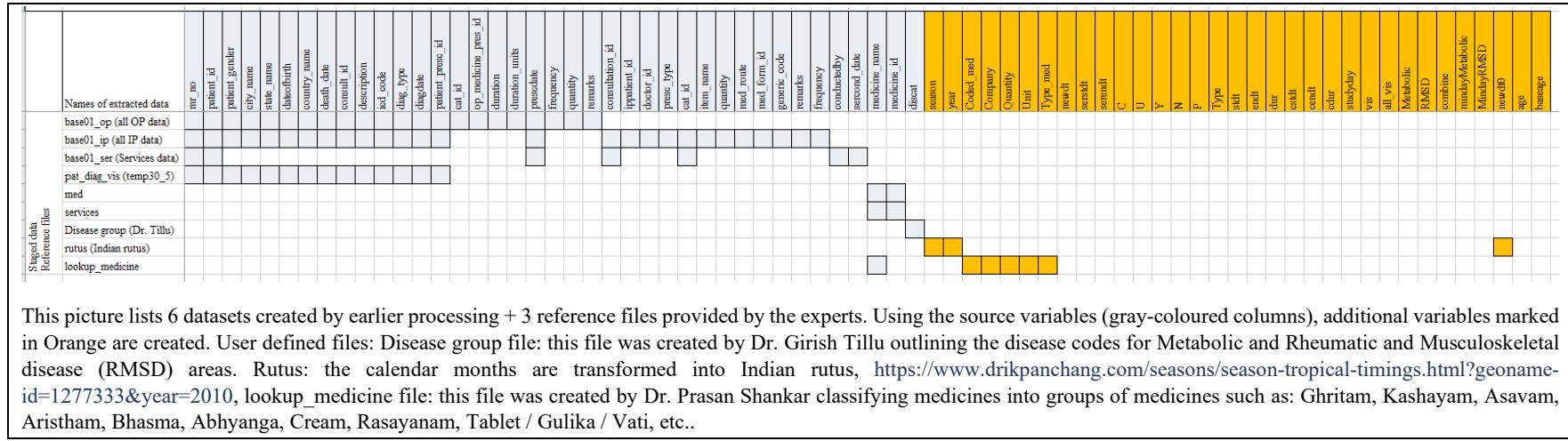
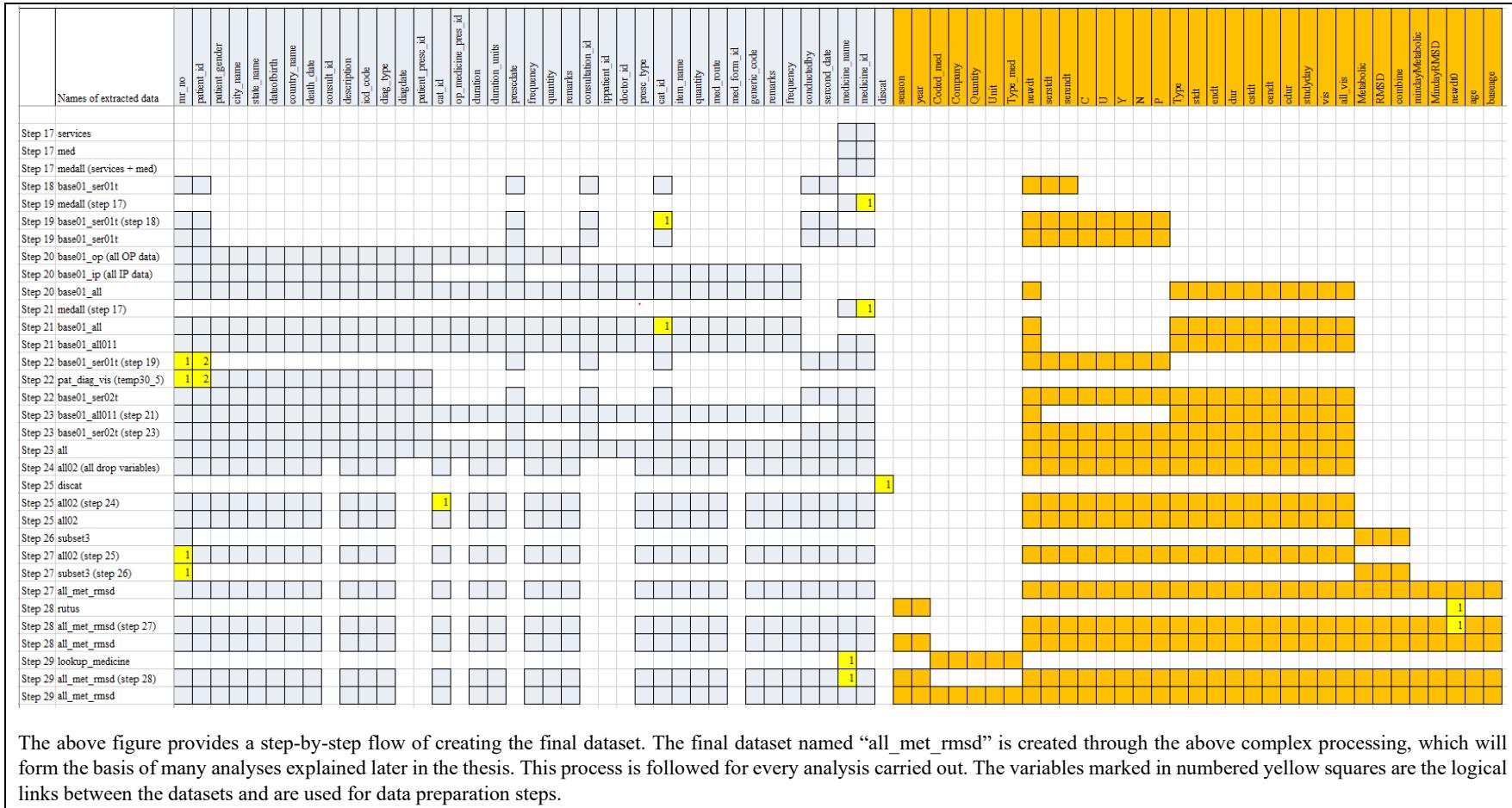
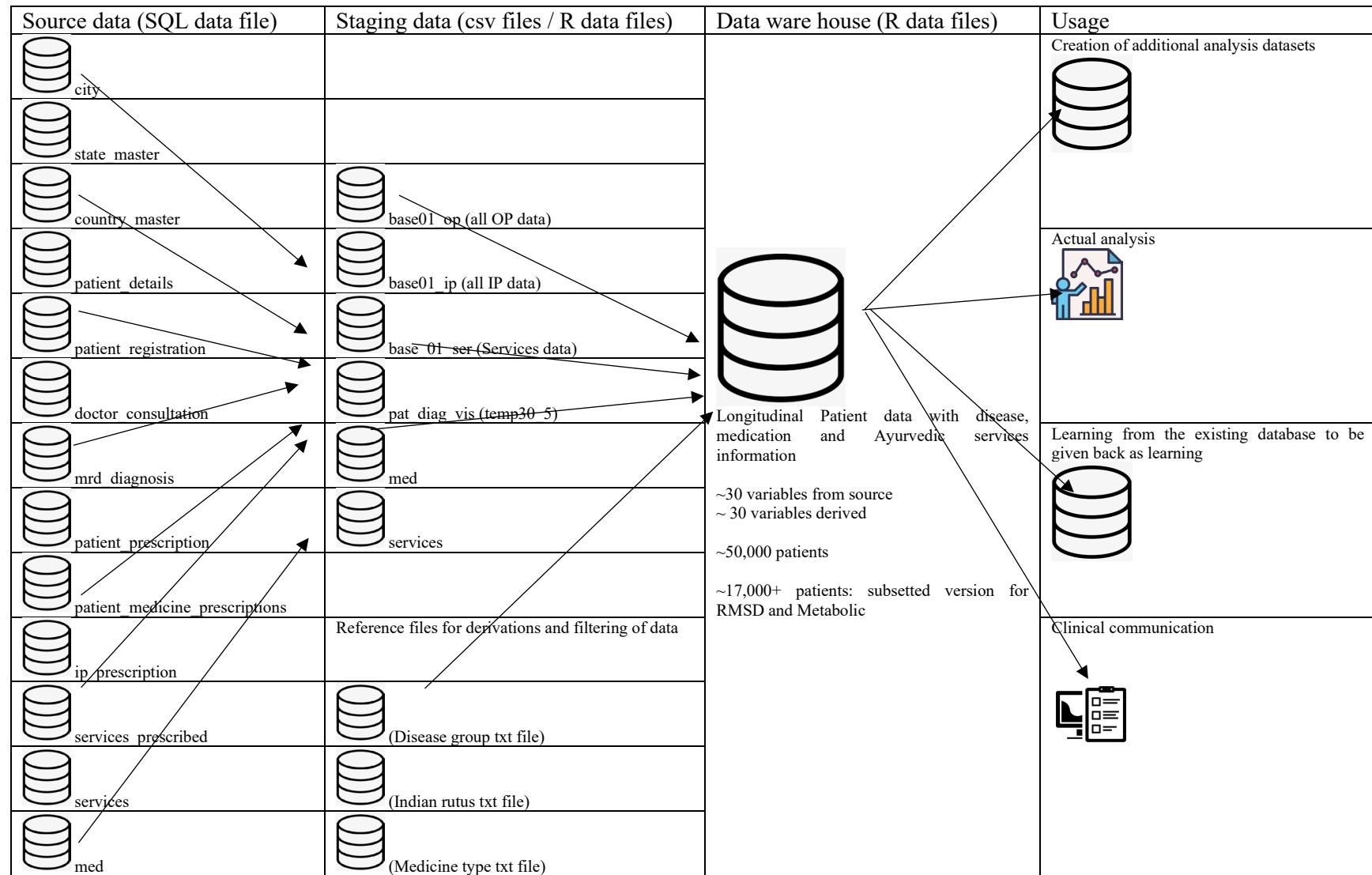


Figure 2-7: Final dataset with 39 source variables and 33 new derived variables



The above figure provides a step-by-step flow of creating the final dataset. The final dataset named “all_met_rmsd” is created through the above complex processing, which will form the basis of many analyses explained later in the thesis. This process is followed for every analysis carried out. The variables marked in numbered yellow squares are the logical links between the datasets and are used for data preparation steps.

Figure 2-8: Data flow from source data to interpretable results



SQL data: source data captured in the database, staging data: logically combined intermediate datasets from source data by software development, Reference files: files needed for deriving certain information which is not present in the source database, Longitudinal data: dataset having 1 record per patient, per visit, per disease and per treatment, the dataset is filtered for the Metabolic and Rheumatic and Musculoskeletal disease (RMSD) patients, analysis is carried out using such derived dataset(s).

2.4 Clinical data understanding

2.4.1 Broad checks on the datasets

As a part of clinical understanding, structural and contents checks were performed for completeness, correctness, to identify duplication, to name a few across 90+ datasets and 500+ variables. Some of these were programmatic checks and some were manual checks to make the data available for exploration and “analysis ready”. Unique values for each variable were checked to understand the value level detail for consistency and variations. The following data and contents review was done for vital sign dataset, lab measurement dataset, treatment dataset, as well as review of clinically important variables. After reviewing the source datasets for clinical understanding, derived datasets were also reviewed.

2.4.2 Contents checks

500+ variables were captured across many datasets for each visit and each patient (Table 6-3) were classified and mapped into the following categories, (1) Ayurvedic data, (2) Background, (3) Disease, (4) Doctor's Notes, (5) Food / Exercise, (6) Hospital Visit, (7) Lab report, (8) Measurement, and (9) Treatment / Procedure. If there was any non-missing data present in a particular variable then a pseudo value “Yes” was assigned, if the data was missing then a pseudo “Blank or No” value was assigned for the purpose of analysis. This data was presented as a listing for each patient for each visit (day) by the categorization presented above. If the data was available, it was presented as a color-coded bar. If the data was missing, then it was presented as a white blank space (Figure 3-2).

2.4.3 Visit pattern analysis

Frequency counts of 4 parameters, (1) new Out-Patients added on that day, (2) total number of patients visiting on that day, (3) total number of In-Patient visits on that day, and (4) total number of Out-Patient visits on that day were calculated for each day to understand the patient flow to hospital from year 2011 to 2016. The calculated information was represented on a calendar.

2.4.4 Patient disease and treatment journey view

Patient profile report generation module was also checked to understand the contents. Two longitudinal interactive views were created to display individual patient data. first version of patient profile contains the following information (Figure 3-4): Patient ID (mr_no), gender, study day, In-Patient visits are displayed in blue colour and Out-Patient visits are displayed in Orange colour. The tooltip of the interactive display holds information about the following data points not displayed on the page: (1) Study day, (2) Total duration of hospital visits, (3) Disease description variable accompanying ACD codes, (4) Medicine provided at that visit, (5) Minday Metabolic: First day on which any metabolic disease has been reported by patient, (6) Minday RMSD: First day on which any RMSD disease has been reported by patient.

Second version of patient profile contains the following information (Figure 3-5): Patient ID (mr_no), gender, base age, category, Code, description, study day. The Diseases were displayed in blue coloured bars and treatments prescribed were marked in orange coloured bars. Disease

duration and treatment duration bars were created as follows: Duration between minimum and maximum reported date for a disease as well as prescribed treatment was calculated, this duration was displayed on the visualization. The tooltip contains information about the following data points not displayed on the page: (1) Daystt: Start of event in days, (2) Disdur: Duration of event in days, (3) Disstt: Start date of event, (4) Diend: End date of event.

2.5 Studying demographics and patient specific factors

Analysis datasets created in the earlier sections (converting clinical data into analyzable format and Clinical data understanding) are used to generate necessary analysis. If the existing variables were sufficient to produce the results, then these were used as is. In case additional information was needed then that was derived as appropriate. Reports using tableau software were created. Multiple types of data visualizations were used so that data was represented appropriately.

Preliminary analysis was carried out by Dr. Girish Tillu and he found that the database contains a lot of patients in Metabolic area and (Rheumatic and Musculoskeletal disease) RMSD area [7]. 10 Metabolic and 97 RMSD disease codes were identified (Table 6-2). The analysis was split into 2 major sections in this thesis. Reports were created for the complete dataset and additional reports were created on a subset of patients' metabolic and RMSD disease areas.

Following interactive reports were created and were analyzed for the complete set of patients to gain insights into patient demographic and patient specific factors: (1) A tabular summary of total number of patients treated (Figure 3-6), (2) Patient analysis by country – a Country-wise visualization on the world map (Figure 3-7), (3) Age distribution by country and gender – 2 boxplot representations (Figure 3-8), (4) A tabular summary of Blood group distribution by gender (Figure 3-9), (5) A boxplot representation of analysis of number of visits and types of visit (IP / OP) (Figure 3-10), (6) Number of diseases reported by gender – a descriptive summary statistics table (Figure 3-11)

Subsequent reports were created for metabolic and RMSD patients: (7) A bubble plot data tabulation for patients reporting RMSD and Metabolic diseases (Figure 3-12), (8) Disease distribution by Age and gender – a boxplot representation (Figure 3-13), (9) A tabular representation of Patient visit duration for Disease categories by Gender (Figure 3-14), using the following logic: The duration between the first visit and the last visit for each patient has been calculated and categorized as follows: ≥ 1 day, ≥ 1 month, ≥ 2 months, ≥ 3 months, ≥ 6 months, ≥ 1 year, ≥ 2 years, ≥ 3 years, ≥ 4 years and ≥ 5 years. In this analysis patients were counted multiple times as per available data for each time period. A patient visiting for more than 5 years was counted in all categories. If a patient discontinued in the 4th month then that patient was counted in Day 1, ≥ 1 month, ≥ 2 months, ≥ 3 months categories. The colour gradient moves from Red to Green denoting low to high number of patients in each category. (10) Seasonal Variations within Metabolic and RMSD disease areas by Indian states (Vasant, Grishma, Varsha, Sharad, Hemant, and Shishir) [107] and gender (Figure 3-15). Pre and Post Disease Classification Analysis was carried out for Metabolic and RMSD disease areas to understand the disease trajectories [108] (Figure 3-16) The underlying data was generated from every day medical

practice at the hospital. Hence the diseases were reported almost at random. The following analysis used first occurrence of any disease as day 1 for an individual patient. Using this as a reference day “before period” and “after period” was derived. “Before period” provides significant amount of “baseline data”, “after period” provides specific insights into what would happen after the onset of the reference disease. The following algorithm was used to create the underlying data for analysis:

1. Each of the 107 diseases (10 Metabolic and 97 RMSD) was considered as a reference disease.
2. Day 1 was calculated as the reference day 1 for individual patient for each disease.
3. Other diseases for the same patient were arranged either before or after compared to this reference disease.
4. Duration was calculated before and after day 1, which is the reference day. This calculation provided the background view as well as future view.
5. This referencing allowed for more informative background disease as well as background medicine information. The duration was split into the following time points:

Table 2-1: Visit window table for Pre and post analysis

Before	After
Day 1 as reference	
Before 1 month	Within 1 month
Before 2 months	Within 2 months
Before 3 to 6 months	Within 3 to 6 months
Before 7 to 12 months	Within 7 to 12 months
Before 2nd year	Within 2nd year
Before 3rd year	Within 3rd year
Before 4th year	Within 4th year
Before 5 year	Within 5 year

2.6 Studying diagnostics and interventions

Diagnostics and interventions were studied using disease - disease, disease - treatment combinations / co-occurrences by using various methods. (1) Ayurvedic Classification of Disease (ACD) and International Classification of Diseases (ICD) [109] mapping exercise was carried out to understand the underlying disease burden (Figure 3-17, Figure 3-18, Figure 3-19, Figure 3-20), (2) Summary table for disease by Prakriti and gender was created (Figure 3-21), (3) Co-morbidity analysis was carried out using 3 different approaches (Figure 3-22, Figure 3-23, Figure 3-24, Figure 3-25, and, Figure 3-26), (4) Treatment and disease analysis at individual patient level was carried out to understand treatment protocol (Figure 3-27, Figure 3-28, Figure 3-29), (5) Area graph representation of diseases was created to show variations related day-to-day, seasons, gender, and diseases (Figure 3-30). (6) Mosaic plot displays were put together for disease and treatment combinations (Figure 3-31, Figure 3-33, Figure 3-34). (7) Cross tabulation of prescribed treatments and disease group by gender was generated, a couple examples for specific disease conditions or specific treatment were shown to provide the utility of this analysis (Figure 3-35). (8) Treatment regimen using bhasma is very specific to Ayurveda, an analysis was carried out to understand the duration of treatment pre and post usage of bhasma (Figure 3-36).

Additional Disease – treatment analysis with pre and post visit window approach was performed as described: (9) Circular view representation was created (Figure 3-37, Figure 3-38), (10) Distance metrics analysis for disease trajectories and medicine trajectories were created (Figure 3-39, Figure 3-40), and (11) Multi-dimensional data representation using radar plot displays were created (Figure 3-41), (12) Dynamic bubble plot visualization was created (Figure 3-42).

International Classification of Diseases (ICD) codes were used in patient paperwork, including hospital records, medical charts, visit summaries, and bills. These codes guarantee that a patient obtains right treatment and were charged appropriately for any medical services. An attempt was made to map Ayurvedic Classification Dictionary (ACD) codes with ICD codes by manually comparing the ACD dictionary. Summary tables and boxplots summarizing the ICD classes with the frequency of patient's visits and classifying by gender along with their duration of visit were created.

Bar graph representation for disease by Prakriti and gender was created.

Co-morbidity analysis was carried out by using 3 different approaches: First approach produced a bubble plot, boxplots, summary statistics tables and frequency tables for number of other diseases reported along with the primary disease. Second approach recreated the same analysis by visit window of each month. Third approach created disease trajectories are visually displayed in a form of collapsible tree (Figure 3-22, Figure 3-23, Figure 3-24, Figure 3-25, and, Figure 3-26).

Algorithm for first approach: (1) A unique combination of Patient ID, gender and reported disease at any given time point was created. (2) Subsequently, a dataset having combination of diseases for an individual patient was created. E.g., if a patient had reported 5 unique diseases, then all the combinations of these 5 diseases were created i.e. 5C_2 combinations were created i.e. 10 combinations. (3) The resulting data had the following structure: Patient ID, Disease1, Disease2,

and Gender. (4) Frequency count of distinct patients was calculated for each Disease1, Disease2 combination and gender. (5) Using this data following analysis was carried out: Summary statistics of age group for each disease by gender; Boxplot of age group for each disease by gender; Bubble plot for each disease where the bubble size was determined by the count of unique patient IDs. For each disease number of other unique diseases by gender were reported. Tooltip on the bubble plot provides information about count of distinct number of patients, and summary statistics for age group. The dashboard is controlled by a “Primary Code” or a reference disease and relevant data is displayed on the page. Other bubbles in the bubble plot, display the diseases reported by this subset of patients at any point in time (these could be clinically related or unrelated or could have occurred before or after the occurrence of reference disease). The tooltip shows minimum, median, and maximum age and distinct counts of patients. A table on the left side shows number of other diseases experienced by the patient (Figure 3-22, Figure 3-23, Figure 3-24).

Algorithm for second approach: Same calculations for first algorithm were followed to create comorbidities, but now in addition the time factor of month was added to get insights into seasonal variation and bubble plots by gender and month using a reference disease were created (Figure 3-25).

Algorithm for third approach: (1) Diseases experienced by each patient were sorted by date and only the first instance of a disease was retained. This chronological list of diseases is labelled as “disease trajectory”. Similar analysis when carried out for medicines, the trajectory created is labelled as “medicine trajectory” (2) For each disease trajectory the frequency counts were created and were displayed as a collapsible tree. (3) The tree has filled blue dots which open additional branches, white filled blue dots are the end of the branch, (N=xx) at each of the branches display number of patients reporting that disease trajectory. Disease trajectories were created using R programming. Final output was stored in Json file. Json file was used as the input to the D3js Java programming. Index.html file was hosted on the Github page to create the interactive page <https://coursephd.github.io> (Figure 3-26).

Treatment and disease analysis at individual patient level was carried out. (1) When a disease was reported for the first time then that was counted as “first time disease reported”, any subsequent repetition was counted as “Repeat”. (2) When a treatment was prescribed for the very first time then that was counted “first time treatment prescribed”, any subsequent repetition was counted as “Repeat”. (3) These two calculations were repeated throughout the complete duration for each patient.

Area graph representation of diseases was created to show variations related to day-to-day changes, seasonal changes, by gender, and diseases. This analysis provides frequency count of patients for each disease by month and by gender. (1) Unique combinations of patients, diseases by date and gender were created, (2) Frequency counts of females were displayed in blue color and counts for males were displayed in orange color. (3) this visual opens for each day, by clicking on “+” sign on the x-axis, providing monthly to weekly to daily view without having to go through multiple visualizations.

A mosaic view of disease and intervention was created to explore the following: (1) Total number of interventions prescribed during one disease. (2) To check if there were possible relationships between different diseases and interventions considering multiple diseases reported and multiple interventions prescribed, layers of visualizations were created in the following manner: (1) TreeMapDisMed-Parameter sheet is used to filter a particular disease, which is displayed as a green colored box, (2) smaller boxes inside each disease display one intervention each, (3) Medicine-count sheet provides information on total number of different interventions prescribed for the selected disease, (4) Medicine-list sheet shows a detailed list of interventions with the total patients prescribed with them as well as total patients suffering from the disease (Figure 3-31).

TreeMapDisMed-Parameter sheet can be used to filter a particular intervention and the whole analysis could be performed from an intervention's perspective. (1) TreeMapDisMed-Parameter sheet is used to filter a particular intervention, which was displayed as a single or multiple green colored boxes across multiple disease boxes, (2) Disease-count sheet provides information on total number of different diseases for which this medicine was prescribed, (4) Medicine-list sheet shows a detailed list of diseases with the total number of patients prescribed with the intervention as well as total patients suffering from different diseases (Figure 3-34).

Cross tabulation of prescribed treatments and disease group by gender was also generated. The interactive visualization was used to create a few examples for specific disease conditions or specific treatment. First example is created using Balaristham and second example is created using bhasma. An attempt was made to understand the impact of usage of Bhasma on patient visit duration. Dataset for individual patients with the following variables was created: Visit duration: cdur – “Total duration in days”: cdur = End visit date – start visit date +1, “Pre bhasma duration”: prebhasmadur = bhasmamin (start date of bhasma intake) – 1, “Post bhasma duration”: postbhasmadur = cdur – bhasmamin (start date of bhasma intake) + 1.

A simple t-test analysis was performed on the created data. The pre bhasma duration and post bhasma duration was analyzed by t-test. This analysis can be carried out by an appropriate non parametric test as well.

Analysis for disease – treatment with pre and post visit window approaches:

The circular visualization allows a single page view of relation between disease – disease and / or disease – treatment across multiple time points. This view shows the following information: (1) A table on the middle row: On day 1 of a disease how many distinct diseases have been reported and how many distinct medicines prescribed, this same information is shown as the green bars inside a circle, (2) Pre and post time windows are displayed and for each of the time window a similar table is represented in the upper section of the visualization. (3) In the lower section of the visualization, 1st row represents the co-occurrence of disease – disease and / or disease – treatment before day 1 of the reference disease. (4) Last row represents the same co-occurrence data after day 1 of the reference disease (Figure 3-37, Figure 3-38).

An attempt was made to understand the disease trajectories for patients by using mathematical distances. There are numerous distance measures available in mathematics and statistics which

allows understanding of similarity and dis-similarity between objects, in our case disease trajectories [110].

Following assumptions were used to derive the disease trajectory: (1) Diseases experienced by each patient were sorted by date and only first instance of a disease was retained. (2) This enabled in creation of a disease trajectory for each patient for each reference disease, before and after the occurrence of the reference disease. (3) Cartesian product of patients was created for each reference disease, so that distances could be calculated. A cartesian product is a set of all possible pairs, in this case all possible pairs of reference disease and other diseases for individual patient. (4) The similarity measure was calculated for each disease trajectory, e.g., Jaccard distance was used as a distance measure for this display [111]. The Jaccard distance highlights similarity between finite sample sets. It is defined as the size of the intersection divided by the size of the union of the sample sets [112]. For our example, this will be calculated as the common diseases reported divided all the diseases reported in each case. (5) Jaccard distance closer to 0 shows dissimilarities and closer to 1 show similarities. (6) The distances were divided into 4 categories 0 to 0.25, 0.25 to 0.5, 0.5 to 0.75 and 0.75 to 1 for data visualization perspective. (7) These calculated distances are displayed as a butterfly plot for easy comparison of underlying values [105]. This plot is a comparative bar plot to display comparison of a continuous variable across groups. Similar Analysis to understand the medicinal trajectory was performed.

Radar plot representation: a multidimensional, comparative view of the different diseases was created to understand at various aspects of the diseases. The radar plot chart presents multidimensional metrics. Radar plots can convey a large amount of information [100]. They provide a standardized view of different indicators on one scale. The following information for each disease was visualized as a percentile and is represented as a dimension on a heptagon (as there are 7 parameters considered in this example): (1) Distinct number of patients for each disease, (2) Number of times a disease is reported, (3) Number for a specific disease (chronological number of disease reported by a patient) e.g. a disease is reported as the very first disease or third disease or fifth disease, etc., (4) Number of diseases before the specific disease, (5) Number of diseases after the specific disease, (6) Number of treatments before the specific disease, (7) Number of treatments after the specific disease. Trellis plot display allows multiple representations of same kind next to each other [99].

Dynamic bubble plot visualization: explanation of an algorithm using Amavaata (ACD code A6.0) as an example: (1) Identified unique patients who have had Amavaata reported at least once, (2) All the other diseases and prescribed medicines for this subset of patients, (3) Created an input Json file to be passed into a D3js java program. The underlying utility generated a dynamic bubble plot. The size of bubble is proportional to the total number of patients. The links display relationships between diseases and treatments. If a bubble is “double clicked” then all the “unrelated data” to that bubble vanishes and only relevant data is retained on the screen. Once double clicked again the complete data is displayed again (Figure 3-42).

Same type of analysis was carried out for the Pre and post period, example for Amavaata (A6.0) by period [https://coursephd.github.io/nodediagram/A2_0byperiod/] Similar, views can be created for any number of diseases and treatments, links below provide similar examples for the disease Prameha (P5.0) and its treatments and comorbidities

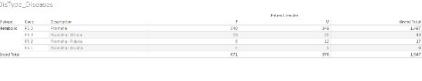
Prameha [https://coursephd.github.io/nodediagram/P5_0_Prameha/]

Prameha by period [https://coursephd.github.io/nodediagram/P5_0_Pramehabyperiod/]

2.7 Summary of methods section

Various methods getting employed have been explained in the earlier sections of chapter 2. These data explorations can be used by different stake holders like Hospital management (HM) from administration point of view, treating doctors (Medics), and by basic researchers (Scientists). Table below (Table 2-2) systematically presents a consolidated view of various analysis, context about different analysis and their possible relationships with each other. The screenshot attached in the table is not of the best resolution but is only representative of the actual analysis. There is a hyperlink provided below each of the figure which takes the user to the actual analysis stored on Tableau website. The user would have freedom to zoom in and out the visualizations as well as additional interactive abilities offered by the system.

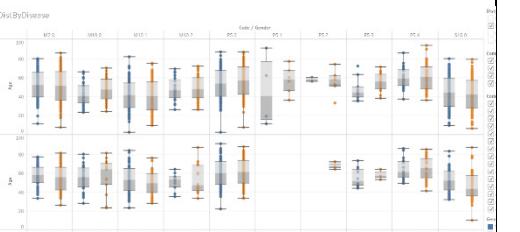
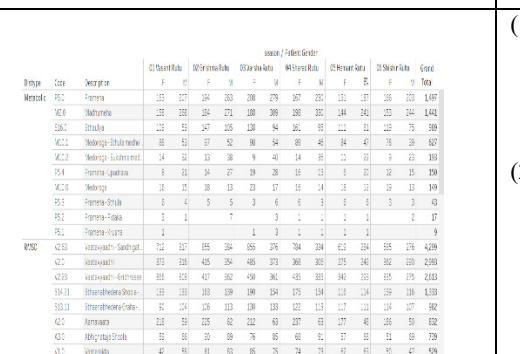
Table 2-2: Proposed methods and analysis use cases

Stake holders	Classification	Type of analysis	Figure number and analysis name (linked to the actual figure)	Snapshot of the analysis (the picture is attached here to provide a quick look into the type of analysis)	Context of the proposed analysis
HM, Medics, Scientists	Clinical data understanding	Tabular frequency table	Figure 3-1: A snippet of disease table by gender		<ul style="list-style-type: none"> (1) Data quality check based on examples of a couple of diseases. (2) Generation of ideas about how “end users” are using the system
HM, Medics, Scientists	Clinical data understanding	Individual patient level data listing	Figure 3-2: Variable classification by categories		<ul style="list-style-type: none"> (1) Understanding data generation process at each visit for each patient to gain present status of data and provide feedback into improvements of system architecture. (2) Improve operational efficiencies of the Hospital Management Information system

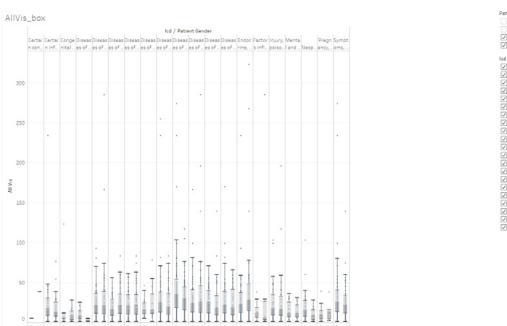
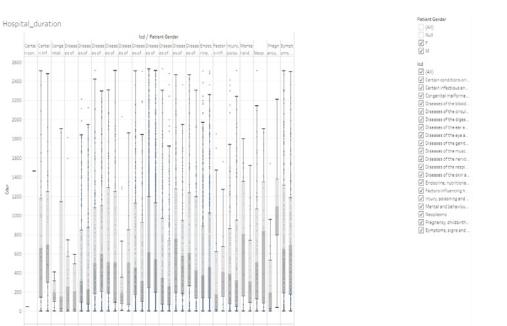
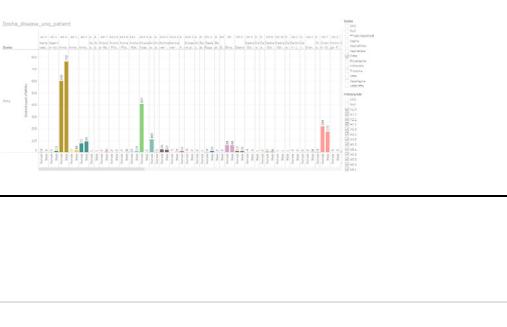
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HM	Clinical data understanding, operational efficiencies	Calendar plot	Figure 3-3: Visit pattern analysis	<p>Sheet 1</p> <table border="1"> <thead> <tr> <th>Month of Var1</th> <th>Week of Var1</th> <th>Sunday</th> <th>Monday</th> <th>Tuesday</th> <th>Wednesday</th> <th>Thursday</th> <th>Friday</th> <th>Saturday</th> </tr> </thead> <tbody> <tr> <td>January</td> <td>Week 1</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>January</td> <td>Week 2</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>January</td> <td>Week 3</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>January</td> <td>Week 4</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>January</td> <td>Week 5</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>January</td> <td>Week 6</td> <td></td> <td></td> <td></td> <td></td> <td></td> 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Medics	Patient disease and treatment journey	Individual patient level data listing	Figure 3-4: Patient visit profile – Horizontal view	<p>Patient_Visit_View</p>	<ul style="list-style-type: none"> (1) An analysis of how a patient journey is documented, how can this study be used prospectively and retrospectively to understand disease progression and treatment protocols (2) Convert treatment ideas into documented material (3) Improvements to the data standards and system architecture 																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
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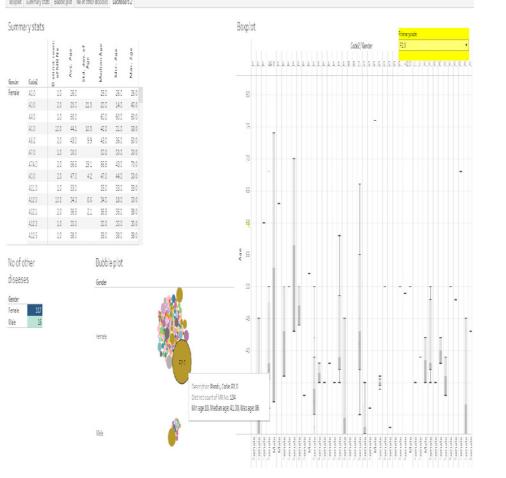
Stake holders	Classification	Type of analysis	Figure number and analysis name (linked to the actual figure)	Snapshot of the analysis (the picture is attached here to provide a quick look into the type of analysis)	Context of the proposed analysis																																																																																			
HM, Medics, Scientists	Study of demographics and patient specific factors	Tabular frequency table	Figure 3-6: Total Number of Patients	<p>01 NoOfPatients 02 Country 03 AgeBoxplotCountry 04 Age</p> <p>Summary of distinct number of patients</p> <table border="1"> <thead> <tr> <th>Common</th> <th>NA</th> <th>Grp OnlyIP</th> <th>OnlyOP</th> <th>Grand Total</th> </tr> </thead> <tbody> <tr> <td>3,491</td> <td>0</td> <td>4,145</td> <td>38,903</td> <td>39,557</td> </tr> </tbody> </table>	Common	NA	Grp OnlyIP	OnlyOP	Grand Total	3,491	0	4,145	38,903	39,557	<ul style="list-style-type: none"> (1) Demographic profiling analysis to understand health seeking behaviours of patients (2) Disease profiling based on preliminary disease analysis, visit patterns and types of visits (In-patient and out-patient visits) (3) Use such analysis to compare against demographic profiling of any other main-stream hospital to understand health seeking behaviours (4) Use disease profiling study to understand epidemiology (5) Use this analysis for defining public health policies to local and central authorities (6) Secondary use of this analysis is to find data quality 																																																																									
Common	NA	Grp OnlyIP	OnlyOP	Grand Total																																																																																				
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HM, Medics, Scientists	Data on world map	Figure 3-7: Country-wise Visualization																																																																																						
HM, Medics, Scientists	Boxplot	Figure 3-8: Age distribution by country, age distribution by gender																																																																																						
HM, Medics, Scientists	Tabular frequency table	Figure 3-9: Blood-group Distribution by gender	<p>07 BloodGroup</p> <table border="1"> <thead> <tr> <th>Blood...</th> <th>Female</th> <th>Male</th> <th>NA</th> <th>Grand Total</th> </tr> </thead> <tbody> <tr> <td>O+</td> <td>6,340</td> <td>6,684</td> <td></td> <td>13,024</td> </tr> <tr> <td>B+</td> <td>4,490</td> <td>4,956</td> <td></td> <td>9,446</td> </tr> <tr> <td>A+</td> <td>2,997</td> <td>3,030</td> <td></td> <td>6,027</td> </tr> <tr> <td>AB+</td> <td>828</td> <td>1,046</td> <td></td> <td>1,874</td> </tr> <tr> <td>O-</td> <td>434</td> <td>447</td> <td></td> <td>881</td> </tr> <tr> <td>B-</td> <td>265</td> <td>259</td> <td></td> <td>524</td> </tr> <tr> <td>A-</td> <td>239</td> <td>179</td> <td></td> <td>417</td> </tr> <tr> <td>AB-</td> <td>80</td> <td>87</td> <td></td> <td>167</td> </tr> <tr> <td>A1+ve</td> <td>30</td> <td>17</td> <td></td> <td>47</td> </tr> <tr> <td>A1-ve</td> <td>6</td> <td>1</td> <td></td> <td>7</td> </tr> <tr> <td>A1B+ve</td> <td>3</td> <td>4</td> <td></td> <td>7</td> </tr> <tr> <td>A2+ve</td> <td>1</td> <td></td> <td></td> <td>1</td> </tr> <tr> <td>A2B+ve</td> <td></td> <td>1</td> <td></td> <td>1</td> </tr> <tr> <td>NA</td> <td></td> <td></td> <td>1</td> <td>1</td> </tr> <tr> <td>Null</td> <td>0</td> <td>0</td> <td></td> <td>0</td> </tr> <tr> <td>Grand Total</td> <td>15,713</td> <td>16,710</td> <td>1</td> <td>32,424</td> </tr> </tbody> </table>	Blood...	Female	Male	NA	Grand Total	O+	6,340	6,684		13,024	B+	4,490	4,956		9,446	A+	2,997	3,030		6,027	AB+	828	1,046		1,874	O-	434	447		881	B-	265	259		524	A-	239	179		417	AB-	80	87		167	A1+ve	30	17		47	A1-ve	6	1		7	A1B+ve	3	4		7	A2+ve	1			1	A2B+ve		1		1	NA			1	1	Null	0	0		0	Grand Total	15,713	16,710	1	32,424
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		Descriptive summary statistics	Figure 3-11: Descriptive summary statistics by number of Diseases by Age and Gender	<table border="1"> <caption>Female</caption> <thead> <tr> <th>Count of</th> <th>Age</th> <th>Avg</th> <th>Std dev</th> <th>Median</th> <th>Min</th> <th>Max</th> </tr> </thead> <tbody> <tr><td>1</td><td>12,433</td><td>46</td><td>30</td><td>18</td><td>1</td><td>96</td></tr> <tr><td>2</td><td>5,652</td><td>48</td><td>30</td><td>18</td><td>2</td><td>93</td></tr> <tr><td>3</td><td>2,459</td><td>49</td><td>31</td><td>17</td><td>2</td><td>93</td></tr> <tr><td>4</td><td>1,215</td><td>51</td><td>51</td><td>17</td><td>2</td><td>87</td></tr> <tr><td>5</td><td>528</td><td>50</td><td>50</td><td>15</td><td>9</td><td>84</td></tr> <tr><td>6</td><td>441</td><td>49</td><td>49</td><td>15</td><td>9</td><td>82</td></tr> <tr><td>7</td><td>182</td><td>53</td><td>52</td><td>13</td><td>12</td><td>79</td></tr> <tr><td>8</td><td>99</td><td>48</td><td>48</td><td>15</td><td>13</td><td>80</td></tr> <tr><td>9</td><td>77</td><td>51</td><td>51</td><td>15</td><td>14</td><td>82</td></tr> <tr><td>10</td><td>29</td><td>53</td><td>51</td><td>21</td><td>33</td><td>86</td></tr> <tr><td>11</td><td>29</td><td>47</td><td>49</td><td>17</td><td>22</td><td>66</td></tr> <tr><td>12</td><td>31</td><td>44</td><td>39</td><td>20</td><td>3</td><td>86</td></tr> <tr><td>13</td><td>2</td><td>56</td><td>56</td><td>21</td><td>41</td><td>71</td></tr> <tr><td>14</td><td>4,163</td><td>46</td><td>45</td><td>19</td><td>2</td><td>101</td></tr> <tr><td>15</td><td>9</td><td>53</td><td>56</td><td>9</td><td>20</td><td>56</td></tr> <tr><td>16</td><td>23</td><td>50</td><td>50</td><td>13</td><td>6</td><td>41</td></tr> <tr><td>17</td><td>9</td><td>30</td><td>18</td><td>20</td><td>18</td><td>71</td></tr> </tbody> </table> <table border="1"> <caption>Male</caption> <thead> <tr> <th>Count of</th> <th>Age</th> <th>Avg</th> <th>Std dev</th> <th>Median</th> <th>Min</th> <th>Max</th> </tr> </thead> <tbody> <tr><td>1</td><td>14,375</td><td>46</td><td>47</td><td>19</td><td>2</td><td>108</td></tr> <tr><td>2</td><td>9,600</td><td>48</td><td>49</td><td>19</td><td>2</td><td>99</td></tr> <tr><td>3</td><td>4,000</td><td>49</td><td>49</td><td>19</td><td>2</td><td>99</td></tr> <tr><td>4</td><td>2,000</td><td>51</td><td>55</td><td>19</td><td>2</td><td>93</td></tr> <tr><td>5</td><td>847</td><td>50</td><td>54</td><td>18</td><td>2</td><td>87</td></tr> <tr><td>6</td><td>749</td><td>49</td><td>49</td><td>18</td><td>2</td><td>84</td></tr> <tr><td>7</td><td>377</td><td>57</td><td>56</td><td>15</td><td>33</td><td>88</td></tr> <tr><td>8</td><td>28</td><td>46</td><td>52</td><td>29</td><td>6</td><td>76</td></tr> <tr><td>9</td><td>23</td><td>51</td><td>51</td><td>23</td><td>45</td><td>11</td></tr> <tr><td>10</td><td>10</td><td>53</td><td>51</td><td>21</td><td>33</td><td>86</td></tr> <tr><td>11</td><td>10</td><td>47</td><td>49</td><td>17</td><td>22</td><td>66</td></tr> <tr><td>12</td><td>11</td><td>44</td><td>39</td><td>20</td><td>3</td><td>86</td></tr> <tr><td>13</td><td>1</td><td>56</td><td>56</td><td>21</td><td>41</td><td>71</td></tr> <tr><td>14</td><td>4,163</td><td>43</td><td>41</td><td>19</td><td>2</td><td>103</td></tr> <tr><td>15</td><td>9</td><td>51</td><td>47</td><td>9</td><td>21</td><td>58</td></tr> <tr><td>16</td><td>23</td><td>41</td><td>41</td><td>0</td><td>41</td><td>41</td></tr> <tr><td>17</td><td>9</td><td>35</td><td>35</td><td>35</td><td>35</td><td>35</td></tr> </tbody> </table>	Count of	Age	Avg	Std dev	Median	Min	Max	1	12,433	46	30	18	1	96	2	5,652	48	30	18	2	93	3	2,459	49	31	17	2	93	4	1,215	51	51	17	2	87	5	528	50	50	15	9	84	6	441	49	49	15	9	82	7	182	53	52	13	12	79	8	99	48	48	15	13	80	9	77	51	51	15	14	82	10	29	53	51	21	33	86	11	29	47	49	17	22	66	12	31	44	39	20	3	86	13	2	56	56	21	41	71	14	4,163	46	45	19	2	101	15	9	53	56	9	20	56	16	23	50	50	13	6	41	17	9	30	18	20	18	71	Count of	Age	Avg	Std dev	Median	Min	Max	1	14,375	46	47	19	2	108	2	9,600	48	49	19	2	99	3	4,000	49	49	19	2	99	4	2,000	51	55	19	2	93	5	847	50	54	18	2	87	6	749	49	49	18	2	84	7	377	57	56	15	33	88	8	28	46	52	29	6	76	9	23	51	51	23	45	11	10	10	53	51	21	33	86	11	10	47	49	17	22	66	12	11	44	39	20	3	86	13	1	56	56	21	41	71	14	4,163	43	41	19	2	103	15	9	51	47	9	21	58	16	23	41	41	0	41	41	17	9	35	35	35	35
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HM, Medics, Scientists	Study of demographics and patient specific factors	Bubble plot	Figure 3-12: Data tabulation for patients reporting RMSD and Metabolic diseases		Analysis similar to described above on a subset of Metabolic and Rheumatic and Musculoskeletal disease (RMSD) patients																																																																																																																																																																																																																																																										

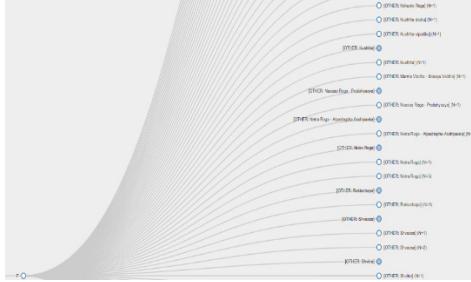
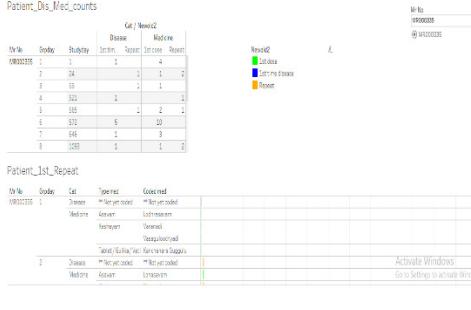
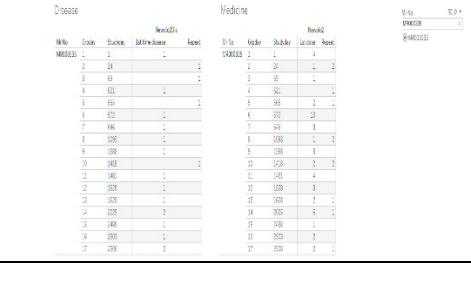
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HM, Medics		Boxplot	Figure 3-13: Disease distribution by age and gender		
		Tabular frequency table	Figure 3-14: Patient visit duration for Disease categories by Gender		
HM, Medics	Disease pattern analysis	Tabular frequency table	Figure 3-15: Disease distribution by Seasonal Variations and gender		<p>(1) Diseases are differently experienced by females and males as well as natural variations affect the prevalence – can we detect if the natural variations are reported in our database</p> <p>(2) A byproduct of this analysis is understanding of data entry and disease classification process at each visit</p>

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HM, Medics	Co-morbidity analysis	Tabular frequency table	Figure 3-16: Pre and Post Disease Classification Analysis		<ul style="list-style-type: none"> (1) Discover disease relationships by creating chronological view (2) Differentiate pre and post diseases so that diagnosis and prognosis can be formed (3) Pre and post differentiation is carried out for the prescribed medicines so that use of medicines could be understood at a summary level 																																																																																																				
HM, Medics, Scientists	Health seeking behaviour and public policy	Tabular frequency table	Figure 3-17: ICD classification by Gender	<table border="1"> <thead> <tr> <th>ICD</th> <th>High</th> <th>Grand Total</th> <th>Patient Gender</th> </tr> </thead> <tbody> <tr> <td>Grand Total</td> <td>8,027</td> <td>4,455</td> <td>Null F M</td> </tr> <tr> <td>Certain conditions originating in the perinatal period</td> <td>2</td> <td>1</td> <td>1 1</td> </tr> <tr> <td>P01</td> <td>2</td> <td>1</td> <td>1</td> </tr> <tr> <td>Certain infectious and parasitic diseases</td> <td>90</td> <td>42</td> <td>40</td> </tr> <tr> <td>A01</td> <td>9</td> <td>6</td> <td>3</td> </tr> <tr> <td>A06</td> <td>1</td> <td>1</td> <td>1</td> </tr> <tr> <td>A15</td> <td>7</td> <td>3</td> <td>4</td> </tr> <tr> <td>A18</td> <td>3</td> <td></td> <td>0</td> </tr> <tr> <td>A20</td> <td>1</td> <td></td> <td>1</td> </tr> <tr> <td>A41</td> <td>1</td> <td></td> <td>1</td> </tr> <tr> <td>A46</td> <td>1</td> <td></td> <td>1</td> </tr> <tr> <td>A51</td> <td>2</td> <td></td> <td>2</td> </tr> <tr> <td>A90</td> <td>2</td> <td></td> <td>2</td> </tr> <tr> <td>A92</td> <td>5</td> <td></td> <td>4</td> </tr> <tr> <td>B01</td> <td>1</td> <td></td> <td>1</td> </tr> <tr> <td>B02</td> <td>5</td> <td></td> <td>5</td> </tr> <tr> <td>B07</td> <td>0</td> <td></td> <td>0</td> </tr> <tr> <td>B08</td> <td>2</td> <td></td> <td>1</td> </tr> <tr> <td>B19</td> <td>6</td> <td></td> <td>6</td> </tr> <tr> <td>B34</td> <td>1</td> <td></td> <td>1</td> </tr> <tr> <td>B35</td> <td>32</td> <td></td> <td>20</td> </tr> <tr> <td>B37</td> <td>4</td> <td></td> <td>4</td> </tr> <tr> <td>B74</td> <td>1</td> <td></td> <td>1</td> </tr> <tr> <td>B85</td> <td>1</td> <td></td> <td>1</td> </tr> </tbody> </table>	ICD	High	Grand Total	Patient Gender	Grand Total	8,027	4,455	Null F M	Certain conditions originating in the perinatal period	2	1	1 1	P01	2	1	1	Certain infectious and parasitic diseases	90	42	40	A01	9	6	3	A06	1	1	1	A15	7	3	4	A18	3		0	A20	1		1	A41	1		1	A46	1		1	A51	2		2	A90	2		2	A92	5		4	B01	1		1	B02	5		5	B07	0		0	B08	2		1	B19	6		6	B34	1		1	B35	32		20	B37	4		4	B74	1		1	B85	1		1	<ul style="list-style-type: none"> (1) ICD classification of disease is used globally to understand the disease burden. What patterns emerge via this analysis, what health seeking behaviors can be understood?
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HM, Medics, Scientists		Boxplot	Figure 3-18: Age distribution by ICD classification and Gender	<p>The boxplot displays the distribution of age for different ICD categories (e.g., A01, A06, A15, A18, A20, A41, A46, A51, A90, A92, B01, B02, B07, B08, B19, B34, B35, B37, B74, B85) categorized by gender (F, M). The Y-axis represents age in years, ranging from 0 to 80. The X-axis shows the ICD categories grouped by gender.</p>																																																																																																					

Stake holders	Classification	Type of analysis	Figure number and analysis name (linked to the actual figure)	Snapshot of the analysis (the picture is attached here to provide a quick look into the type of analysis)	Context of the proposed analysis
HM, Medics, Scientists		Boxplot	Figure 3-19: Visit distribution by ICD classification and Gender		
HM, Medics, Scientists		Boxplot	Figure 3-20: Duration distribution by ICD classification and Gender		
Medics, Scientists	Disease and Prakriti analysis	Barplot	Figure 3-21: Disease classification by Prakriti and Gender		What does Prakriti and disease data

Stake holders	Classification	Type of analysis	Figure number and analysis name (linked to the actual figure)	Snapshot of the analysis (the picture is attached here to provide a quick look into the type of analysis)	Context of the proposed analysis
Scientists	Co-morbidity analysis	Bubble plot + Boxplot + Descriptive summary statistics	Figure 3-22: Co-morbidity analysis approach 1 example 1: Vaatavyadhi		Disease co-morbidities generate insights
		Bubble plot + Boxplot + Descriptive summary statistics	Figure 3-23: Co-morbidity analysis approach 1 example 2: Pandu		

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Scientists		Bubble plot + Boxplot + Descriptive summary statistics	Figure 3-24: Co-morbidity analysis approach 1 example 3: Madhumeha	<table border="1"> <thead> <tr> <th>Gender</th> <th>No of other diseases</th> <th>Count</th> </tr> </thead> <tbody> <tr><td>Female</td><td>0</td><td>12</td></tr> <tr><td>Female</td><td>1</td><td>12</td></tr> <tr><td>Female</td><td>2</td><td>12</td></tr> <tr><td>Female</td><td>3</td><td>12</td></tr> <tr><td>Female</td><td>4</td><td>12</td></tr> <tr><td>Female</td><td>5</td><td>12</td></tr> <tr><td>Female</td><td>6</td><td>12</td></tr> <tr><td>Female</td><td>7</td><td>12</td></tr> <tr><td>Female</td><td>8</td><td>12</td></tr> <tr><td>Female</td><td>9</td><td>12</td></tr> <tr><td>Female</td><td>10</td><td>12</td></tr> <tr><td>Female</td><td>11</td><td>12</td></tr> <tr><td>Female</td><td>12</td><td>12</td></tr> <tr><td>Male</td><td>0</td><td>12</td></tr> <tr><td>Male</td><td>1</td><td>12</td></tr> <tr><td>Male</td><td>2</td><td>12</td></tr> <tr><td>Male</td><td>3</td><td>12</td></tr> <tr><td>Male</td><td>4</td><td>12</td></tr> <tr><td>Male</td><td>5</td><td>12</td></tr> <tr><td>Male</td><td>6</td><td>12</td></tr> <tr><td>Male</td><td>7</td><td>12</td></tr> <tr><td>Male</td><td>8</td><td>12</td></tr> <tr><td>Male</td><td>9</td><td>12</td></tr> <tr><td>Male</td><td>10</td><td>12</td></tr> <tr><td>Male</td><td>11</td><td>12</td></tr> <tr><td>Male</td><td>12</td><td>12</td></tr> </tbody> </table>	Gender	No of other diseases	Count	Female	0	12	Female	1	12	Female	2	12	Female	3	12	Female	4	12	Female	5	12	Female	6	12	Female	7	12	Female	8	12	Female	9	12	Female	10	12	Female	11	12	Female	12	12	Male	0	12	Male	1	12	Male	2	12	Male	3	12	Male	4	12	Male	5	12	Male	6	12	Male	7	12	Male	8	12	Male	9	12	Male	10	12	Male	11	12	Male	12	12	
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Scientists		Bubble plot + Tabular frequency table	Figure 3-25: Co-morbidity analysis approach 2	<table border="1"> <thead> <tr> <th>Gender</th> <th>NoOf_Other_diseases</th> <th>Count</th> </tr> </thead> <tbody> <tr><td>Female</td><td>0</td><td>12</td></tr> <tr><td>Female</td><td>1</td><td>12</td></tr> <tr><td>Female</td><td>2</td><td>12</td></tr> <tr><td>Female</td><td>3</td><td>12</td></tr> <tr><td>Female</td><td>4</td><td>12</td></tr> <tr><td>Female</td><td>5</td><td>12</td></tr> <tr><td>Female</td><td>6</td><td>12</td></tr> <tr><td>Female</td><td>7</td><td>12</td></tr> <tr><td>Female</td><td>8</td><td>12</td></tr> <tr><td>Female</td><td>9</td><td>12</td></tr> <tr><td>Female</td><td>10</td><td>12</td></tr> <tr><td>Female</td><td>11</td><td>12</td></tr> <tr><td>Female</td><td>12</td><td>12</td></tr> <tr><td>Male</td><td>0</td><td>12</td></tr> <tr><td>Male</td><td>1</td><td>12</td></tr> <tr><td>Male</td><td>2</td><td>12</td></tr> <tr><td>Male</td><td>3</td><td>12</td></tr> <tr><td>Male</td><td>4</td><td>12</td></tr> <tr><td>Male</td><td>5</td><td>12</td></tr> <tr><td>Male</td><td>6</td><td>12</td></tr> <tr><td>Male</td><td>7</td><td>12</td></tr> <tr><td>Male</td><td>8</td><td>12</td></tr> <tr><td>Male</td><td>9</td><td>12</td></tr> <tr><td>Male</td><td>10</td><td>12</td></tr> <tr><td>Male</td><td>11</td><td>12</td></tr> <tr><td>Male</td><td>12</td><td>12</td></tr> </tbody> </table>	Gender	NoOf_Other_diseases	Count	Female	0	12	Female	1	12	Female	2	12	Female	3	12	Female	4	12	Female	5	12	Female	6	12	Female	7	12	Female	8	12	Female	9	12	Female	10	12	Female	11	12	Female	12	12	Male	0	12	Male	1	12	Male	2	12	Male	3	12	Male	4	12	Male	5	12	Male	6	12	Male	7	12	Male	8	12	Male	9	12	Male	10	12	Male	11	12	Male	12	12	
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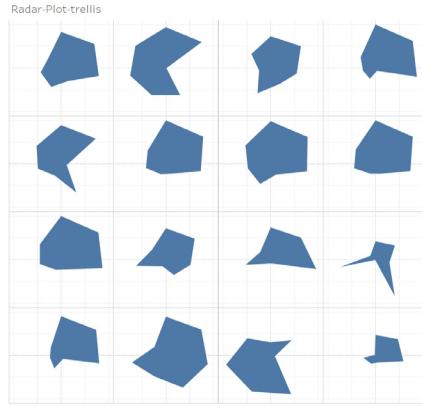
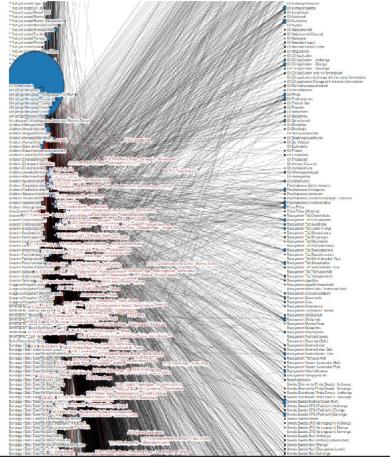
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Medics, Scientists		Collapsible tree diagram	Figure 3-26: Co-morbidity analysis approach 3: collapsible tree view		
Medics	Patient disease and treatment journey	Individual patient level data listing + Tabular frequency table	Figure 3-27: Patient Disease and Treatment administration by Study Day		<ul style="list-style-type: none"> (1) An analysis of how a patient journey is documented, how can this study be used prospectively and retrospectively to understand disease progression and treatment protocols (2) This could help study the severity of the disease, co-morbidities and the number of medications prescribed to treat the condition (3) This can also provide an overview of the practicing physician's style of treatment and may be help draw parallels in treating medical conditions (4) Improvements to the data standards and system architecture is a byproduct of this analysis
		Individual patient level data listing + Tabular frequency table	Figure 3-28: Patient Disease by Study Day and Treatment administration by Study Day		

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Medics		Individual patient level data listing + Tabular frequency table	Figure 3-29: Patient Cumulative Disease and Treatment administration by Visit	<p>The left table, titled "Patient_dis_med_Cumulative", shows individual patient data across 16 visits. The right table, titled "%Patient_dis_med_Cumulative", shows the same data as a percentage of the total population.</p> <table border="1"> <thead> <tr> <th>Mr No</th> <th>Cumday2</th> <th>Disease</th> <th>Medicine</th> </tr> </thead> <tbody> <tr><td>M0000335</td><td>TilVisit1</td><td>1</td><td>4</td></tr> <tr><td></td><td>TilVisit2</td><td>1</td><td>5</td></tr> <tr><td></td><td>TilVisit3</td><td>1</td><td>6</td></tr> <tr><td></td><td>TilVisit4</td><td>2</td><td>2</td></tr> <tr><td></td><td>TilVisit5</td><td>2</td><td>4</td></tr> <tr><td></td><td>TilVisit6</td><td>7</td><td>3</td></tr> <tr><td></td><td>TilVisit7</td><td>8</td><td>3</td></tr> <tr><td></td><td>TilVisit8</td><td>9</td><td>22</td></tr> <tr><td></td><td>TilVisit9</td><td>10</td><td>3</td></tr> <tr><td></td><td>TilVisit10</td><td>10</td><td>4</td></tr> <tr><td></td><td>TilVisit11</td><td>11</td><td>4</td></tr> <tr><td></td><td>TilVisit12</td><td>12</td><td>24</td></tr> <tr><td></td><td>TilVisit13</td><td>13</td><td>4</td></tr> <tr><td></td><td>TilVisit14</td><td>15</td><td>4</td></tr> <tr><td></td><td>TilVisit15</td><td>16</td><td>4</td></tr> <tr><td></td><td>TilVisit16</td><td>17</td><td>4</td></tr> </tbody> </table> <table border="1"> <thead> <tr> <th>Mr No</th> <th>Cumday2</th> <th>Disease</th> <th>Medicine</th> </tr> </thead> <tbody> <tr><td>M0000335</td><td>TilVisit1</td><td>100.00%</td><td>100.00%</td></tr> <tr><td></td><td>TilVisit2</td><td>50.00%</td><td>50.00%</td></tr> <tr><td></td><td>TilVisit3</td><td>33.33%</td><td>66.67%</td></tr> <tr><td></td><td>TilVisit4</td><td>50.00%</td><td>50.00%</td></tr> <tr><td></td><td>TilVisit5</td><td>40.00%</td><td>60.00%</td></tr> <tr><td></td><td>TilVisit6</td><td>70.00%</td><td>30.00%</td></tr> <tr><td></td><td>TilVisit7</td><td>72.73%</td><td>27.27%</td></tr> <tr><td></td><td>TilVisit8</td><td>75.00%</td><td>25.00%</td></tr> <tr><td></td><td>TilVisit9</td><td>76.52%</td><td>23.48%</td></tr> <tr><td></td><td>TilVisit10</td><td>74.48%</td><td>28.57%</td></tr> <tr><td></td><td>TilVisit11</td><td>73.33%</td><td>26.67%</td></tr> <tr><td></td><td>TilVisit12</td><td>75.20%</td><td>24.80%</td></tr> <tr><td></td><td>TilVisit13</td><td>74.47%</td><td>23.53%</td></tr> <tr><td></td><td>TilVisit14</td><td>78.86%</td><td>21.55%</td></tr> <tr><td></td><td>TilVisit15</td><td>80.00%</td><td>20.00%</td></tr> <tr><td></td><td>TilVisit16</td><td>80.95%</td><td>19.05%</td></tr> </tbody> </table>	Mr No	Cumday2	Disease	Medicine	M0000335	TilVisit1	1	4		TilVisit2	1	5		TilVisit3	1	6		TilVisit4	2	2		TilVisit5	2	4		TilVisit6	7	3		TilVisit7	8	3		TilVisit8	9	22		TilVisit9	10	3		TilVisit10	10	4		TilVisit11	11	4		TilVisit12	12	24		TilVisit13	13	4		TilVisit14	15	4		TilVisit15	16	4		TilVisit16	17	4	Mr No	Cumday2	Disease	Medicine	M0000335	TilVisit1	100.00%	100.00%		TilVisit2	50.00%	50.00%		TilVisit3	33.33%	66.67%		TilVisit4	50.00%	50.00%		TilVisit5	40.00%	60.00%		TilVisit6	70.00%	30.00%		TilVisit7	72.73%	27.27%		TilVisit8	75.00%	25.00%		TilVisit9	76.52%	23.48%		TilVisit10	74.48%	28.57%		TilVisit11	73.33%	26.67%		TilVisit12	75.20%	24.80%		TilVisit13	74.47%	23.53%		TilVisit14	78.86%	21.55%		TilVisit15	80.00%	20.00%		TilVisit16	80.95%	19.05%	
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Medics, Scientists	Disease pattern analysis	Area plot	Figure 3-30: Area graph representation of diseases	<p>This area plot displays the monthly prevalence of different diseases. The Y-axis represents the percentage of patients affected, ranging from 0% to 100%. The X-axis shows months from April to March. Diseases are color-coded: blue for ARI, orange for VCI, red for RSV, and green for PCL. The plot shows seasonal trends and varying prevalence rates for each disease.</p>	<ul style="list-style-type: none"> (1) Due to this analysis representation, information on many diseases can be viewed in very short space (diseases plotted side by side) (2) Diseases vary by seasons, by gender as well as some diseases are more prevalent than others which can be seen, and clinical interpretations can be drawn (3) Operational and clinical insights can be generated with help of this visualization 																																																																																																																																								
Medics, Scientists	Co-morbidities and concomitant medications	Mosaic plot	Figure 3-31: Mosaic plot: Disease and treatment representation example 1: Prameha	<p>This mosaic plot illustrates the relationship between diseases (rows) and treatments (columns). The plot is divided into smaller rectangles of varying sizes, where the size of each rectangle represents the frequency or strength of the association between a specific disease and treatment combination. The legend indicates the color coding for different categories of diseases and treatments.</p>	<ul style="list-style-type: none"> (1) In ayurveda, a treatment is used for multiple diseases and multiple treatments are used for the same disease based on the context of disease. This relationship gives rise to many associations between disease and treatment (2) Many to many relationships which are hard to visualize are generated through this analysis 																																																																																																																																								

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Medics, Scientists		Tabular frequency table	Figure 3-32: Disease and treatment example 2: P5.0: Prameha and Oil: Kottamchukkadi	<table border="1"> <thead> <tr> <th>Medicine</th> <th>Code</th> <th>Category</th> <th>Count</th> <th>Percentage</th> </tr> </thead> <tbody> <tr> <td>Prameha</td> <td>P5.0</td> <td>Prameha</td> <td>4694</td> <td>14.66</td> </tr> <tr> <td>Oil:Kottamchukkadi</td> <td></td> <td>Oil:Kottamchukkadi</td> <td>324</td> <td>22.25</td> </tr> <tr> <td></td> <td></td> <td>Total</td> <td>4018</td> <td>7.04</td> </tr> </tbody> </table>	Medicine	Code	Category	Count	Percentage	Prameha	P5.0	Prameha	4694	14.66	Oil:Kottamchukkadi		Oil:Kottamchukkadi	324	22.25			Total	4018	7.04	<p>(3) This analysis produces a mosaic display for diseases showing what kinds of treatments are prescribed</p> <p>(4) Another mosaic display is created for treatments showing what kinds of diseases are getting treated by the underlying treatment</p> <p>(5) Clinically meaningful as well as not so meaningful relationships are visualized, rare disease – disease combinations or disease – medicine combinations also can be studied</p>																																																																							
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Mosaic plot	Figure 3-34: Mosaic plot Disease and treatment representation example 4: Treatment: Oil: Kottamchukkadi	<p>The mosaic plot displays the distribution of diseases and treatments. The x-axis represents different treatments, and the y-axis represents different diseases. The size of the rectangles indicates the frequency of each combination.</p>																																																																																														
Tabular frequency table	Figure 3-35: Cross tabulation of prescribed treatments and disease group by gender Example 1	<table border="1"> <thead> <tr> <th rowspan="2">Medicine Name</th> <th colspan="3">Metabolic</th> <th colspan="3">DisType / Patient Gender</th> <th rowspan="2">Grand Total</th> </tr> <tr> <th>F</th> <th>M</th> <th>Total</th> <th>E</th> <th>M</th> <th>Total</th> </tr> </thead> <tbody> <tr> <td>Balerishtam</td> <td>29</td> <td>10</td> <td>39</td> <td>2</td> <td>1</td> <td>3</td> <td>3</td> </tr> <tr> <td>Balerishtam 450 ml</td> <td>143</td> <td>80</td> <td>223</td> <td>16</td> <td>9</td> <td>25</td> <td>225</td> </tr> <tr> <td>Balerishtam 450 ml [sna]</td> <td>13</td> <td>9</td> <td>22</td> <td>9</td> <td>5</td> <td>14</td> <td>22</td> </tr> <tr> <td>Balerishtam 450 ML SNA</td> <td>5</td> <td>14</td> <td>19</td> <td>2</td> <td>1</td> <td>3</td> <td>14</td> </tr> <tr> <td>Balerishtam 450 ml Vaidya</td> <td>188</td> <td>122</td> <td>280</td> <td>9</td> <td>5</td> <td>14</td> <td>282</td> </tr> <tr> <td>Balerishtam AVP</td> <td>2</td> <td>1</td> <td>3</td> <td>1</td> <td>1</td> <td>2</td> <td>3</td> </tr> <tr> <td>Balerishtam [AVP]</td> <td>393</td> <td>256</td> <td>649</td> <td>11</td> <td>8</td> <td>19</td> <td>616</td> </tr> <tr> <td>Balerishtam Rajah</td> <td>1</td> <td>1</td> <td>2</td> <td>1</td> <td>1</td> <td>2</td> <td>2</td> </tr> <tr> <td>Balerishtam(Arya)</td> <td>24</td> <td>12</td> <td>36</td> <td>1</td> <td>1</td> <td>2</td> <td>37</td> </tr> <tr> <td>Grand Total</td> <td>677</td> <td>465</td> <td>1,142</td> <td>17</td> <td>13</td> <td>30</td> <td>1,154</td> </tr> </tbody> </table>	Medicine Name	Metabolic			DisType / Patient Gender			Grand Total	F	M	Total	E	M	Total	Balerishtam	29	10	39	2	1	3	3	Balerishtam 450 ml	143	80	223	16	9	25	225	Balerishtam 450 ml [sna]	13	9	22	9	5	14	22	Balerishtam 450 ML SNA	5	14	19	2	1	3	14	Balerishtam 450 ml Vaidya	188	122	280	9	5	14	282	Balerishtam AVP	2	1	3	1	1	2	3	Balerishtam [AVP]	393	256	649	11	8	19	616	Balerishtam Rajah	1	1	2	1	1	2	2	Balerishtam(Arya)	24	12	36	1	1	2	37	Grand Total	677	465	1,142	17	13	30	1,154
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Medics, Scientists	Co-morbidities and concomitant medications	Circular data representation	Figure 3-37: Circular view: Co-occurrences of disease – disease Example 1		<p>(1) This analysis provides a view for a disease – disease combination or disease – medicine combination longitudinally (day 1 of disease, diseases reported at different time points before and after day 1)</p> <p>(2) Disease and treatment information is represented on a circular display with green spokes representing co-occurrences of disease combination or disease – medicine</p>																																																																																																																																																																																																																																																																																														

Stake holders	Classification	Type of analysis	Figure number and analysis name (linked to the actual figure)	Snapshot of the analysis (the picture is attached here to provide a quick look into the type of analysis)	Context of the proposed analysis
Medics, Scientists		Circular data representation	Figure 3-38: Circular view: Co-occurrences of disease – treatment Example 2		(3) Clinically meaningful as well as not so meaningful relationships are visualized, rare disease – disease combinations or disease – medicine combinations also can be studied
Scientists	Similarity analysis in disease and medicine trajectories	Butterfly plot	Figure 3-39: Pre and Post distance analysis for disease: M2.0: Madhumeha		(1) Disease trajectories (chronological list of diseases reported) and medicine trajectories (chronological list of medicines prescribed) are generated to study if similar diseases are experienced after an onset of a particular disease (2) This analysis helps in understanding biological changes, represented by subsequent reported diseases triggered by an underlying disease
		Butterfly plot	Figure 3-40: Pre and Post distance analysis for medicines given for diseases: P5.0, V2.23, V2.63		(3) Similarly, which medicines are prescribed provide insights into treatment protocols

Stake holders	Classification	Type of analysis	Figure number and analysis name (linked to the actual figure)	Snapshot of the analysis (the picture is attached here to provide a quick look into the type of analysis)	Context of the proposed analysis
Scientists	Multi-dimensional data analysis	Radar plot	Figure 3-41: Radar plot	<p>Radar-Plot-trellis</p> 	<ul style="list-style-type: none"> (1) This analysis developed showed 7 parameters on 7 vertices. Different diseases were displayed next to each other as trellis radar display. (2) If there are different shapes for different diseases then this suggests that there are underlying differences in the data representing differences in diseases.
Scientists	Co-morbidities and concomitant medications	Dynamic bubble plot	Figure 3-42: Dynamic bubble plot: Example 1: Disease: A6.0: Amavaata		<ul style="list-style-type: none"> (1) Intricate relationship between disease and medicines in a very short space, at present this type of data representation approach may not have a direct application, but consultation with "end users" may provide appropriate use case.

3 Results

3.1 Converting real life clinical data into analyzable format

3.1.1 Details of the database

The database has approximately 200 datasets (Figure 2-3). They cover various components of hospital's day-to-day functions right from operational data to the patient level clinical information. High level of classification of data types is as below:

1. Operational datasets:
 - a. Hospital charges – In Patient (IP), Out Patient (OP)
 - b. Operation theater charges
 - c. Inventory of equipment
 - d. Doctor charges
2. Reference dictionaries
 - a. Disease codes
 - b. Ayurvedic services
 - c. Medication names
 - d. Master list of Laboratory tests
 - e. Names of city, state, countries
3. Doctor details
 - a. Doctor ID
 - b. Relevant ward information
 - c. Internal / Visiting / Part time / Full time
4. Patient information
 - a. Patient details
 - b. Visit details
 - c. Vital signs
 - d. Registration details
 - e. Discharge details
 - f. Lab data details
 - g. Diet details
5. Datasets related to managing access levels, datasets related to pharmacy stocks, datasets related to scheduling appoints, datasets related to purchase orders, and other IT related contexts used by various teams in hospital

For this study, the following data was not used to in accordance with the patient data protection and privacy, financial privacy as well as hospital management confidentiality thus avoiding any controversies:

1. Hospital monetary details
2. Doctor's details (Name and ID of individual doctor)

3. Patient details of sensitive nature such as name, phone number, socio economic status, health insurance details

3.1.2 Data Extracted from Hospital Database

In our study, we had different versions of data, details in the table below.

Table 3-1: Versions of data used for analysis

Data version	Version 1	Version 2
Approach	CSV files provided by the Hospital IT support	Data extraction via the SQL DB connect
Date time frame	From start of the hospital to Oct 2016	From start of the hospital to Oct 2017
Data domains	Lab Vital signs Diagnosis	All the available data in the hospital database
Type of extraction	Full extraction of available domains	Full extraction of all the available hospital data

The analysis was carried out in the study using these 2 different versions of the data, version of the data has been provided along with each of the analysis for clarity.

3.2 Clinical data understanding

3.2.1 Broad checks on the datasets

This paragraph summarizes observations from structural review of the datasets. In a well-defined database, patients should have the primary key as Patient ID: mr_no (in our case), but the underlying database considers unique visit for each patient as a primary key between tables (Patient_ID). In general, a variable containing same information across tables should have the same name, but in our case, each table has a different variable, making it difficult to create logical links across tables. E.g., Consultation_ID from doctor_consultation and Patient_ID from patient_registration had the same information; Visit_ID from mrd_diagnosis and Patient_ID from doctor_consultation meant the same. The case report form allowed for multiple diseases and multiple treatments to be recorded for each patient, this causes a “clinical logic” challenge – the potential 1-1 relation between a disease and a treatment is lost, this had to be derived outside of the database using expert understanding which would require investment of time and efforts from Ayurvedic vaidyas. There were multiple versions of the same table available in the database (as a programmer, it is well understood that older copies are retained in the system), but due to

unavailability of the documentations increased the complexity. Potential approaches to address these challenges are provided in chapter 4 section [4.2.8](#).

This section outlines observations from the clinical data review of individual case report forms:

Vital sign dataset: Vital sign measurements include parameters like body temperature, blood pressure, body surface area, height, and weight. The existing database has various vital signs parameters listed one below the other. The current structure has one record per patient per visit per parameter. For a lot of visits vital sign information was missing, or partially filled. There were certain records with implausible values for certain parameters such as height and weight having 0 value. Blood pressure values having character data. Potential approaches to address these challenges are provided in chapter 4 sections [4.2.1](#), [4.2.5](#).

Lab measurement dataset: Findings were similar to the Vital signs database. Along with the patient identifier information, only laboratory test name and laboratory measurements were present. In case a patient had the laboratory investigations outside of the hospital that data got stored in a scanned image format. Apart from this the dataset did not contain the date of sample, reference ranges, laboratory parameter units, fasting status etc. A single lab test had multiple names. E.g., Alanine Aminotransferase was captured in the dataset in the following different ways:

Alanine Aminotransferase

Alanine Aminotransferase ALT (SGPT)(UV Kinetic)

Alanine Aminotransferase (SGPT)(UV Kinetic)

Alanine Aminotransferase ALT (SGPT)

Alanine Aminotransferase ALT (SGPT)(UV Kinetic)

S.G.PT (UV kinetic)

SGPT (UV kinetic)

ERYTHROCYTE SEDIMENTATION RATE was captured in the dataset in the following different ways:

ERYTHROCYTE SEDIMENTATION RATE

ERYTHROCYTE SEDIMENTATION RATE (ESR)

ERYTHROCYTE SEDIMENTATION RATE (ESR)

Potential approaches to address these challenges are provided in chapter 4 sections [4.2.3](#), [4.2.5](#).

Treatment dataset: the treatment or dosing or medication dataset does not get exported into a structured file for easy understanding and analysis. Which treatment was prescribed for which disease was not easily understandable based on the system generated report. Potential approaches to address these challenges are provided in chapter 4 sections [4.2.4](#), [4.2.8](#).

Medical coding and clinically important variables: the medical records for patients were captured differently by different doctors, nurses and other medical staff. Same information was found in

more than one variable. Acronyms were used inconsistently. Answer for more than one question was captured in one variable. Due to “free text nature” of variables simple questions like Yes / No had many different data values. Potential approaches to address these challenges are provided in chapter 4 section 4.2.5.

Classification and Sub-classification of the Doshas / Diseases: It was observed that the main disease classification by kapha, pitta, vata has disparity in numbers. As an example the table below show the variation in the counts of the diseases and their sub-classification. Potential approaches to address these challenges are provided in chapter 4 section 4.2.6

Figure 3-1: A snippet of disease table by gender

DisType_Diseases

Distype	Code	Description	Patient Gender			Grand Total
			F	M		
Metabolic	P5.0	Prameha	648	849		1,497
	P5.3	Prameha - Sthula	23	20		43
	P5.2	Prameha - Pidaka	5	12		17
	P5.1	Prameha - Krusha	4	5		9
Grand Total			671	876		1,547

DisType_Diseases

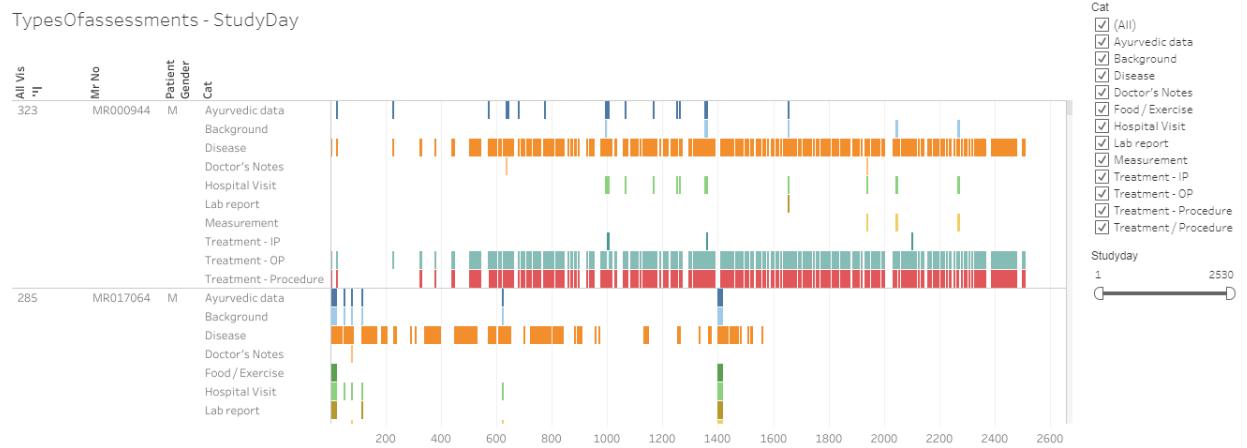
Distype	Code	Description	Patient Gender			Grand Total
			F	M		
RMSD	A2.0	Aamavaata	652	180		832
	A2.3	Aamavaata - Vaataja	27	7		34
	A2.1	Aamavaata - Kaphaja	13	4		17
	A2.2	Aamavaata - Pittaja	4	3		7
Grand Total			679	190		869

Frequency of Prameha (P5.0) and Aamavaata by gender has been displayed. The frequency of patients is substantially lower for classification by Sthula, Pidaka and Krusha as well as Kapha, Vaata, and Pitta. Data version: 2011 to Oct 2017. Link to analysis: [Link](#)

3.2.2 Contents checks

The analysis below shows that for majority of the patients and for majority of the visits, the disease data and medication (Treatment /Procedure) were non-missing. Most of the other categories were not entered as consistently as they should have been. If this was the expected data collection pattern then these findings should not be considered as any issues.

Figure 3-2: Variable classification by categories



500+ variables are captured for each visit and each patient are classified into the following categories, (1) Ayurvedic data, (2) Background, (3) Disease, (4) Doctor's Notes, (5) Food / Exercise, (6) Hospital Visit, (7) Lab report, (8) Measurement, and (9) Treatment / Procedure. If there is any non-missing data present in a particular category then “Yes” is assigned, if the data is missing then “No” value is assigned. This data is presented as a listing for each patient for each visit (day). When the data is available it is presented as a color-coded bar and when it is missing then it is presented as a white blank space. Data version: 2011 to Oct 2017. Link to analysis: [Link](#)

Two example screenshots are shown below as to what was observed while content check was performed.

CRFname_variable number_variable label	Unique values	Unique patients	Variable classification category
sec001_var008_Diabetes	1064	4124	Background

sec001_var008_Diabetes: represents CRF page number 1, labelled as “History of Present Illness” and variable number 8 “Diabetes”. Based on the label of the variable, this variable is considered as a part of “Background” information. This variable “Diabetes” has 1064 unique values entered by different doctors for different patients. Data is available for 4124 distinct patients.

CRFname_variable number_variable label	Unique values	Unique patients	Variable classification category
sec001_var018_Associated Complaint with Onset & Duration	5102	4549	Disease

sec001_var018_Associated Complaint with Onset & Duration: presents CRF page 1 “History of Present Illness” and variable number 8 “Associated Complaint with Onset & Duration”. This variable “Associated Complaint with Onset & Duration” has 5102 different values entered by different doctors for different patients. Data is available for 4549 distinct patients.

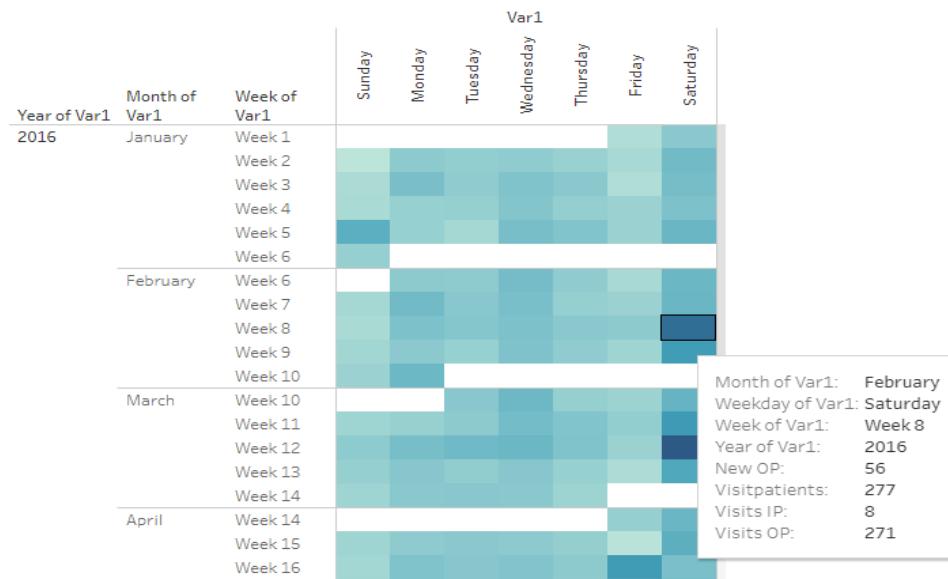
The large number of unique values show that the data entry rules are not being followed consistently, and each doctor or each nurse might have a different interpretation of the rules. In addition to this, looking at the unique number of patients, the data has not been entered for all the patients, hypothetically giving rise to missing data. Potential approaches to address these challenges are provided in chapter 4 section 4.2.8.

3.2.3 Visit pattern analysis

Each of the cell displayed on a calendar display was coloured in shades of blue from light blue to dark blue showing increasing frequency count of number of patients. From 2011 to 2016, the number of patients visiting hospital on weekdays was less than the number of patients visiting on weekends. In-Patients were considerably less than Out-Patients. Overall number of patients coming to hospital have been increasing year on year. Potential approaches to address additional patient burden are provided in chapter 4 section 4.2.1.

Figure 3-3: Visit pattern analysis

Sheet 1



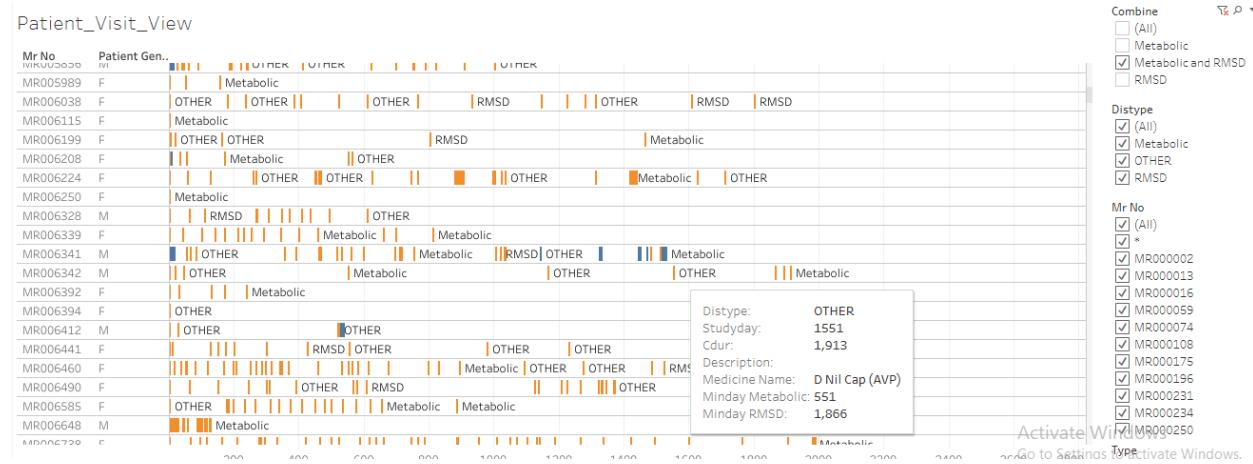
Frequency counts of 4 parameters, (1) new Out-Patients added on that day, (2) total number of patients visiting on that day, (3) total number of In-Patient visits on that day, and (4) total number of Out-Patient visits on that day are calculated for each day to understand the patient flow to hospital from year on year. Light blue to dark blue shows increasing frequency count of number of patients Data version: 2011 to Oct 2016. Link to analysis: [Link](#)

3.2.4 Patient disease and treatment journey view

Multiple representations of data allow the end user to review data with different perspectives. Patient profile reports provide detailed view of individual patient's disease condition, prescribed medication, co-morbidities along with basic demographic information. Treating doctors and researchers will greatly benefit from this visual display. This representation (Figure 3-4) provides the patient an understanding of the disease chronology as well as the prescribed medication and

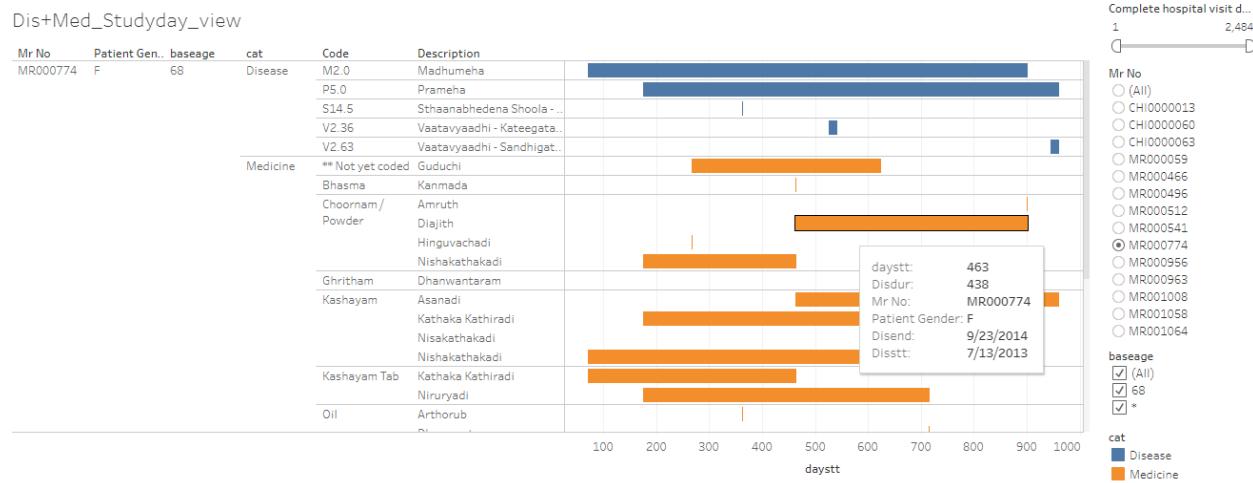
progress. Interpretations drawn from these representations and potential approaches to improve current version of patient profiles used at the hospital are provided in chapter 4 sections 4.2.8.

Figure 3-4: Patient visit profile – Horizontal view



Mr No: Patient ID, Patient gender, x-axis: duration of hospital visits, Orange bar: Out-patient visit, Blue bar: In-patient visit, Metabolic: when a metabolic disease is reported, RMSD: when a Rheumatic and Musculoskeletal disease is reported, OTHER: other diseases are reported. Patients listed have at least one of the RMSD or metabolic diseases. Tooltip has a lot of information relevant to each visit. Data version: 2011 to Oct 2017. Link to analysis: [Link](#)

Figure 3-5: Patient visit profile – Vertical view



Mr No: Patient ID, Patient gender, baseage Age at the very first hospital visit, category: Disease and medicine, Code: ACD code, Description: disease description, x-axis: duration of disease and medicine, Tooltip has a lot of information relevant to each visit. Data version: 2011 to Oct 2017. Link to analysis: [Link](#) to get the above display subset Mr No = MR000774

3.3 Studying demographics and patient specific factors

Results related to complete set of patients: While exploring the basic data, the following high-level picture appeared: For the 5-year time frame from 2011 to 2016, the database contained approximately 40,000 unique patients (Figure 3-6), 90% of patients were from India and remaining

10% patients were from more than 50 different countries (Figure 3-7). The proportion of male and female patient was approximately 50%. Median age for females was marginally higher than males across all visit types (Figure 3-8). Approximately 90% of patients were Out-Patients and 10% were In-Patients (Figure 3-1). Approximately 12,000+ female patients and 14,000+ male patients had reported only a single disease (Figure 3-11), these patients could have come only once to the hospital and may not have come back at all after reporting the first disease. There were a few outliers observed having more than 10 disease conditions across the years. The maximum age of 108 years was a possible case of data issue. Similar anomalies were seen in a few other groups, e.g., patients reporting 23 diseases, is this accurate? This warrants additional data checks from operational and clinical perspective. Blood group is collected only for ~32,500 out of ~40,000 patients. There was missing data for almost 20% of patients. Blood group distribution was largely in line with the Indian blood group distribution (Figure 3-9). Potential approaches to improve current situation and interpretations are provided in chapter 4 section 4.3.

Figure 3-6: Total Number of Patients

01 NoOfPatients	02 Country	03 AgeBoxplotCountry	04 Age
-----------------	------------	----------------------	--------

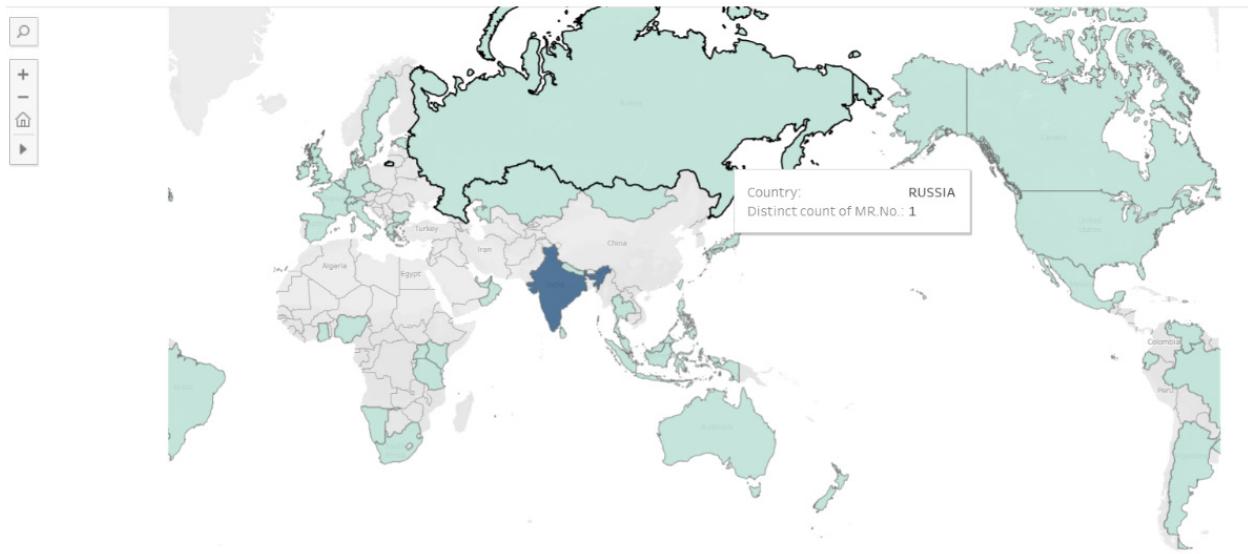
Summary of distinct number of patients

Grp				
Common	NA	OnlyIP	OnlyOP	Grand Total
3,491	0	4,145	38,903	39,557

Grad Total: Total number of patients used in the analysis, OnlyIP: patients having only In-Patient visits, OnlyOP: patients having only Out-Patient visits, Common: Patients having both type of visits. Data version: 2011 to Oct 2016. Link to analysis: [Link](#)

Figure 3-7: Country-wise Visualization

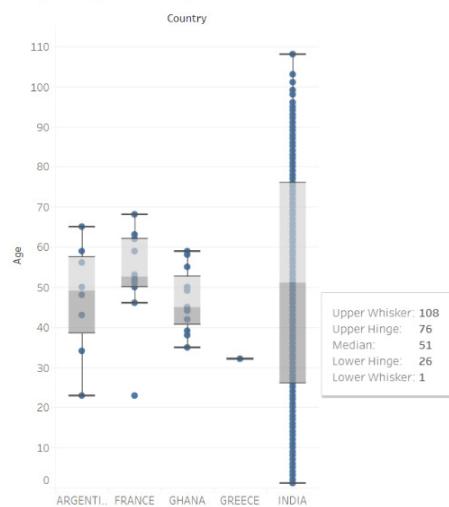
02 Country



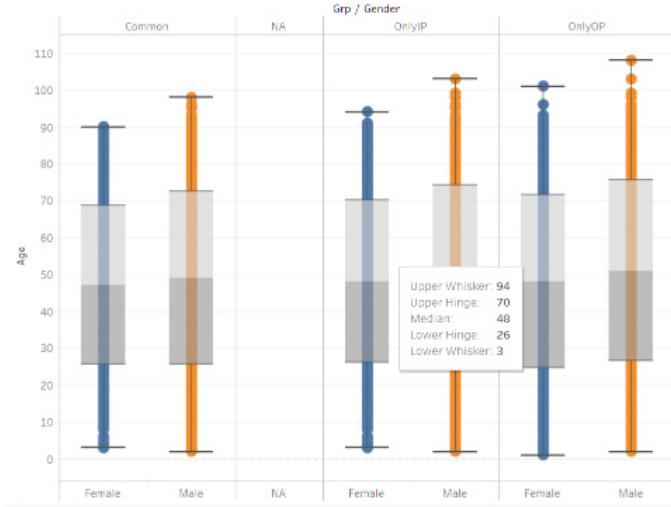
Unique number of patients are plotted on the world map, the map shows that at least 1 patient data is coming from 50+ countries, 95% or more patients are from India. Data version: 2011 to Oct 2016. Link to analysis: [Link](#)

Figure 3-8: Age distribution by country, age distribution by gender

03 AgeBoxplotCountry



04 AgeBoxplotGroup



Boxplot representation: Age distribution is presented for each country and then by type of patient and gender, OnlyIP: patients having only In-Patient visits, OnlyOP: patients having only Out-Patient visits, Common: Patients having both type of visits Data version: 2011 to Oct 2016. Link to analysis: [Link01](#), [Link02](#)

Figure 3-9: Blood-group Distribution by gender

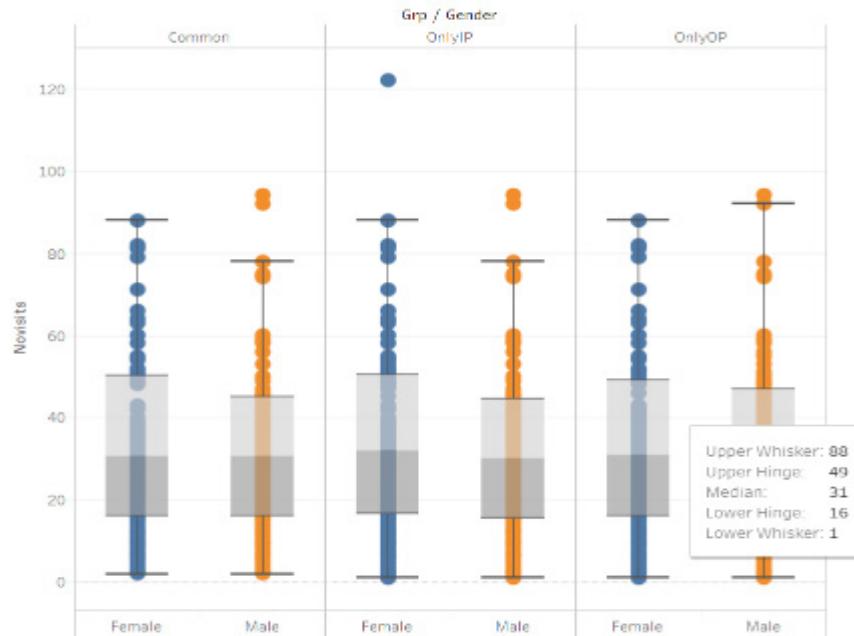
07 BloodGroup

Blood... F	Gender			Grand Total
	Female	Male	NA	
O+	6,340	6,684		13,024
B+	4,490	4,956		9,446
A+	2,997	3,030		6,027
AB+	828	1,046		1,874
O-	434	447		881
B-	265	259		524
A-	239	178		417
AB-	80	87		167
A1 +ve	30	17		47
A1 -ve	6	1		7
A1B +ve	3	4		7
A2 +ve	1			1
A2B +ve		1		1
NA			1	1
Null	0	0		0
Grand Total	15,713	16,710	1	32,424

Tabular frequency distribution table for Blood-group by gender. Data version: 2011 to Oct 2016. Link to analysis: [Link](#)

Figure 3-10: Number of Visits, and Visit Types

05 NoOfVisitsBox



Boxplot representation of number of Visits, and Visit Types, Data version: 2011 to Oct 2016. Link to analysis: [Link](#)

Figure 3-11: Descriptive summary statistics by number of Diseases by Age and Gender

05a NoOfDis_age

Nodiseases	Female								Male							
	Count	Age	Avg. Age	Median	Std. dev.	Age	Avg. Age	Median	Std. dev.	Age	Avg. Age	Median	Std. dev.	Min. Age	Max. Age	
1	12,884	46	46	18	1	96	46	45	19	2	108					
2	5,652	48	50	18	2	93	48	47	19	2	96					
3	2,426	48	48	17	2	93	2,002	50	49	18	2	98				
4	1,215	51	51	17	2	87	898	53	55	19	2	93				
5	526	50	50	15	9	84	477	53	54	18	2	87				
6	342	48	48	17	9	81	199	50	47	15	6	84				
7	182	53	52	13	12	79	140	57	56	15	33	88				
8	99	48	48	15	13	80	28	46	52	23	6	76				
9	77	54	52	15	4	78	22	58	65	11	39	67				
10	25	53	51	21	33	86	20	50	51	5	43	57				
11	23	47	49	17	22	66	14	49	44	14	35	63				
12	31	44	39	24	9	82	6	64	64	0	64	64				
15	2	56	56	21	41	71										
NA	4,263	46	45	19	2	101	5,627	43	41	19	2	103				
13	8	53	56	9	30	56	13	51	47	8	31	58				
23							6	41	41	0	41	41				
14	9	30	18	20	18	71	1	35	35		35	35				

Descriptive summary statistics by number of diseases reported, by gender. Nodiseases: Number of diseases reported in the database. Data version: 2011 to Oct 2016. Link to analysis: [Link](#)

Results for the metabolic and RMSD disease areas: Out of ~40,000 patients, there were ~14,000 patients having reported at least 1 metabolic and/or 1 RMSD disease condition. It was quite evident that there were a lot more patients in the RMSD group compared to the metabolic group (Figure

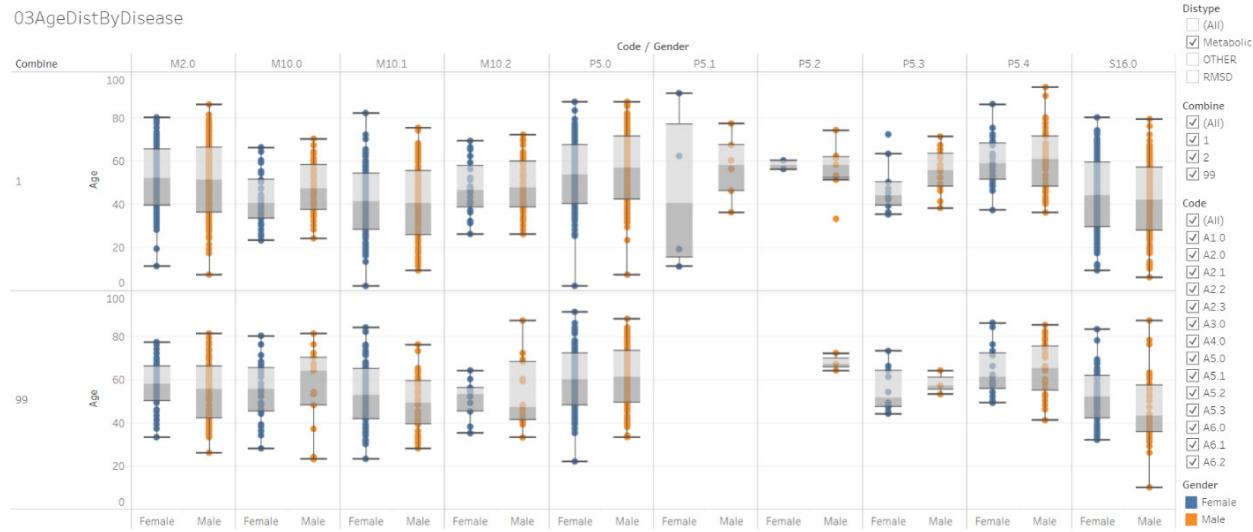
3-12). Large number of patients were visiting the hospital only for 1 visit, ~62% patients were dropping off in first month of treatment. ~15% of patients having at least one RMSD disease were still visiting the hospital after 1 year of first ever visit to the hospital. Boxplot representation of age showed variability in age across disease type and gender (Figure 3-13). Presentation of disease burden by gender, Indian seasons (rutas) and disease category provides data about possible variations reported for different diseases (Figure 3-15). (1) Prameha, (2) Madhumeha, and (3) Sthaulya were the top three most frequently reported metabolic diseases where as (1) Vaatavyaadhi – Sandhigata Vaata, (2) Vaatavyaadhi, (3) Vaatavyaadhi – Gridhrasee, (4) Sthaanabhedana Shoola – Katee Shoola and (5) Sthaanabhedana Graha – Katee Graha were the top five most frequently reported RMSD diseases. Prameha and Madhumeha were reported more by males than females. There were more female patients with disease condition Sthaulya. In general, RMSD diseases were reported in more females than males. For RMSD disease group, 51 out of 97 diseases were reported in ≤ 10 patients. Metabolic diseases were not varying across seasons, while RMSD diseases had some seasonal variations (Figure 3-15). The before and after visualization of data allows to build a disease and medicinal trajectories (Figure 3-16). These should be useful for determining diagnostic and prognostic relationships.

Figure 3-12: Data tabulation for patients reporting RMSD and Metabolic diseases



Bubble plot: 1 = Patients with at least 1 metabolic diseases, 2 = Patients with at least 1 Rheumatic, Musculoskeletal (RMSD) diseases, 99 = Patients with at least one disease from each of the groups, Data version: 2011 to Oct 2016. Link to analysis: [Link](#)

Figure 3-13: Disease distribution by age and gender



Boxplot representation of age by disease. Orange: male, Blue: female. Individual column represents a disease. 1 = Patients with at least 1 metabolic diseases, 2 = Patients with at least 1 Rheumatic, Musculoskeletal (RMSD) diseases, 99 = Patients with at least one disease from each of the groups, Data version: 2011 to Oct 2016. Link to analysis: [Link](#)

The columns in the above image are different diseases from Metabolic and RMSD categories. (Refer [Link](#) for codes and de-codes)

Figure 3-14: Patient visit duration for Disease categories by Gender

Durlvr	Dur	Combine / Gender								Grand Total	
		1		2		99					
Female	Male	Female	Male	Female	Male	Female	Male	Female	Male		
Null	Null	42	49	275	228	53	41				688
0	>=1 day	1,134	1,537	5,751	4,763	582	447				14,214
1	>=1 month	425	590	2,255	1,634	354	267				5,525
2	>=2 months	334	480	1,854	1,374	315	239				4,596
3	>=3 months	294	433	1,650	1,227	292	225				4,121
6	>=6 months	223	322	1,257	944	249	196				3,191
12	>=1 year	148	203	857	665	184	147				2,204
24	>=2 years	81	103	444	335	102	95				1,160
36	>=3 years	38	48	215	159	55	51				566
48	>=4 years	17	16	62	47	24	19				185
60	>=5 years	4	2	18	11	10	6				51
Grand Total		1,147	1,554	5,821	4,821	587	453				14,383

1 = Patients with at least 1 metabolic diseases, 2 = Patients with at least 1 Rheumatic, Musculoskeletal (RMSD) diseases, 99 = Patients with at least one disease from each of the groups, Data version: 2011 to Oct 2016. Link to analysis: [Link](#)

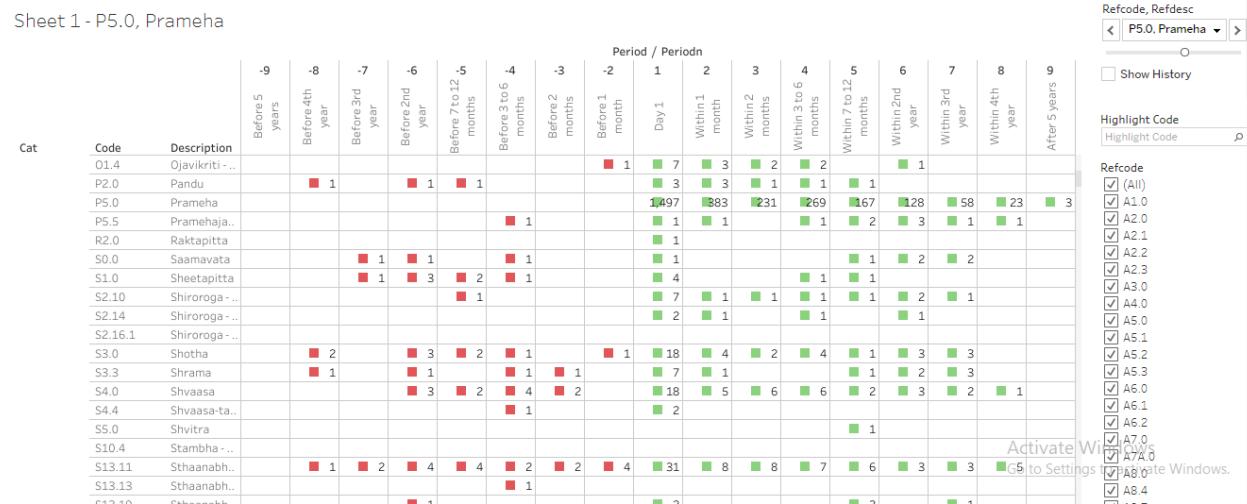
Figure 3-15: Disease distribution by Seasonal Variations and gender

Distype	Code	Description	season / Patient Gender																		
			01 Vasant Ritu		02 Grishma Ritu		03 Varsha Ritu		04 Sharad Ritu		05 Hemant Ritu		06 Shishir Ritu		Grand Total						
Metabolic	P5.0	Prameha	163	207	194	263	208	279	167	230	151	187	166	203	1,497						
	M2.0	Madhumeha	158	268	184	271	188	309	198	330	144	241	153	244	1,441						
	S16.0	Sthaulya	109	59	147	105	138	94	161	95	111	81	119	75	989						
	M10.1	Medoroga - Sthula medho ..	88	53	97	52	98	54	89	46	84	47	78	39	627						
	M10.2	Medoroga - Sukshma med..	14	32	13	38	9	40	14	36	11	29	9	23	193						
	P5.4	Prameha - Upadrava	8	21	14	27	19	28	16	15	6	20	12	15	150						
	M10.0	Medoroga	16	15	18	13	23	17	16	14	18	12	19	13	149						
	P5.3	Prameha - Sthula	6	4	5	5	3	6	6	3	6	6	3	3	43						
	P5.2	Prameha - Pidaka	3	1			7		3	1	1	1			2	17					
	P5.1	Prameha - Krusha	1					1	3	1	1	1			9						
RMSD	V2.63	Vaatavyadhi - Sandhigat..	712	317	855	384	855	376	784	334	619	284	585	276	4,299						
	V2.0	Vaatavyadhi	373	316	415	354	485	373	368	306	275	249	362	290	2,993						
	V2.23	Vaatavyadhi - Gridhrasee	366	308	417	362	450	361	435	335	342	293	335	275	2,613						
	S14.21	Sthaanabhedena Shoola - ..	133	133	163	139	190	154	175	154	116	114	139	116	1,333						
	S13.11	Sthaanabhedena Graha - ..	90	104	106	113	130	133	122	113	117	111	114	107	982						
	A2.0	Aamavaata	218	59	225	62	212	63	237	63	177	48	186	50	832						
	A3.0	Abhighataja Shoola	59	66	90	89	76	85	68	91	57	68	51	69	739						
	V1.0	Vaatarakta	42	58	61	83	85	75	74	73	62	63	50	47	529						
	S14.0	Sthaanabhedena Shoola	73	42	80	53	51	43	68	51	46	49	74	44	523						
	V2.36	Vaatavyadhi - Kategata..	52	41	54	60	62	61	42	29	16	29	33	35	404						
	S14.7	Sthaanabhedena Shoola - ..	21	21	32	30	21	31	32	31	26	16	28	21	233						
	S14.17	Sthaanabhedena Shoola - ..	14	15	30	18	28	20	29	27	19	18	7	11	206						
	V2.9	Vaatavyadhi - Asthigata ..	26	20	19	19	21	19	42	15	36	20	21	8	206						
	V2.75	Vaatavyadhi - Vaatakant..	21	5	26	14	43	14	29	9	20	5	18	8	164						
	S13.19	Sthaanabhedena Graha - ..	14	15	12	18	18	17	12	10	12	14	15	14	121						
	V2.30	Vaatavyadhi - Jaanugata..	12	7	20	13	10	5	7	10	4	4	8	3	92						
	S15.31	Sthaanabhedena Shoola - ..	11	9	9	7	14	7	11	16	14	6	9	5	89						
	S14.2	Sthaanabhedena Shoola - ..	4	6	15	7	9	6	12	5	9	6	11	9	92						

Distype: Metabolic and RMSD, Code: ACD disease code, Description: disease description, seasons are presented as: Vasant ritu, Grishma ritu, Varsha ritu, Sharad ritu, Hemant ritu, and Shishir ritu, Data version: 2011 to Oct 2017. Link to analysis: [Link](#)

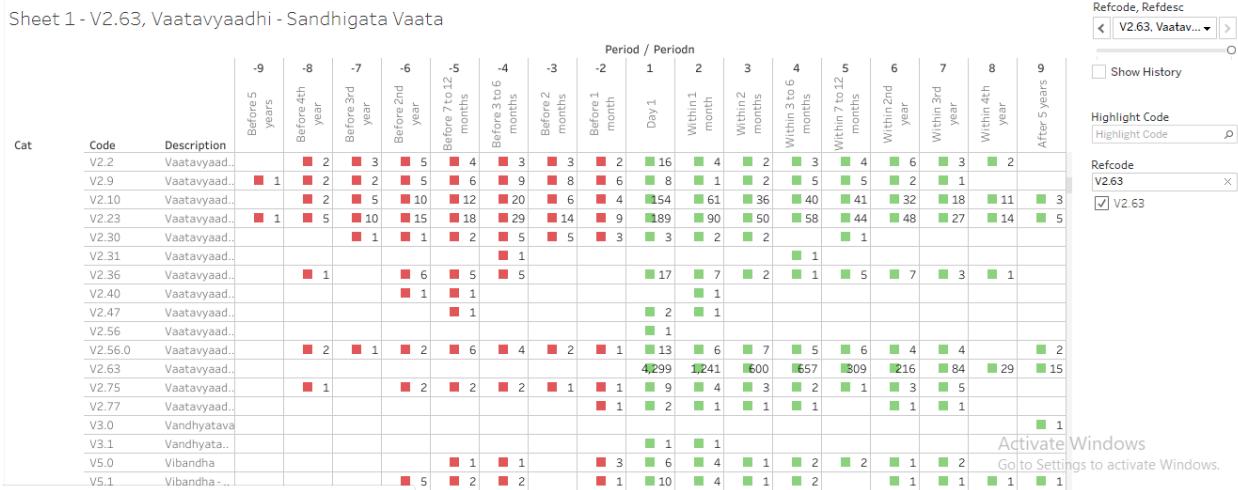
Figure 3-16: Pre and Post Disease Classification Analysis

Example 1: Prameha



Cat: category of disease and medicine, Code: ACD code, prescribed medicine types, pre and post visit window w.r.t. the 1st day of each of the reference diseases, Data version: 2011 to Oct 2017. Link to analysis: [Link](#) to get the display for Prameha, go to "Refcode, Refdesc" filter and select P5.0, Prameha.

Example 2 Vaatavyadhi – Sandhigata Vaata



Cat: category of disease and medicine, Code: ACD code, prescribed medicine types, pre and post visit window w.r.to the 1st day of each of the reference diseases, Data version: 2011 to Oct 2017. Link to analysis: [Link](#) to get the display for Vaatavyaadhi – Sandhigata Vaata, go to “Refcode, Refdesc” filter and select V2.63, Vaatavyaadhi – Sandhigata Vaata.

3.4 Studying diagnostics and interventions

Almost all the ICD categories were represented in the analysis. Some of the ICD classes had more patients than other categories. Age distribution showed natural variation. Visit distribution and duration for which patients were visiting hospital look like the earlier analysis. The ACD and ICD mapping exercise showed that the current hospital data demonstrates all the types of diseases being catered to at the hospital. (Figure 3-17, Figure 3-18, Figure 3-19, Figure 3-20)

The bar graph representation (Figure 3-21) provided a view of the spread of the patient population their diseases versus their prakriti classification seen at the hospital. The prakriti type as well as disease type can be filtered. It also provided a view of the combination of the gender and the prakriti manifesting into the kind of doshas and the most prevalent doshas for the combination.

Observations from the first Co-morbidity approach (Figure 3-22, Figure 3-23, Figure 3-24): This display provided a comprehensive view of the disease clusters. Comorbidities were easily identified, some of them are clinically relevant, and some of them are not. Bubble size provided comparative view of number of patients reporting a specific disease. The age group distribution for each gender was available. Some diseases were reported more by males or by females, easy to spot on the graph. Box named “Number of other diseases” provided a contextual display about number of co-morbidities. Some diseases had higher number of co-morbidities, some had lower number. Variations were seen amongst gender as well. This analysis did not consider the before or after nature of time points, hence did not provide insights into the causal relationships between diseases. The second co-morbidity approach provided views on the seasonal variations of diseases as well as seasonal co-morbidities (Figure 3-25). The third co-morbidity approach provided the following: The collapsible tree showed progression of diseases as experienced by patients and reported in the database. The tree showed approximately 12,500 lines of data in very short space. Some diseases were experienced more by males than by females. Some diseases were only reported by one of the genders. Some diseases had many more branches than a few others. Some

of the disease trajectories had very few numbers of patients. Some of the trajectories may be clinically meaningful and some may not be meaningful (Figure 3-26).

Treatment and disease analysis at individual patient level: This analysis was explained using example patient MR000335: For this patient there were 17 visits in the database, there were 17 distinct diseases reported and 45 distinct treatments, services prescribed. 4 out of 17 diseases were repeated and 10 out of 45 treatments had been repeated. When a new disease was reported, usually a new treatment or treatments re-reported, if there was only a new treatment added then it could indicate, the earlier treatment may not have worked, or it described the treatment regimen. If only new diseases were added and no new treatment was added, then the same treatment could work for multiple diseases. These visualizations allow the treating doctor insights into newer diseases getting reported as well as what newer treatments have been prescribed at what time points (Figure 3-27, Figure 3-28, Figure 3-29).

Area graph representation of diseases provided information about 800+ diseases, almost all diseases present in the database in very short space. Due to the data visualization scheme variations caused by day-to-day, seasons, gender, and diseases could be interpreted very easily. The interactive nature of visualization allowed for real time subset of diseases. One of the 4 diseases displayed has very few patients compared to other 3 diseases showing different nature of diseases (Figure 3-30).

Cross tabulation of prescribed treatments and disease group by gender was generated. First example is created using Balaristham. The source variable captured the quantity + unit + company name in the same variable, which did not allow for 100% accurate numerical calculations, but still provided a good idea. Only 30 patients having metabolic diseases were prescribed the medicine whereas 1,142 patients with RMSD were prescribed. Second example is created using bhasma: approximately 287 patients out of 17,406, 1.5% of patients are prescribed bhasmas (at least treatments having word “bhasma”) for various diseases (Figure 3-35, Figure 3-36). Summary statistics and hypothesis testing was conducted to conclude any impact of bhasma on visit duration. 514 patients were identified with at least 1 bhasma treatment. The mean duration of treatment before 1st bhasma treatment was 14.8 days, min - max duration was reported as (1, 111) whereas the mean duration of treatment after 1st bhasma treatment was 10.6 days, min - max duration was reported as (0, 89). The t-test at 5% significance level shows statistically significant difference between duration of treatment before bhasma treatment and duration of treatment after bhasma treatment.

Circular display, how to read the visualization? Figure 3-37 and Figure 3-38 show 2 examples of 2 combinations, the first example had many green bars, and the second combination had very few green bars. Details about the display: For each reference disease 1 page was created. Each page was controlled by a combination of “Reference disease + disease”, “Reference disease + medicine”

Refcode, Refdesc

V2.23, Vaatavyaadhi ... ▾

Show History

HighlightCode

A6.0:Amlapitta

Reference disease window:

Reference disease or medicine window:

Tables displayed in the top part of the display: there were 9 columns created for each time point.

01 Day 1 District count of Tab Code	02 1 month District count of Tab Med	03 2 months District count of Tab Code	04 3 to 6 months District count of Tab Med	05 7 to 12 months District count of Tab Code	06 2nd year District count of Tab Med	07 3rd year District count of Tab Code	08 4th year District count of Tab Med	09 5 years District count of Tab Code
---	--	--	--	--	---	--	---	---

2 columns were displayed in each time point to display “count of distinct number of diseases” and “count of distinct number of medicines”.

Count of distinct number of diseases:

Distinct count
of Tab Code

Count of distinct number of medicines:

Distinct count
of Tab Med

There were 3 rows for “Before period”, “Day 1” and “After period” with 2 lines in each period. Day 1 cell showed the start day of reference disease “V2.23: Vaatavyadhi – Gridhrasee”, This example showed 137 total number of distinct diseases reported and 664 total number of distinct medicines prescribed on day 1 for this combination of reference disease “V2.23: Vaatavyadhi – Gridhrasee” and disease “A6.0: Amlapitta”.

The first line in the Day 1 cell showed, 1 disease – which is “A6.0: Amlapitta” and 81 distinct medicines prescribed. These 81 different treatments could have been prescribed for “A6.0: Amlapitta”.

		01 Day 1	
		Distinct count of Tab Code	Distinct count of Tab Med
01	In		
Before	O.		
	T..		
02 Day 1	In	1.0	81.0
	O.	136.0	664.0
	T..	137.0	664.0

Cells in the “Before period” line provided the following information:

This example shows 1 month before “V2.23: Vaatavyadhi – Gridhrasee”, there were 61 distinct diseases and 298 distinct medicines reported.

The first line in the cell shows, 1 disease – which is “A6.0: Amlapitta” and 11 distinct medicines prescribed. These 11 different treatments could have been prescribed for “A6.0: Amlapitta”.

		01 Day 1		02 1 month	
		Distinct count of Tab Code	Distinct count of Tab Med	Distinct count of Tab Code	Distinct count of Tab Med
01	In			1.0	11.0
Before	O.			60.0	294.0
	T..			61.0	298.0

Cells in the “After period” line provide the following information:

This example shows 1 month before “V2.23: Vaatavyadhi – Gridhrasee”, there were 96 distinct diseases and 633 distinct medicines reported.

The first line in the cell shows, 1 disease – which is “A6.0: Amlapitta” and 49 distinct medicines prescribed. These 49 different treatments could have been prescribed for “A6.0: Amlapitta”.

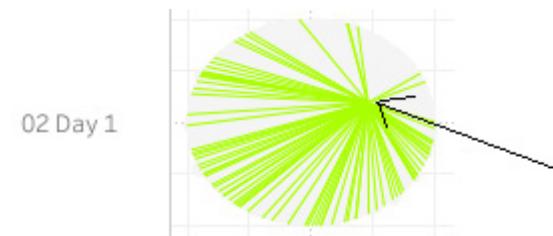
		01 Day 1		02 1 month	
		Distinct count of Tab Code	Distinct count of Tab Med	Distinct count of Tab Code	Distinct count of Tab Med
03 After	In			1.0	49.0
	O.			96.0	633.0
	T..			97.0	635.0
Grand Total		137.0	664.0	114.0	706.0

The bottom section follows the same structure as the top section. The following table provided distinct number of diseases reported and distinct number of medicines prescribed for this particular combination. There were 308 diseases and 1,357 medicines reported for this combination of reference disease “V2.23: Vaatavyadhi – Gridhrasee” and disease “A6.0: Amlapitta”.

Distinct diseases / medicines	
Disease	Medicine
308	1,357

Explanation about the circular view:

The starting point marked the position of the other disease in this case, “A6.0: Amlapitta”, The green colored spokes going from point of origin were different treatments prescribed. These were showing 664 distinct medicines prescribed on day 1.



Hovering tooltip provided details about the disease, treatment name and count of number of patients:



The inner circle displayed the diseases. And the outer circle displayed the treatments.

Distance based Pre and post analysis: in the example for the disease M2.0 (Madhumeha), disease trajectory distances were plotted (Figure 3-39). (1) Madhumeha was reported by 1,441 patients at least once. (2) Of these 567 patients reported only Madhumeha and no other disease thereafter. For such patients, the disease trajectory calculation was not possible, hence these patients were removed from the analysis. (3) The following table showed details of patient count. The disease trajectory calculation was based on 874 patients comprising of 530 males and 344 females

patient_gender	numtype	ncount
M	Only 1 dis	377
F	Only 1 dis	190
M	> 1 dis	530
F	> 1 dis	344

Out of 530 male patients: (1) 201 patients had diseases reported before the first reported instance of M2.0, (2) 460 patients had at least one other disease reported other than M2.0 on or after the first reported instance of M2.0, (3) Disease trajectory for 70 patients could not be calculated since the next reported disease was M2.0.

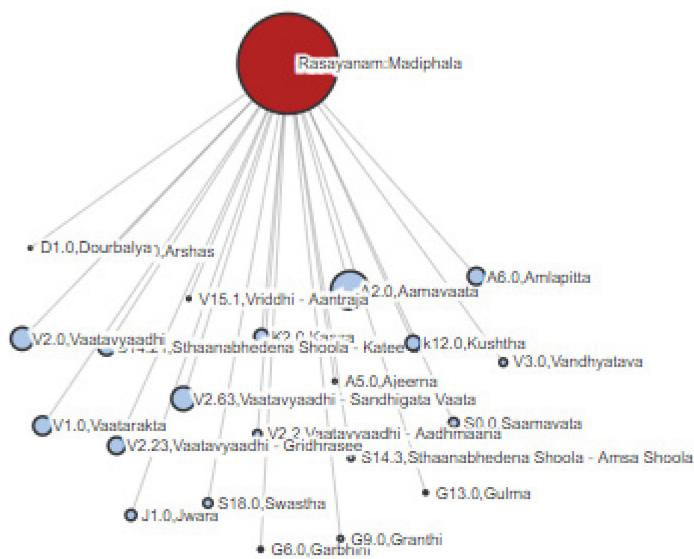
Out of 344 female patients: (1) 140 patients had diseases reported before the first reported instance of M2.0, (2) 291 patients had at least one disease other than M2.0 reported on or after the first reported instance of M2.0, (3) Disease trajectory for 53 patients could not be calculated since the next reported disease was M2.0.

patient_gender	numtype	refday2	ncount
M	> 1 dis	Before	201
M	> 1 dis	After	460
F	> 1 dis	Before	140
F	> 1 dis	After	291

The trajectories were calculated for these patients and displayed for the before and after period. More number of patients had disease trajectories in the “after onset” section. More than 73% of males lie in the score >0.25 and around 36% of them lie in the score >0.5 which could confirm that there were similar diseases experienced by the patients post the onset of the reference disease. Similarly, around 64% of females lie in the score >0.25 and around 24% of them lie in the score >0.5 which could confirm that there were similar diseases experienced by the patients post the onset of the reference disease. A few more examples of similar kind were shown for diseases: P5.0: Prameha, V2.23: Vaatavyaadhi - Gridhrasee, V2.63: Vaatavyaadhi - Sandhigata Vaata (Figure 3-40).

The radar plot shows multi-dimensional data in a short space, 7 different parameters were shown on 7 vertices. Different shapes suggest that there were underlying differences to the data structure.

Dynamic bubble plot visualization showed intricate relationships and details in a limited space, one more analysis method to see multi-dimensional data (Figure 3-42). Using data for Amavaata (A6.0), in the snapshot below, we could see the patients with Aamvata who received Rasayanam Madiphala and in addition what were the other diseases that these patients reported.



Another view which showed the further detailed view of Aamvata patients having received Rasayanam Madiphala and further having reported Stanbheedana Kathee Shoola disease and further its treatment. Further, the big bubble here closer to Stanbheedana Kathee Shoola disease was Aamdosha which showed that Stanbheedana Kathee Shoola was also one of the diseases reported by Aamdosha patients.

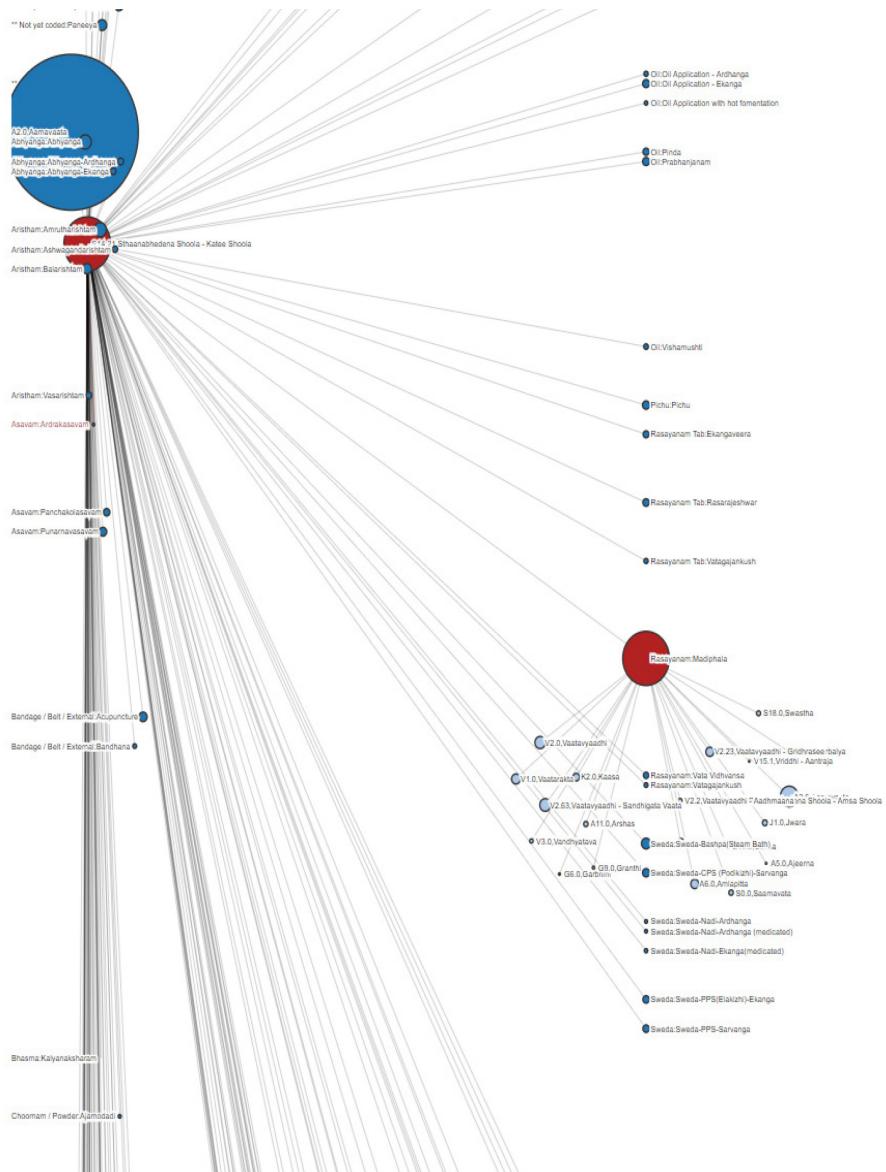


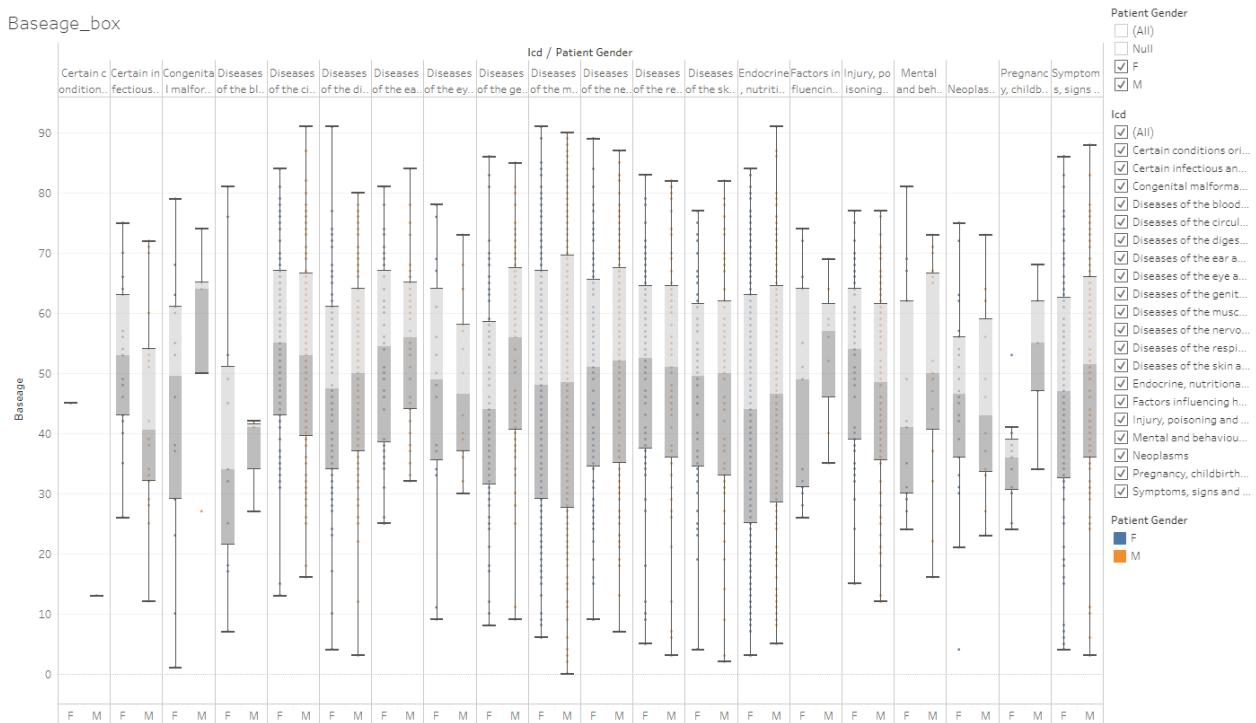
Figure 3-17: ICD classification by Gender

ICDFreq

Icd	High	Grand Total	Patient Gender		
			Null	F	M
Grand Total		8,027	1	4,455	3,571
Certain conditions originating in the perinatal period	Total	2		1	1
P91		2		1	1
Certain infectious and parasitic diseases	Total	90		42	48
A01		9		6	3
A06		1		1	
A15		7		3	4
A18		3			3
A30		1		1	
A41		1		1	
A46		1		1	
A81		2		2	
A90		2		2	
A92		5		4	1
B01		1		1	
B02		5			5
B07		8		5	3
B08		2		1	1
B19		6			6
B34		1			1
B35		32		12	20
B37		4		4	
B74		1		1	
B82		1			1

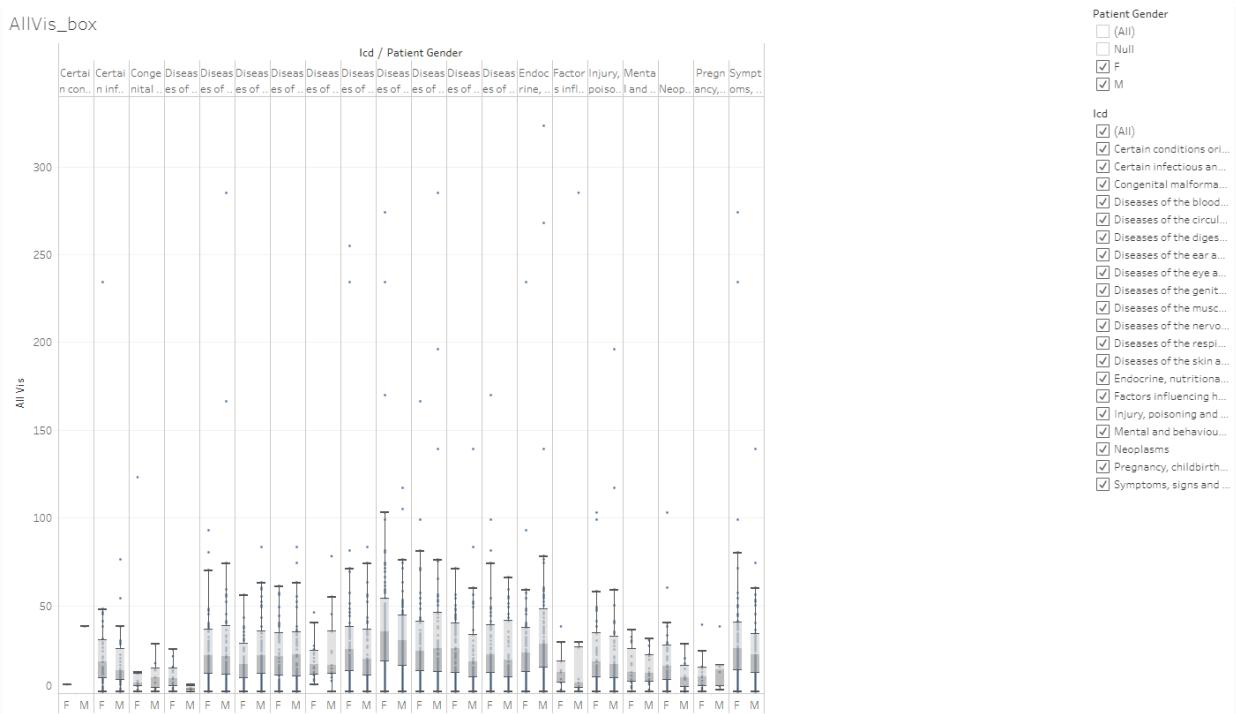
ICD classification and ICD classification high level categories, frequency counts by gender. Data version: 2011 to Oct 2017. Link to analysis: [Link](#)

Figure 3-18: Age distribution by ICD classification and Gender



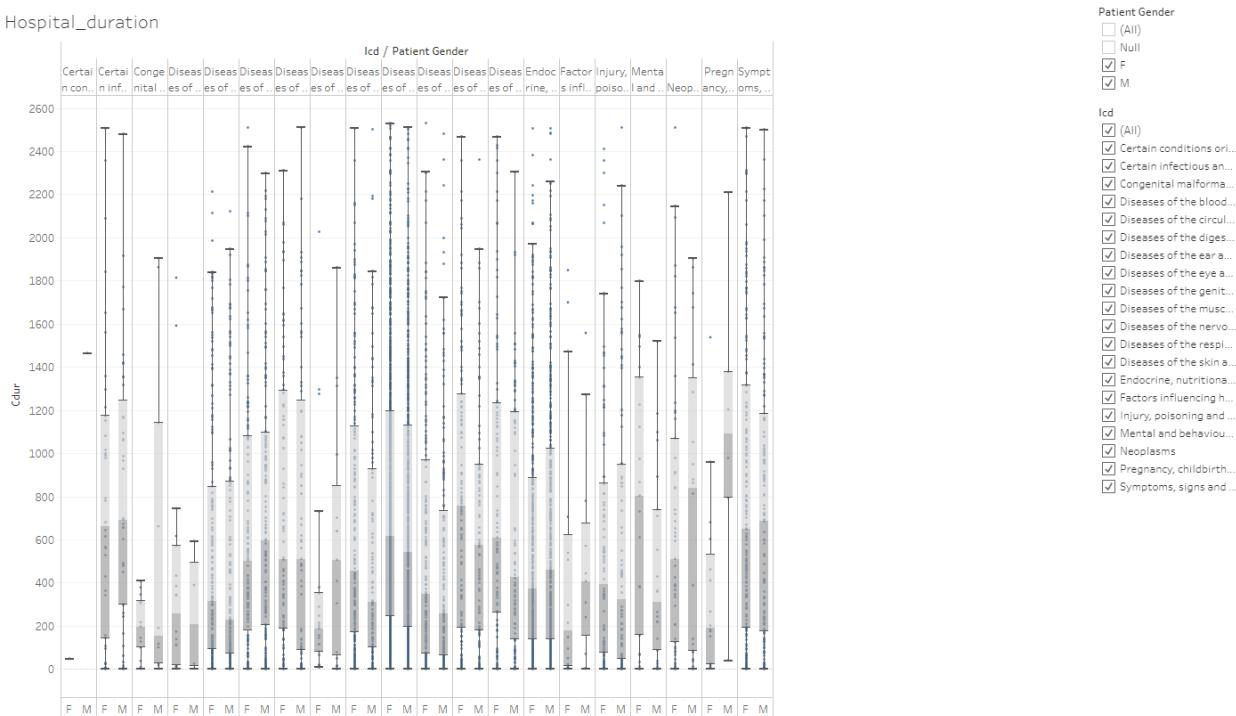
Boxplot representation of age by ICD classification and gender, Data version: 2011 to Oct 2017. Link to analysis: [Link](#)

Figure 3-19: Visit distribution by ICD classification and Gender



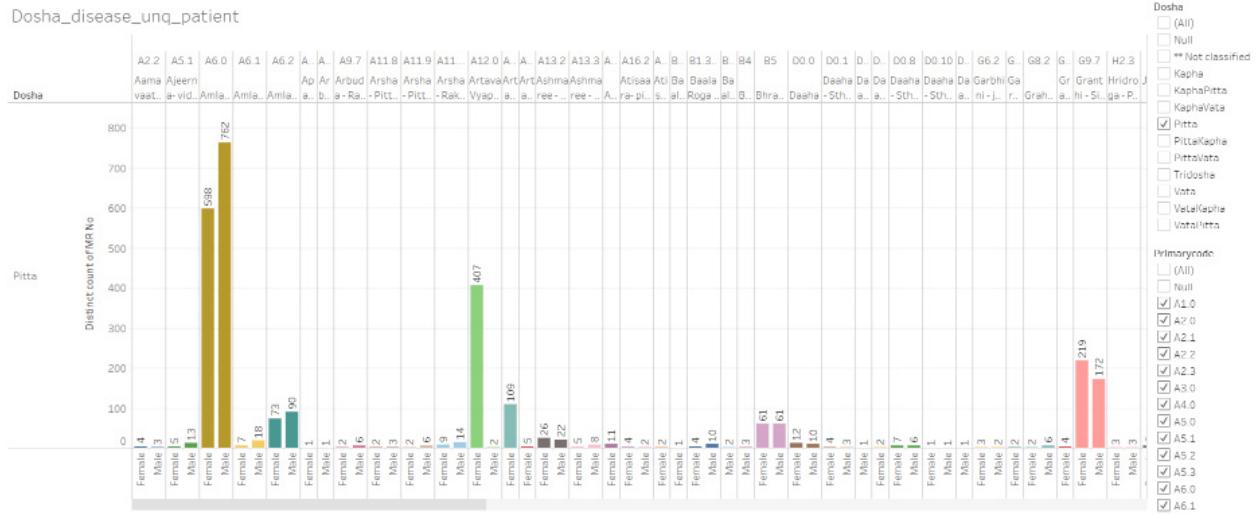
Boxplot representation of hospital number of visits by ICD classification and gender, Data version: 2011 to Oct 2017. Link to analysis: [Link](#)

Figure 3-20: Duration distribution by ICD classification and Gender



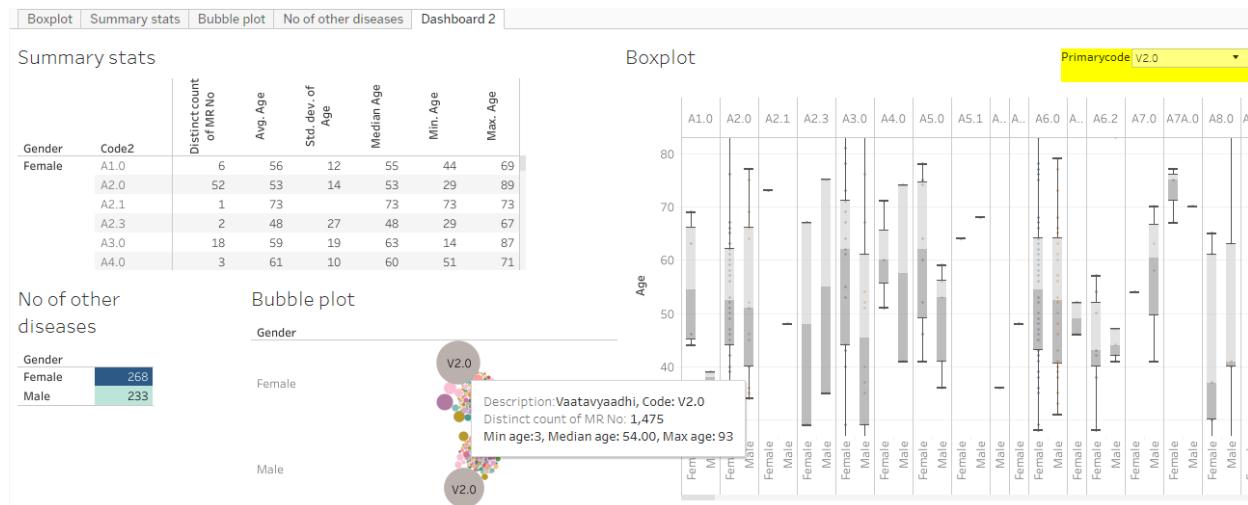
Boxplot representation of hospital visit duration by ICD classification and gender, Data version: 2011 to Oct 2017. Link to analysis: [Link](#)

Figure 3-21: Disease classification by Prakriti and Gender



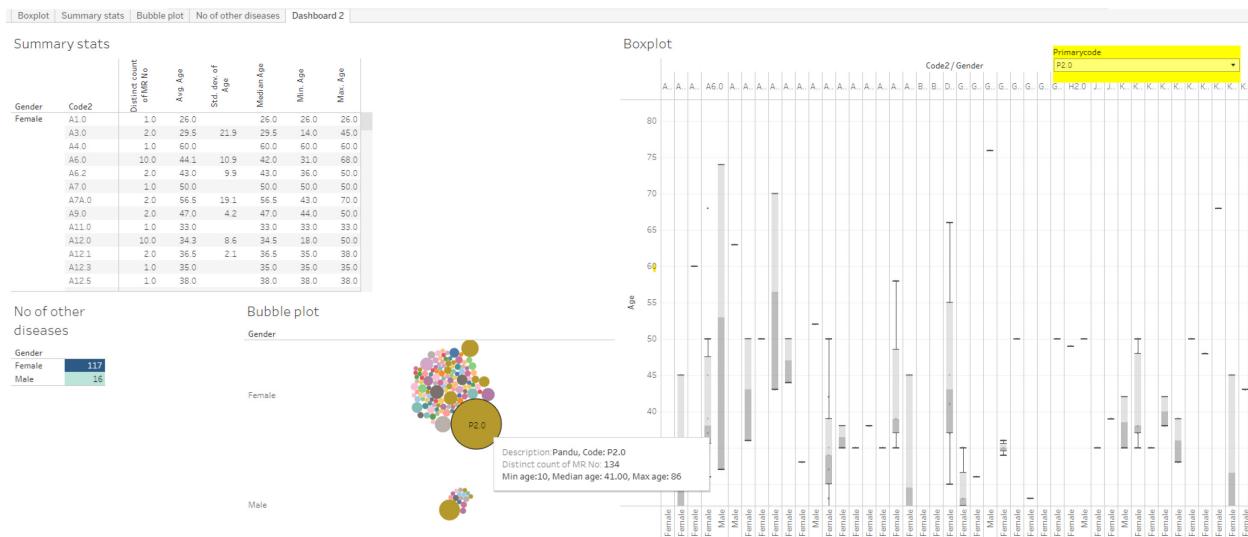
Dosha: Prakriti type, x-axis: male and female grouped by individual disease, y-axis: frequency counts of unique patients, Data version: 2011 to Oct 2016. Link to analysis: [Link](#) to get the above display subset Dosha for Pitta.

Figure 3-22: Co-morbidity analysis approach 1 example 1: Vaatavyadhi



Summary stats section: descriptive statistics details by gender and other diseases reported, No of other disease: distinct number of other diseases reported by patients who had reported the primary disease, Bubble plot: frequency count of distinct patients by disease, Boxplot: age distribution by disease and gender, Data version: 2011 to Oct 2016. Link to analysis: [Link](#) to get the above display subset Primarycode = V2.0

Figure 3-23: Co-morbidity analysis approach 1 example 2: Pandu



Summary stats section: descriptive statistics details by gender and other diseases reported, No of other disease: distinct number of other diseases reported by patients who had reported the primary disease, Bubble plot: frequency count of distinct patients by disease, Boxplot: age distribution by disease and gender, Data version: 2011 to Oct 2016. Link to analysis: [Link](#) to get the above display subset Primarycode = P2.0

Figure 3-24: Co-morbidity analysis approach 1 example 3: Madhumeha



Summary stats section: descriptive statistics details by gender and other diseases reported, No of other disease: distinct number of other diseases reported by patients who had reported the primary disease, Bubble plot: frequency count of distinct patients by disease, Boxplot: age distribution by disease and gender, Data version: 2011 to Oct 2016. Link to analysis: [Link](#) to get the above display subset Primarycode = M2.0

Figure 3-25: Co-morbidity analysis approach 2



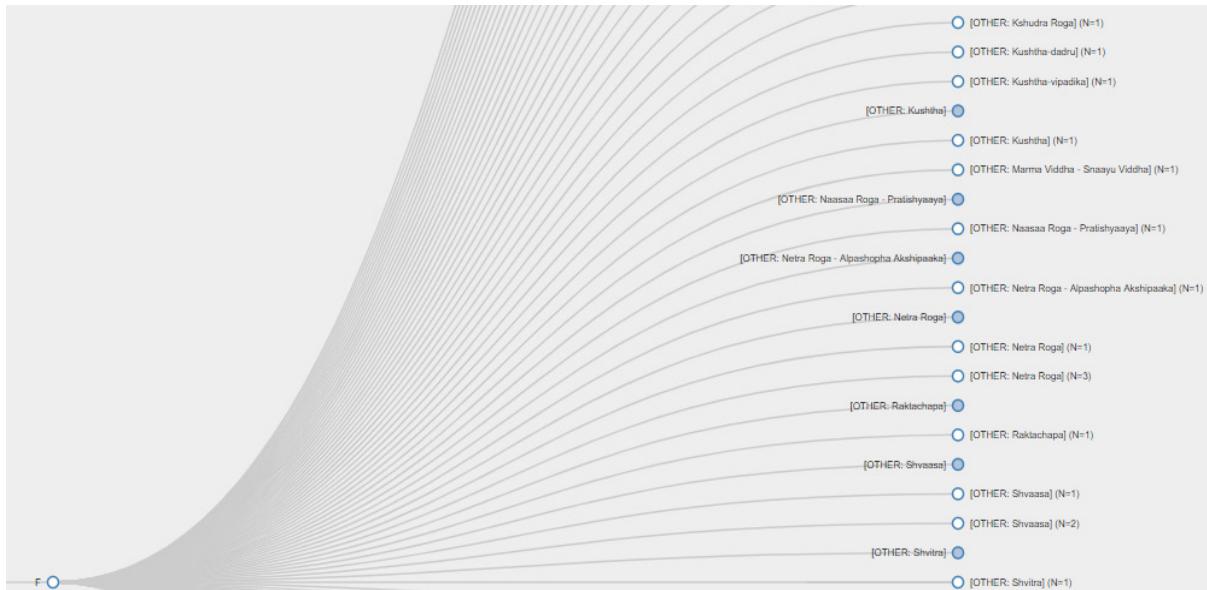
Upper section: bubble plots for the reference disease and other diseases reported, bubble size is based on number of distinct patients. Lower sections: unique number of other diseases reported for the reference disease. 1, 2, ..., 12: January to December month, Data version: 2011 to Oct 2016. Link to analysis: [Link](#) to get the above display subset Primarycode = V2.0

Figure 3-26: Co-morbidity analysis approach 3: collapsible tree view

Initial view of the tree



After clicking on F (Female), the collapsible tree opens up



An example of a disease experienced only by one gender



<https://coursephd.github.io/>

Figure 3-27: Patient Disease and Treatment administration by Study Day

Patient_Dis_Med_counts							Mr No
Mr No	Grday	Studyday	Cat / Newold2		Medicine		Newold2
			Disease	1st tim..	Repeat	1st dose	
MR000335	1	1		1	4		1st dose
	2	24		1	1	2	1st time disease
	3	69		1	1		Repeat
	4	521	1		1		
	5	565		1	2	1	
	6	572	5		10		
	7	646	1		3		
	8	1093	1		1	2	

Patient_1st_Repeat				
Mr No	Grday	Cat	Type med	Coded med
MR000335	1	Disease	** Not yet coded	** Not yet coded
		Medicine	Asavam	Lodhrasavam
			Kashayam	Varanadi
				Vasaguloochyadi
			Tablet/Gulika/Vati	Kanchanara Guggulu
	2	Disease	** Not yet coded	** Not yet coded
		Medicine	Asavam	Lohasavam

The report displays individual patient data. Upper left part: Mr No: Patient ID, study day, Disease reported 1st time and repeated, medicine reported 1st time and repeated, Lower part of the report displays individual patient data for each day and distinguishes 1st dose, 1st disease and Repeat reporting for the same. Data version: 2011 to Oct 2017. Link to analysis: [Link](#) to get the above display subset Mr No = MR000335

Figure 3-28: Patient Disease by Study Day and Treatment administration by Study Day

Disease					Medicine				
Mr No	Grpday	Studyday	Newold2Dis		Mr No	Grpday	Studyday	Newold2	
			1st time disease	Repeat				1st dose	Repeat
MR000335	1	1		1	MR000335	1	1	4	
	2	24				2	24	1	2
	3	69				3	69	1	
	4	521	1			4	521		1
	5	565		1		5	565	2	1
	6	572	1			6	572	10	
	7	646	1			7	646	3	
	8	1093	1			8	1093	1	2
	9	1388	1			9	1388	3	
	10	1418		1		10	1418	2	2
	11	1481	1			11	1481	4	
	12	1528	1			12	1528	3	
	13	1628	1			13	1628	2	1
	14	2025	2			14	2025	6	1
	15	2488	1			15	2488	1	
	16	2503	1			16	2503	2	
	17	2508		2		17	2508	2	1

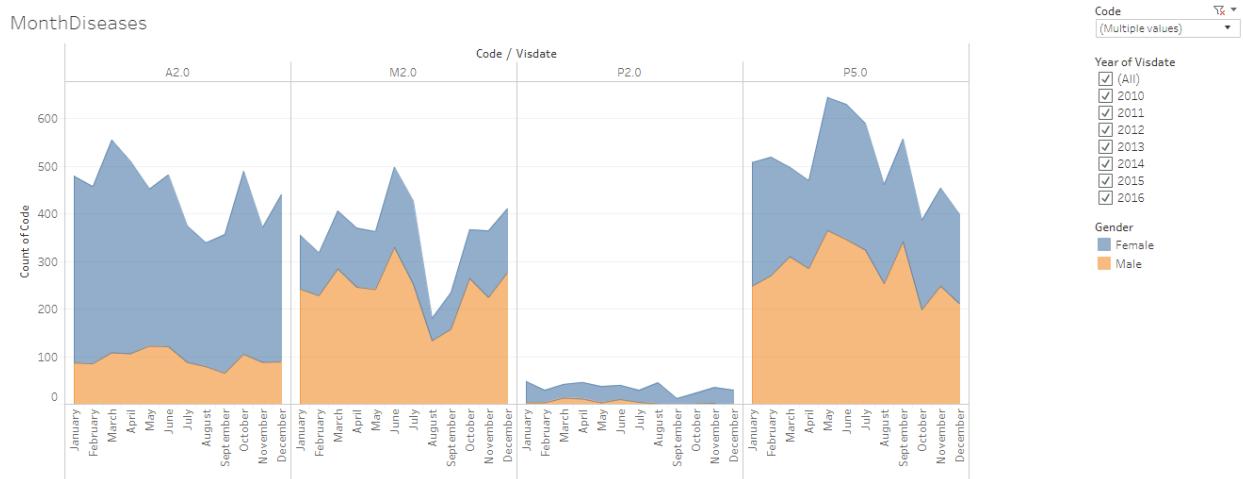
The report displays individual patient data. Panel on the left hand: number of diseases reported at a particular visit, panel on the right hand: number of prescribed treatments reported at a particular visit, Data version: 2011 to Oct 2017. Link to analysis: [Link](#) to get the above display subset Mr No = MR000335

Figure 3-29: Patient Cumulative Disease and Treatment administration by Visit

Patient_dis_med_Cumulative					%Patient_dis_med_Cumulative				
Mr No	Cumday2	Cat / Newold2		Mr No	Cumday2	Cat / Newold2		Mr No	Cumday2
		Disease	Medicine			Disease	Medicine		
1st time disease	Repeat	1st dose	Repeat	1st time disease	Repeat	1st dose	Repeat	1st time disease	Repeat
MR000335	Till visit 1	1		4	MR000335	Till visit 1	100.00%	100.00%	
	Till visit 2	1	1	5		50.00%	50.00%	71.43%	28.57%
	Till visit 3	1	2	6		33.33%	66.67%	75.00%	25.00%
	Till visit 4	2	2	6		50.00%	50.00%	66.67%	33.33%
	Till visit 5	2	3	8		40.00%	60.00%	66.67%	33.33%
	Till visit 6	7	3	18		70.00%	30.00%	81.82%	18.18%
	Till visit 7	8	3	21		72.73%	27.27%	84.00%	16.00%
	Till visit 8	9	3	22		75.00%	25.00%	78.57%	21.43%
	Till visit 9	10	3	25		76.92%	23.08%	80.65%	19.35%
	Till visit 10	10	4	27		71.43%	28.57%	77.14%	22.86%
	Till visit 11	11	4	31		73.33%	26.67%	79.49%	20.51%
	Till visit 12	12	4	34		75.00%	25.00%	80.95%	19.05%
	Till visit 13	13	4	36		76.47%	23.53%	80.00%	20.00%
	Till visit 14	15	4	42		78.95%	21.05%	80.77%	19.23%
	Till visit 15	16	4	43		80.00%	20.00%	81.13%	18.87%
	Till visit 16	17	4	45		80.95%	19.05%	81.82%	18.18%

The report displays individual patient data. Panel on the left hand: absolute values of diseases and prescribed treatments till particular visits, panel on the right hand side: % values of diseases and prescribed treatments till particular visits, Data version: 2011 to Oct 2017. Link to analysis: [Link](#)

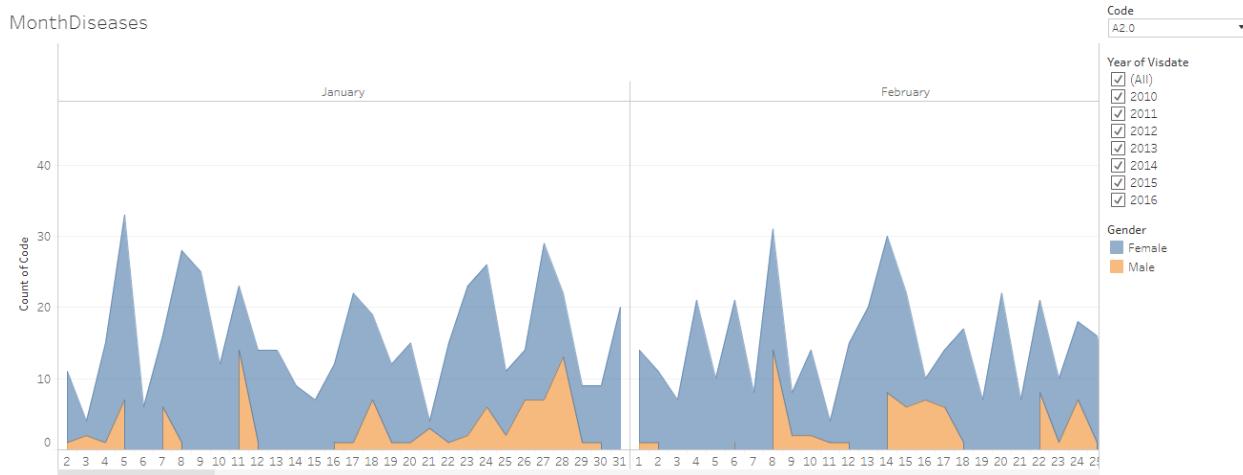
Figure 3-30: Area graph representation of diseases



Area graph representation of diseases: x-axis: Month, y-axis: frequency count of unique patients, disease code: the underlying data for each disease, peach colour: counts for male, blue colour: counts for female.

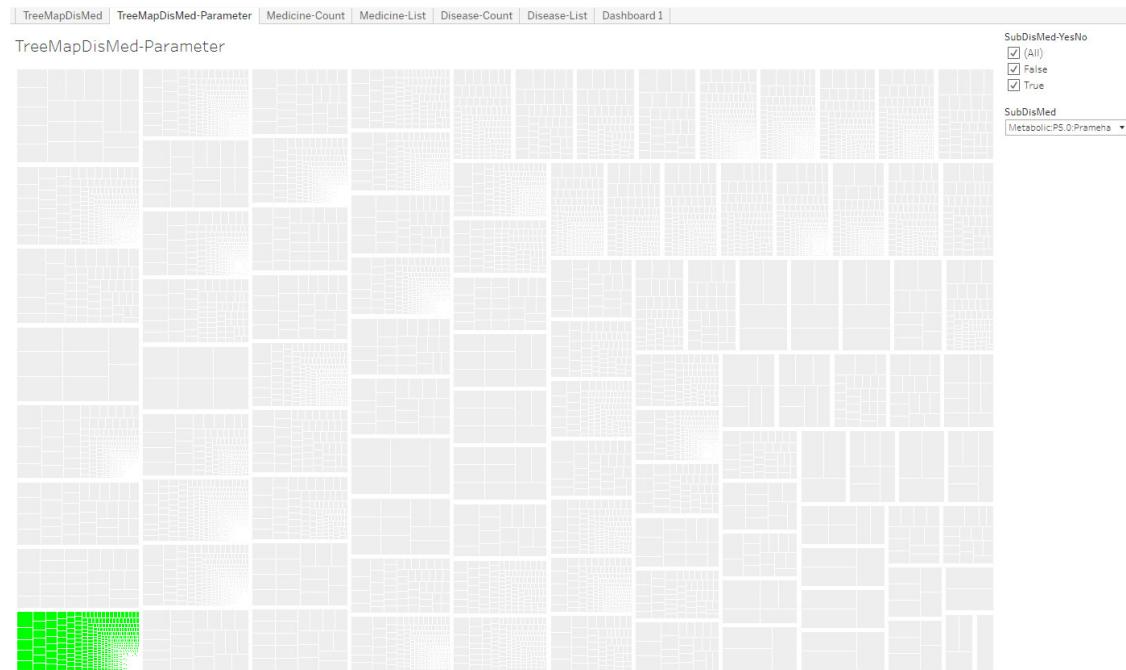


x-axis can be expanded to convert the monthly view to more granular unit (week, day).

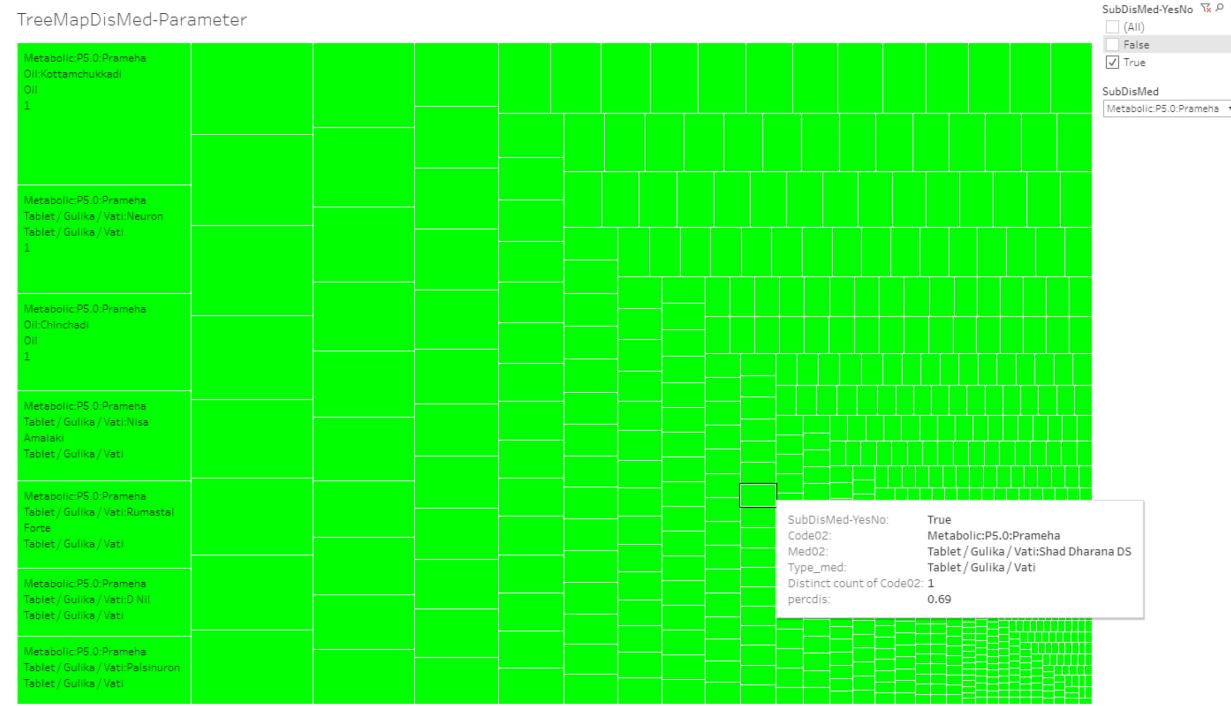


The original data displayed in the 1st part of the presentation is opened for daily view for a particular disease code A2.0, Data version: 2011 to 2016. Link to analysis: [Link](#) to get the above display subset the Code for (A2.0, M2.0, P2.0, P5.0)

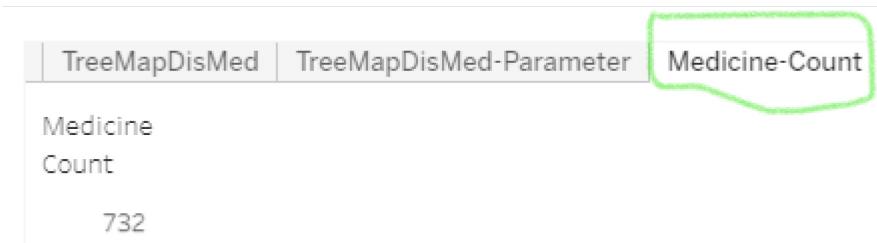
Figure 3-31: Mosaic plot: Disease and treatment representation example 1: Prameha



Mosaic plot: Each box is one disease, the selected disease is marked in Green colour, smaller boxes inside each disease display one intervention each, Data version: 2011 to Oct 2017. Link to analysis: [Link](#) to get the above display subset SubDisMed = Metabolic: P5.0: Prameha



The snapshot above is the zoomed version of the Prameha block which highlights one of the many treatments prescribed for the same.



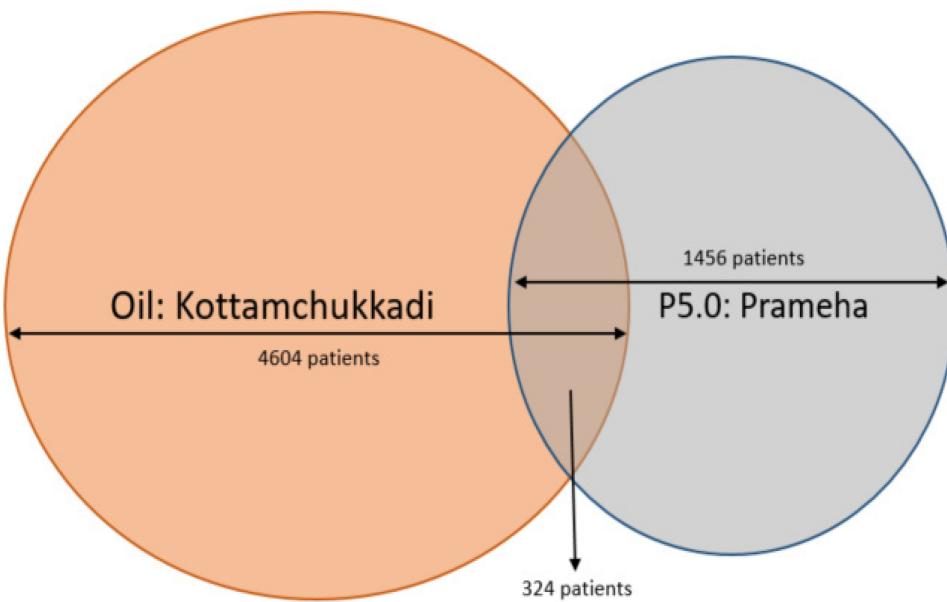
The Medicine count tab provides the information on total number of different medicines prescribed for Prameha. There are 732 distinct interventions.

Medicine-List							SubDisMed	
Med02	Code02	totpatmed	totpatdis	n	F	percdis	percmed	SubDisMed
Oil:Kottamchukkadi	Metabolic:P5.0:Prameha	4604	1456	324	22.25	7.04		Abc
Tablet/Gulika/Vati:Neuron	Metabolic:P5.0:Prameha	2065	1456	247	16.96	11.96		Abc
Oil:Chinchadi	Metabolic:P5.0:Prameha	2947	1456	221	15.18	7.5		Abc
Tablet/Gulika/Vati:Nisa Amalaki	Metabolic:P5.0:Prameha	798	1456	206	14.15	25.81		Abc
Tablet/Gulika/Vati:Rumastal Forte	Metabolic:P5.0:Prameha	1844	1456	199	13.67	10.79		Abc
Tablet/Gulika/Vati:D Nil	Metabolic:P5.0:Prameha	549	1456	155	10.65	28.23		Abc
Tablet/Gulika/Vati:Palsimuron	Metabolic:P5.0:Prameha	1511	1456	154	10.58	10.19		Abc
Tablet/Gulika/Vati:Diabecon DS	Metabolic:P5.0:Prameha	476	1456	145	9.96	30.46		Abc
Liniment:Myostal	Metabolic:P5.0:Prameha	1991	1456	145	9.96	7.28		Abc
Tablet/Gulika/Vati:Cervilon	Metabolic:P5.0:Prameha	1151	1456	143	9.82	12.42		Abc
Kashayam:RasnasaPthakam	Metabolic:P5.0:Prameha	1866	1456	133	9.13	7.13		Abc
Kashayam:Prasaranyadi	Metabolic:P5.0:Prameha	974	1456	124	8.52	12.73		Abc
Kashayam:Rasnaerandadi	Metabolic:P5.0:Prameha	2265	1456	122	8.38	5.39		Abc
Tablet/Gulika/Vati:Nuro - XT	Metabolic:P5.0:Prameha	1026	1456	120	8.24	11.7		Abc
Kashayam:Rasnayograj Guggulu	Metabolic:P5.0:Prameha	967	1456	117	8.04	12.1		Abc
Kashayam:Asanadi	Metabolic:P5.0:Prameha	418	1456	113	7.76	27.03		Abc
Tablet/Gulika/Vati:Rumalaya Forte	Metabolic:P5.0:Prameha	1175	1456	106	7.28	9.02		Abc
Kashayam Tab:Rasnaerandadi	Metabolic:P5.0:Prameha	1182	1456	100	6.87	8.46		Abc
Kashayam:Sahacharadi	Metabolic:P5.0:Prameha	1603	1456	92	6.32	5.74		Abc
Tablet/Gulika/Vati:Trayodasanga Guggulu	Metabolic:P5.0:Prameha	1830	1456	88	6.04	4.81		Abc
Tablet/Gulika/Vati:Lumbatton	Metabolic:P5.0:Prameha	1433	1456	84	5.77	5.86		Abc
Tablet/Gulika/Vati:Ksheerabala	Metabolic:P5.0:Prameha	594	1456	76	5.22	12.79		Abc
Kashayam:Ashtavargam	Metabolic:P5.0:Prameha	548	1456	76	5.22	13.87		Abc
Tablet/Gulika/Vati:Flexy	Metabolic:P5.0:Prameha	562	1456	73	5.01	12.99		Abc
Oil:Narayana	Metabolic:P5.0:Prameha	374	1456	73	5.01	19.52		Abc
Oil:Mirlvenna	Metabolic:P5.0:Prameha	2329	1456	69	4.74	2.96		Abc
Oil:Sahacharadi	Metabolic:P5.0:Prameha	1100	1456	67	4.6	6.09		Abc
Kashayam:Maharasnayograj Guggulu	Metabolic:P5.0:Prameha	660	1456	67	4.6	10.15		Abc
Tablet/Gulika/Vati:Chandraprabha	Metabolic:P5.0:Prameha	612	1456	66	4.53	10.78		Abc
Tablet/Gulika/Vati:Trayodasanga Guggulu DS	Metabolic:P5.0:Prameha	1249	1456	65	4.46	5.2		Abc
Tablet/Gulika/Vati:Mehamil	Metabolic:P5.0:Prameha	214	1456	59	4.05	27.57		Abc
Tablet/Gulika/Vati:Glukostat	Metabolic:P5.0:Prameha	175	1456	57	3.91	32.57		Abc
Oil:Pinda	Metabolic:P5.0:Prameha	937	1456	57	3.91	6.08		Abc
Rasayanan:Vasant Kusumakar Plain	Metabolic:P5.0:Prameha	535	1456	55	3.78	10.28		Abc
Tablet/Gulika/Vati:Sallaki M R	Metabolic:P5.0:Prameha	2972	1456	54	3.71	1.82		Abc
Kashayam:Kathaka Kathiradi	Metabolic:P5.0:Prameha	167	1456	53	3.64	31.74		Abc
Tablet/Gulika/Vati:Dia P	Metabolic:P5.0:Prameha	134	1456	51	3.5	38.06		Abc

A detailed list of medicines with the total patients prescribed with them as well as total patients suffering from Prameha are displayed in the snapshot above.

Figure 3-32: Disease and treatment example 2: P5.0: Prameha and Oil: Kottamchukkadi

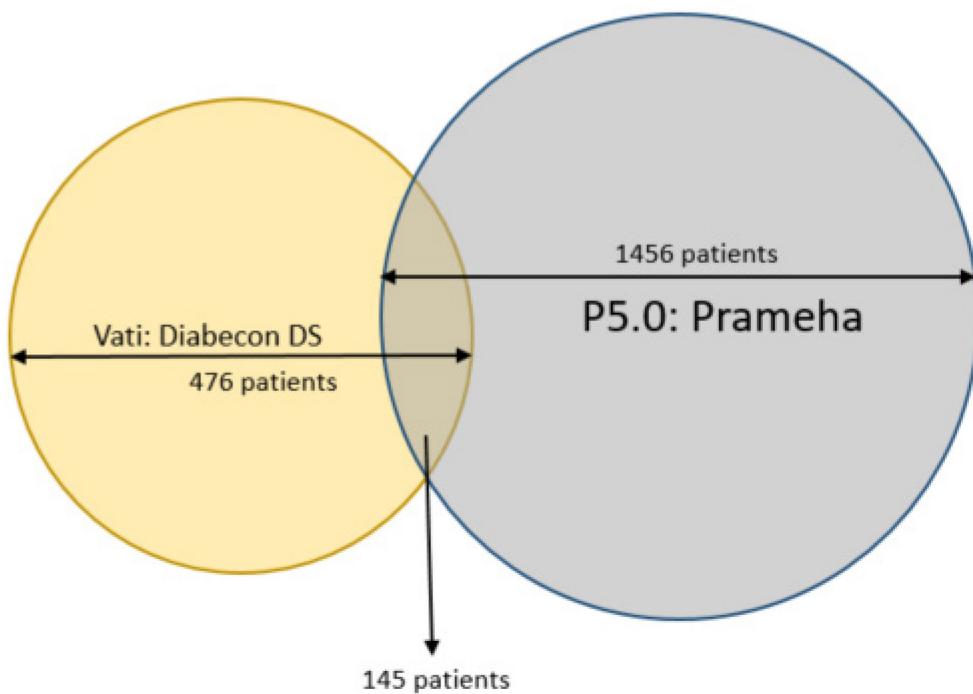
Medicine-List							
Med02	Code02	totpatmed	totpatdis	n	F	percdis	percmed
Oil:Kottamchukkadi	Metabolic:P5.0:Prameha	4604	1456	324	22.25	7.04	



Totpatmed shows that there are 4,604 patients who have been prescribed with Oil: Kottamchukkadi; Totpatdis shows that there are 1,456 patients who are diagnosed with Prameha; this shows that the treatment is not Prameha specific. The n count of 324 shows the patients who had Prameha and were prescribed Oil: Kottamchukkadi. Percdis shows that 22.25% i.e. 324 / 1456 of patients having Prameha are prescribed this particular treatment. Percmed shows that only 7% of the time this medicine has been prescribed for Prameha patients.

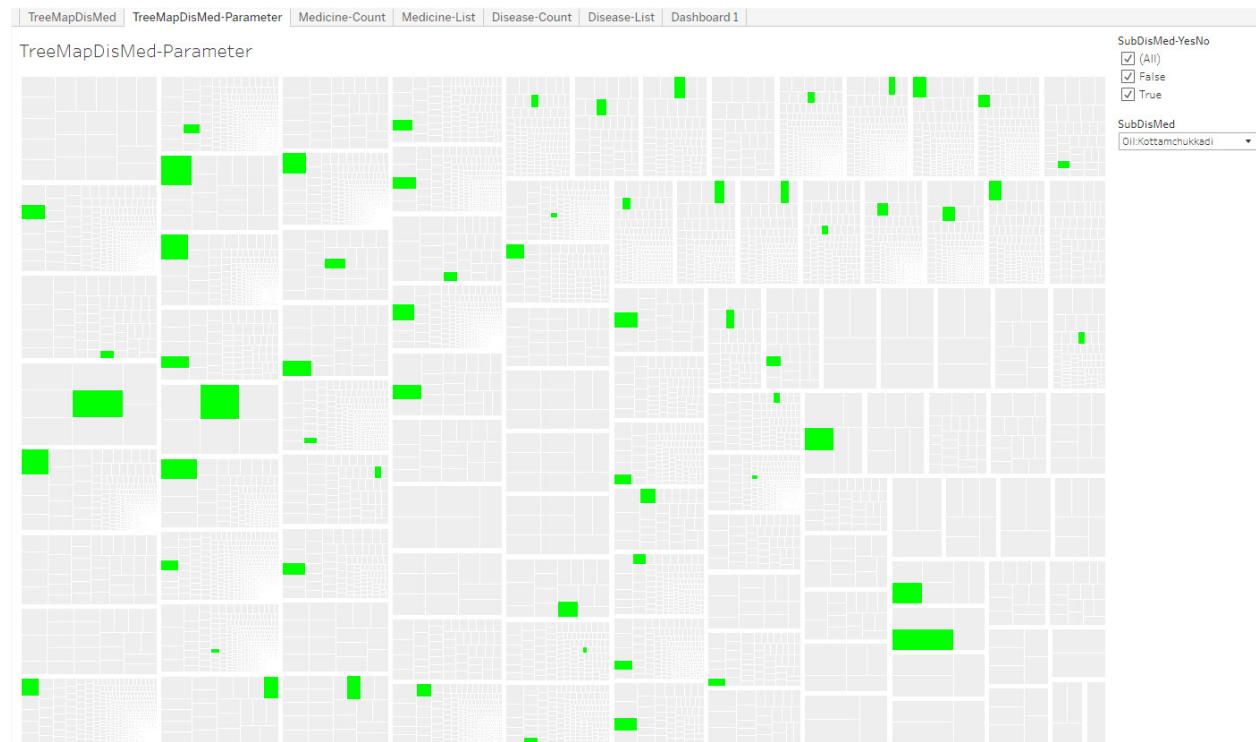
Figure 3-33: Disease and treatment example 3: P5.0: Prameha and Vati: Diabecon DS

Tablet / Gulika / Vati:Diabecon DS	Metabolic:P5.0:Prameha	476	1456	145	9.96	30.46
------------------------------------	------------------------	-----	------	-----	------	-------



Totpmed shows that there are 476 patients who have been prescribed with Vati: Diabecon DS; Totpatdis shows that there are 1,456 patients who are diagnosed with Prameha; this shows that the treatment could be more prescribed to Prameha patients. The n count of 145 shows the patients who had Prameha and were prescribed Vati: Diabecon DS. Percdis shows that 9.96% i.e. 145 / 1,456 of patients having Prameha are prescribed this particular treatment. Percmed shows that only 30.46% of the time this medicine has been prescribed for Prameha patients.

Figure 3-34: Mosaic plot Disease and treatment representation example 4: Treatment: Oil: Kottamchukkadi



Mosaic plot: Each box is one disease, the selected disease is marked in Green colour, smaller boxes inside each disease display one intervention each, Data version: 2011 to Oct 2017. Link to analysis: [Link](#) to get the above display subset SubDisMed = Oil: Kottamchukkadi



Disease-
Count

62

The Disease count tab provides the information on total number of different diseases for which the intervention was prescribed. There are 62 distinct diseases.

Medicine-List							
Med02	F	Code02	totpatmed	totpatdis	n	F	percdis
Oil:Kottamchukkadi		RMSD.V2.63:Vaatavyaad..	4604	4160	1506	36.2	32.71
		RMSD.V2.23:Vaatavyaad..	4604	2476	1274	51.45	27.67
		RMSD.S13.11:Sthaanabh..	4604	942	490	52.02	10.64
		RMSD.V2.0:Vaatavyaadhi..	4604	2822	396	14.03	8.6
		RMSD.S14.21:Sthaanabh..	4604	1227	326	26.57	7.08
		Metabolic:P5.0:Prameha ..	4604	1456	324	22.25	7.04
		RMSD.A2.0:Aamavaata..	4604	790	205	25.95	4.45
		RMSD.A3.0:Abhigataja S..	4604	703	78	11.1	1.69
		RMSD.S13.19:Sthaanabh..	4604	120	65	54.17	1.41
		RMSD.V1.0:Vaatarkta..	4604	506	62	12.25	1.35
		RMSD.V2.36:Vaatavyaad..	4604	361	51	14.13	1.11
		RMSD.S14.0:Sthaanabhe..	4604	508	50	9.84	1.09
		RMSD.V2.9:Vaatavyaadhi..	4604	203	44	21.67	0.96
		Metabolic:M10.1:Medoro..	4604	590	42	7.12	0.91
		Metabolic:M2.0:Madhum..	4604	1395	40	2.87	0.87
		RMSD.S14.7:Sthaanabhe..	4604	227	35	15.42	0.76
		RMSD.S14.17:Sthaanabh..	4604	189	26	13.76	0.56
		RMSD.V2.75:Vaatavyaad..	4604	162	20	12.35	0.43
		RMSD.V2.30:Vaatavyaad..	4604	78	18	23.08	0.39
		Metabolic:S16.0:Sthaulya ..	4604	911	18	1.98	0.39
		RMSD.S15.42:Sthaanabh..	4604	73	15	20.55	0.33
		RMSD.S15.36:Sthaanabh..	4604	75	14	18.67	0.3
		RMSD.S15.31:Sthaanabh..	4604	86	13	15.12	0.28
		RMSD.V2.77:Vaatavyaad..	4604	55	11	20	0.24
		Metabolic:M10.0:Medoro..	4604	139	11	7.91	0.24
		Metabolic:P5.4:Prameha ..	4604	140	9	6.43	0.2
		RMSD.S14.3:Sthaanabhe..	4604	79	8	10.13	0.17
		RMSD.V2.68:Vaatavyaad..	4604	49	7	14.29	0.15
		RMSD.S14.24:Sthaanabh..	4604	29	7	24.14	0.15
		RMSD.S14.18:Sthaanabh..	4604	34	7	20.59	0.15
		RMSD.V2.47:Vaatavyaad..	4604	24	6	25	0.13
		RMSD.S10.4:Stambha -Gr..	4604	31	6	19.35	0.13
		RMSD.A2.3:Aamavaata..	4604	30	5	16.67	0.11
		Metabolic:M10.2:Medoro..	4604	188	5	2.66	0.11
		RMSD.V2.42:Vaatavyaad..	4604	52	4	7.69	0.09
		RMSD.S14.4:Sthaanabhe..	4604	68	4	5.88	0.09
		RMSD.S14.13:Sthaanabh..	4604	45	3	6.67	0.07

A detailed list of diseases with the total patients prescribed with the treatment as well as total patients suffering from different diseases are displayed.

Figure 3-35: Cross tabulation of prescribed treatments and disease group by gender Example 1

MedType_DisType

Medicine Name	Distype / Patient Gender							
	Metabolic			RMSD			Total	Grand Total
	F	M	Total	F	M			
Balarishtam						29	10	39
Balarishtam 450 ml	3	2	5	143	80	223	225	
Balarishtam 450 ml [sna]						16	9	25
Balarishtam 450 ml KPL						13	9	22
Balarishtam 450 ML SNA						9	5	14
Balarishtam 450 ml Vaidya	3	2	5	158	122	280	282	
Balarishtam [KPL]						2	1	3
Balarishtam [AVP]	11	8	19	353	256	609	616	
Balarishtam Rajah						1	1	2
Balarishtam(Arya)	1	1	2	24	12	36	37	
Grand Total	17	13	30	677	465	1,142	1,154	

Cross tabulation of medicine, disease type and patient gender, Medicine name: source data collected on Case Report Form, Distype: Metabolic and RMSD groups derived in the analysis dataset. Patient Gender: source data. Only 30 patients having metabolic diseases were prescribed the medicine whereas 1,142 patients with RMSD were prescribed. This reflects the ayurvedic principle of who should be prescribed any aristham. Data version: 2011 to Oct 2017. Link to analysis: [Link](#) to get the above display subset Medicine name = Balarishtam

Figure 3-36: Cross tabulation of prescribed treatments and disease group by gender Example 2

MedType_DisType

Medicine Name	Distype / Patient Gender						
	Metabolic			RMSD			Grand Total
	F	M	Total	F	M	Total	
Abhrak bhasma (Dooth) 2gm				2	1	3	3
Abhraka Bhasma 1g (Sahasraputi) Dhoot					1	1	1
Abhraka Bhasma 5g [101] (AVP)	3	2	5	1	2	3	8
Abhraka Bhasma AVP	3	2	5	2	1	3	8
Abhraka Bhasma Dooth-100Butas	1	2	3	2	6	8	10
Abhrakam bhasma				2		2	2
Apamarga kshara Bhasma					1	1	1
Godhanti Bhasma 50gm [SDM]	1		1	16	4	20	20
Hajrulayahda Bhasma (Baidyanath)	1	5	6	3	8	11	17
Heeraka Bhasma 100mg [Dooth]				2		2	2
Kanmada Bhasma(10gm) (AVP)	4	4	8	2	2	4	11
Kashis Bhasma (Baidyanath)				1		1	1
Pravala bhasma	1		1	2	2	4	5
Pravala Bhasma Tab Dooth	1		1		1	1	2
Pravala Basmam (AVP)	1		1	1		1	2
Pravala Basmam Cap - 100				10	2	12	12
Pravala Basmam Cap (Kottakkal)	2		2	98	35	133	133
Rajatabhasma Cap (Kottakkal)	1		1				1
Roupya (Rajatha) Bhasma					1	1	1
Roupya (Rajatha) Bhasma 5 gm (Dooth)				2	1	3	3
Sameerapannaga Bhasma (Dooth)				2		2	2
sanka bhasmam				2		2	2
sankha bhasma				1	1	2	2
Sankha Bhasma(AVP)	1			1		1	1
Shilajith Bhasma	1	2	3				3
Shuddha Shilajit Bhasma		1	1				1
Tankan Bhasma 10gm		1	1	1	1	2	3
Tankan Bhasma (Baidyanath)		2	2	3	2	5	7
Tapyadi Loha Bhasma (Dooth)	1		1	3	1	4	4
Trivanga Bhasma (Dooth)	1	1	2				2
Vanga Bhasma 5g (Dhoot)	1	2	3				3
Yashada Bhasma 5gm (Dooth)	3	6	9	10	12	22	28
Grand Total	24	30	54	161	82	243	287

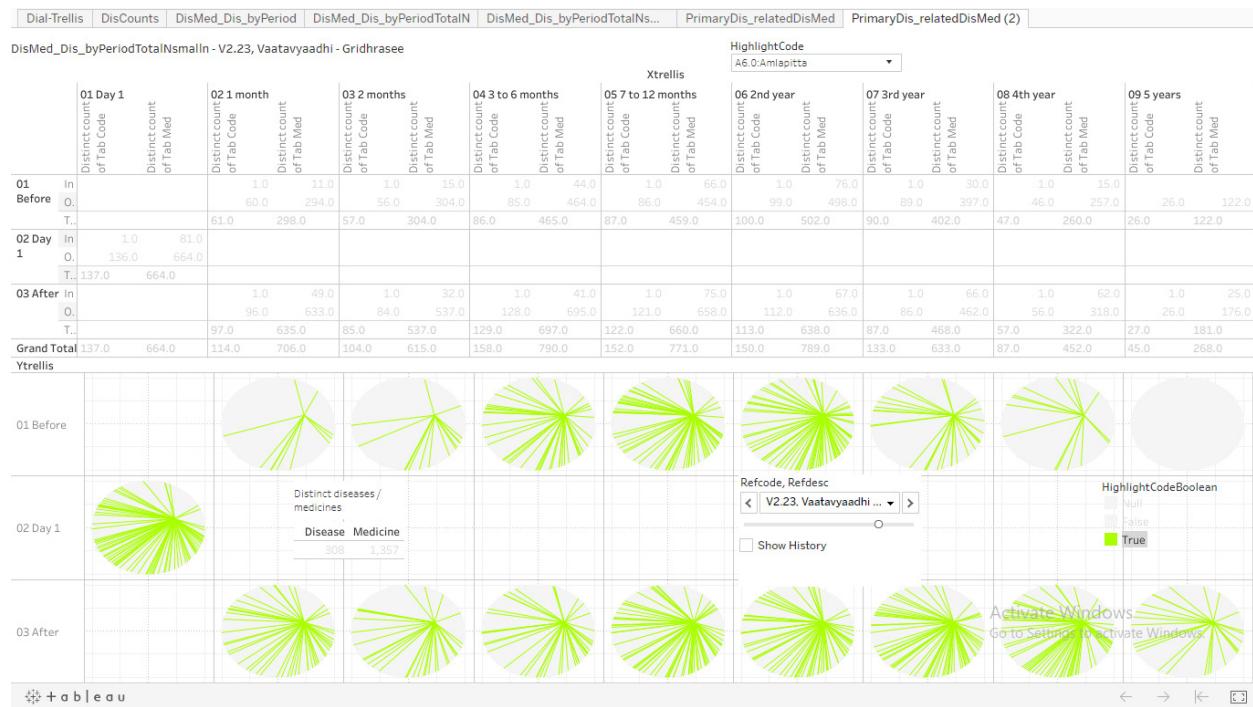
Cross tabulation of medicine, disease type and patient gender, Medicine name: source data collected on Case Report Form, Distype: Metabolic and RMSD groups derived in the analysis dataset. Patient Gender: source data. Only 287 (1.5%) patients have been prescribed bhasma. This reflects the ayurvedic principle of using bhasma based treatment wisely. Data version: 2011 to Oct 2016. Link to analysis: [Link](#) to get the above display subset Medicine name = Bhasma

Table 3-2: Summary statistics and t-test for bhasma usage

Overall (N=514)	welch Two Sample t-test
Pre_Bhasma	
Mean (SD) 14.8 (14.0)	
Median [Min, Max] 9.00 [2.00, 111]	
Post_Bhasma	
Mean (SD) 10.6 (14.5)	
Median [Min, Max] 6.00 [0, 89.0]	

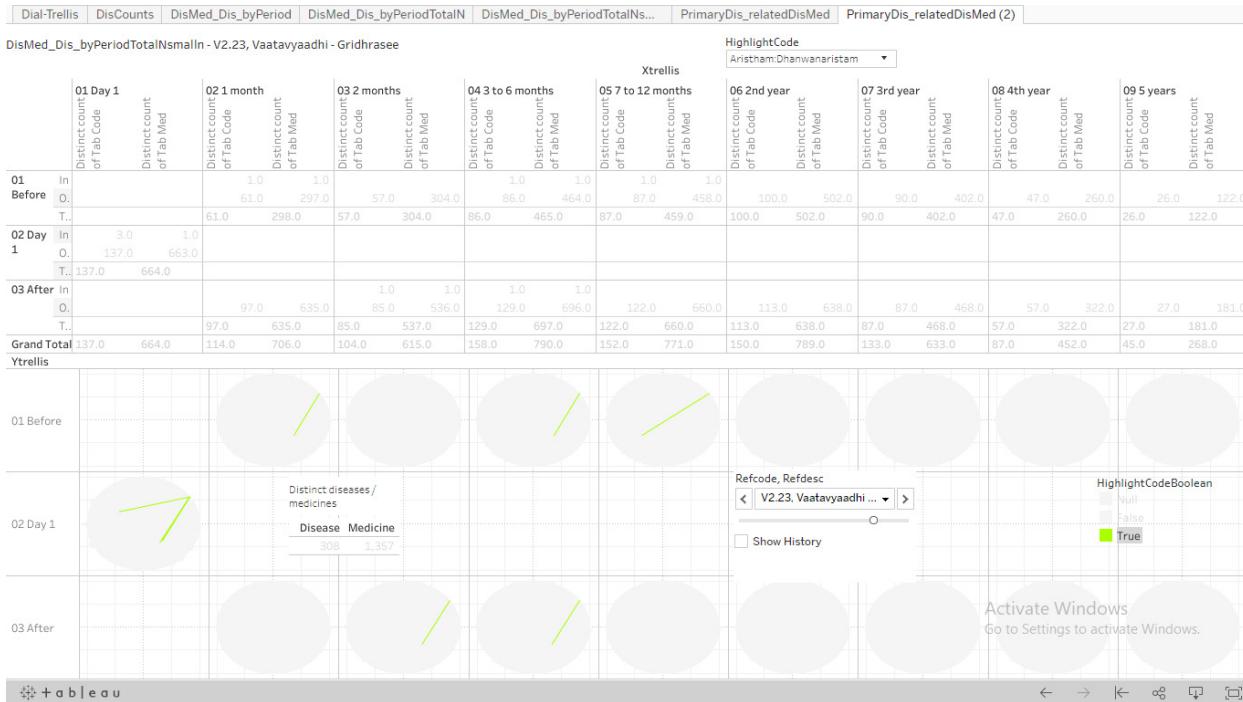
Patients who were prescribed at least one “bhasma” treatments are summarized, Pre_Bhasma: Duration of treatment before the 1st bhasma treatment, Post_Bhasma: Duration of treatment after the 1st bhasma treatment, Data version: 2011 to Oct 2017
https://github.com/coursephd/PostgreSQL/blob/master/110_rasa_aushadhi_analysis.R

Figure 3-37: Circular view: Co-occurrences of disease – disease Example 1



Example 1: Disease: A6.0: Amavaata and Reference Disease: V2.23: Vaatavyadhi – Gridhrasee, Upper section: Pre and post time windows, count of distinct diseases and count of distinct medicines prescribed at the given time point. Lower section: 1st row represents the co-occurrence of disease – disease and / or disease – treatment before day 1 of the reference disease. Middle row: On day 1 count of distinct diseases and count of distinct medicines prescribed. Last row represents the same co-occurrence data after day 1 of the reference disease. Green bars inside a circle show co-occurrence of chosen disease – disease and / or disease – treatment combination, Data version: 2011 to Oct 2017. Link to analysis: [Link](#) to get the above display subset Refcode, Refdesc = V2.23 Vaatavyadhi – Gridhrasee and HighlightCode = A6.0: Amlapitta

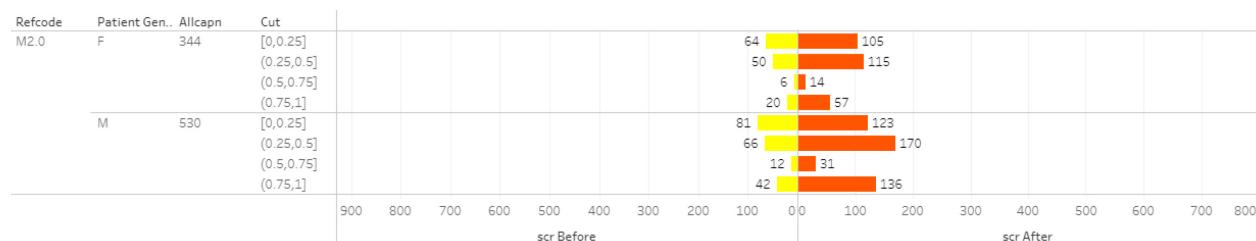
Figure 3-38: Circular view: Co-occurrences of disease – treatment Example 2



Example 2: Treatment: Arishtam:Dhanwanaristham and Reference Disease: V2.23: Vaatavyadhi – Gridhrasee, Upper section: Pre and post time windows, count of distinct diseases and count of distinct medicines prescribed at the given time point. Lower section: 1st row represents the co-occurrence of disease – disease and / or disease – treatment before day 1 of the reference disease. Middle row: On day 1 count of distinct diseases and count of distinct medicines prescribed. Last row represents the same co-occurrence data after day 1 of the reference disease. Green bars inside a circle show co-occurrence of chosen disease – disease and / or disease – treatment combination, Data version: 2011 to Oct 2017. Link to analysis: [Link](#) to get the above display subset Refcode, Refdesc = V2.23: Vaatavyadhi – Gridhrasee and HighlightCode = Arishtam:Dhanwanaristham

Figure 3-39: Pre and Post distance analysis for disease: M2.0: Madhumeha

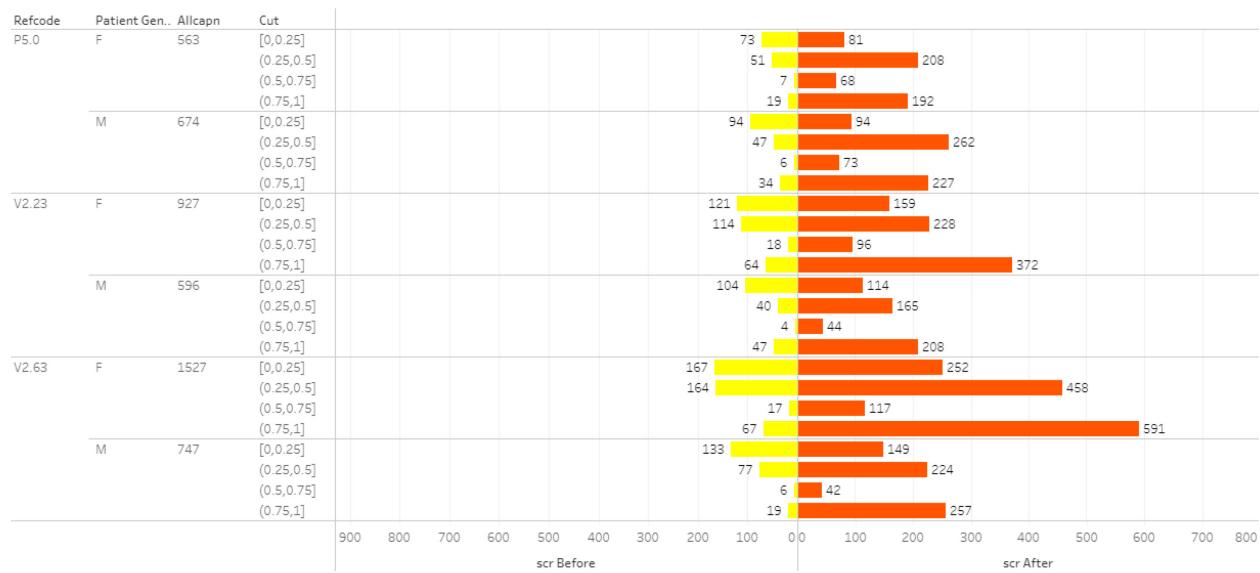
DiseaseMaxDist



Butterfly plot display of pre and post distance analysis for disease trajectories. Refcode: reference disease, Patient gender, Allcapn: Total number of patients in each of the categories, Cut: Jaccard distance, scr Before: patients falling in a particular category before day 1 of reference disease, scr After: patients falling in a particular category after day 1 of reference disease, Data version: 2011 to Oct 2017. Link to analysis: [Link](#) to get the above display subset Refcode = M2.0

Figure 3-40: Pre and Post distance analysis for medicines given for diseases: P5.0, V2.23, V2.63

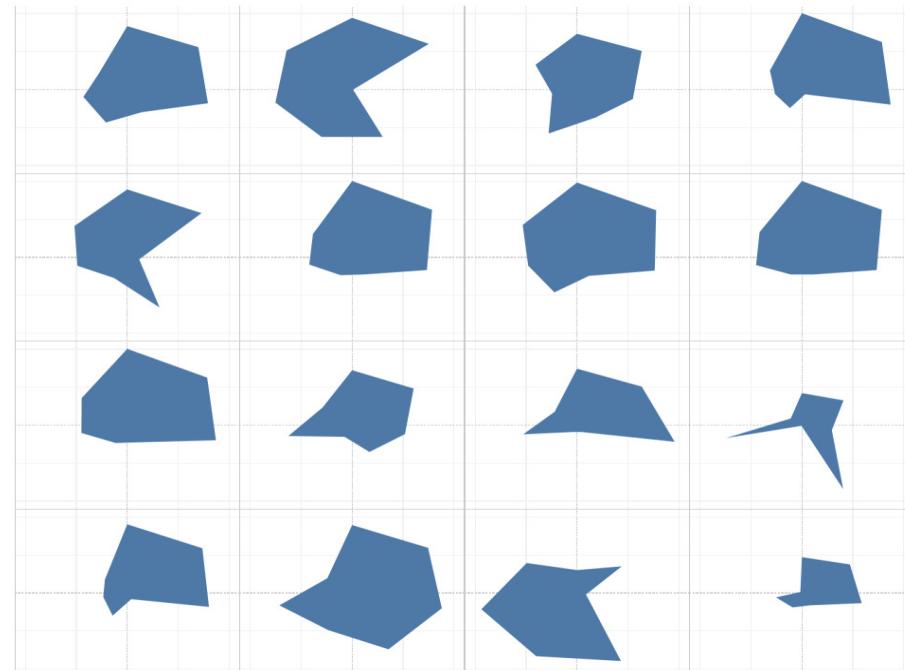
DiseaseMaxDist



Butterfly plot display of pre and post distance analysis for medicine trajectories. Refcode: reference disease, Patient gender, Allcapn: Total number of patients in each of the categories, Cut: Jaccard distance, scr Before: patients falling in a particular category before day 1 of reference disease, scr After: patients falling in a particular category after day 1 of reference disease. This distance calculation was done on the basis of trajectory of prescribed treatments, Data version: 2011 to Oct 2017. Link to analysis: [Link](#) to get the above display subset for Refcode in (P5.0, V2.23, V2.63)

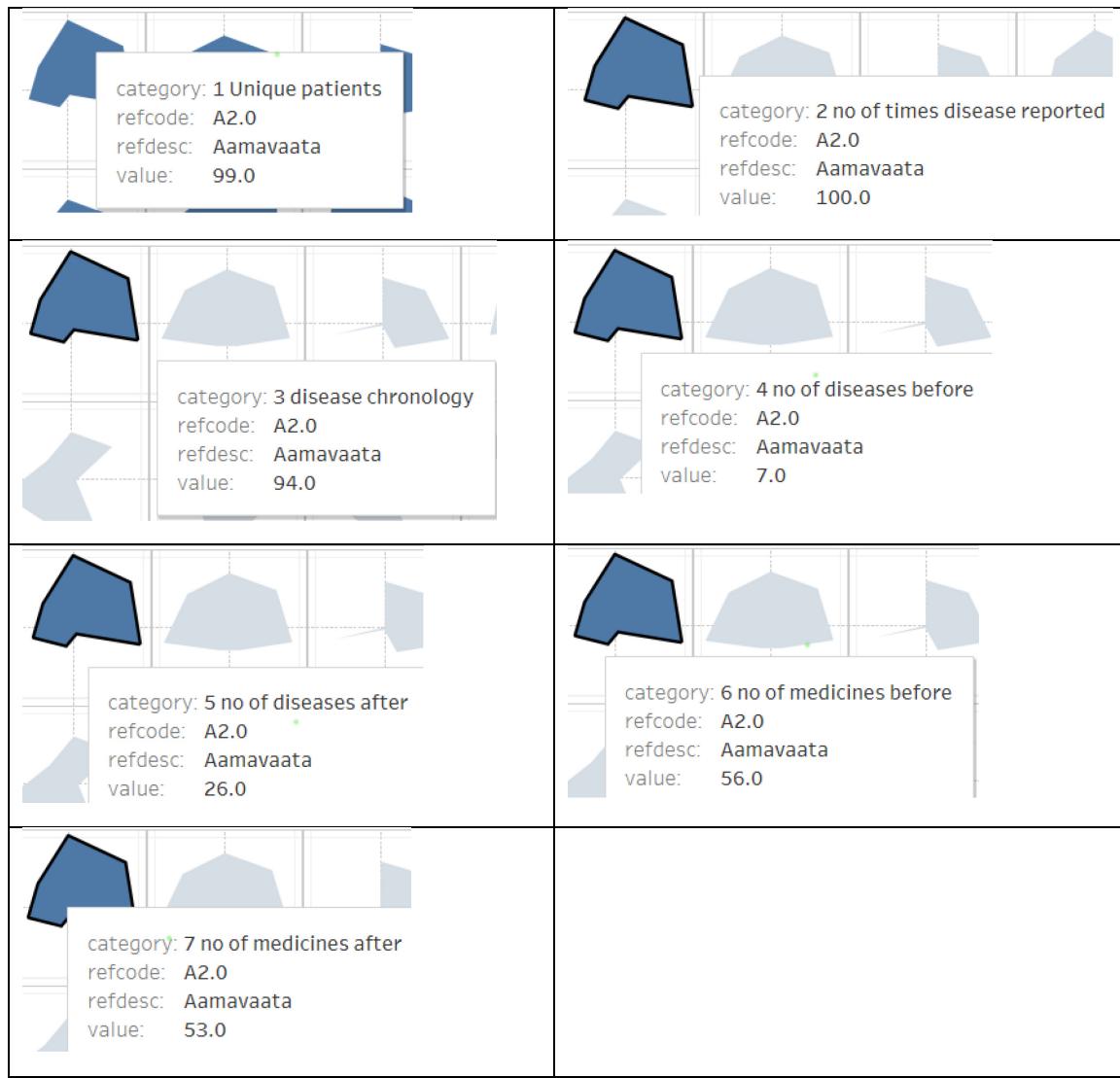
Figure 3-41: Radar plot

Radar-Plot-trellis



Radar plot showing multiple diseases displayed side by side.

Example 1: Multidimensional view a single disease: A6.0: Aamavaata



7 parameters displayed on one plot: (1) Unique patients, (2) Number of times disease reported, (3) Disease chronology, (4) Number of diseases reported before the reference disease, (5) Number of disease reported after the reference disease, (6) Number of medicines prescribed before the reference disease, (7) Number of medicines prescribed after the reference disease, Data version: 2011 to Oct 2017. Link to analysis: [Link](#)

Example 2: Multiple disease comparison

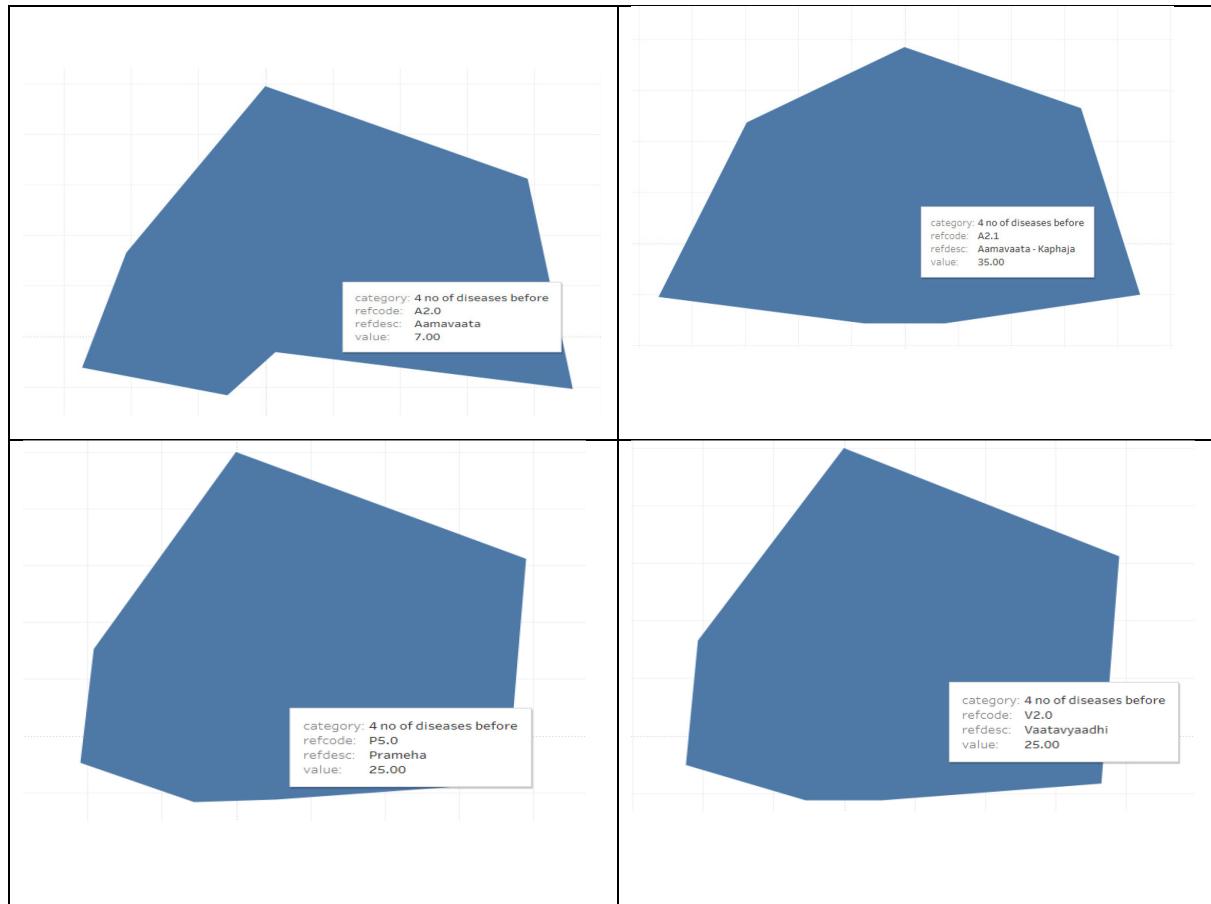
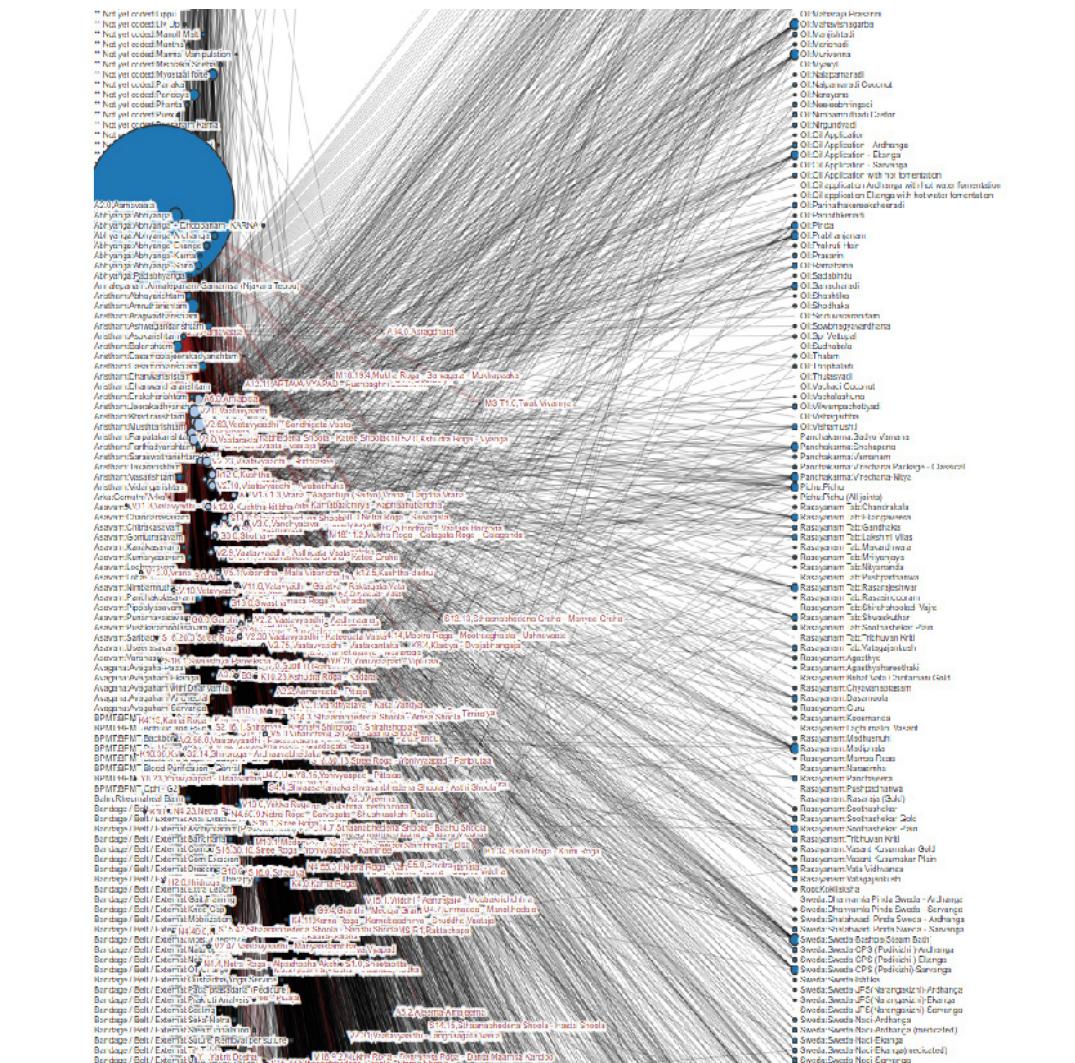


Figure 3-42: Dynamic bubble plot: Example 1: Disease: A6.0: Amavaata



This dynamic bubble plot shows relations between diseases and medicines, the bubble plot size is based on number of unique patients, Data version: 2011 to Oct 2017, Amavaata [https://coursephd.github.io/nodediagram/A2_0/]

4 Discussions

4.1 Converting real life clinical data into analyzable format

The TDU / I-AIM team should be congratulated first before any discussion to create an electronic database right from the inception of the hospital. This foresight has allowed us to have significant amount of data. There are a lot of learnings from this exercise which can be beneficial to many institutes and hospitals.

Conversion of real-life clinical data from an individual data point to a logical dataset was done. Logical relationships were established post inspection of the datasets and the columns. Relational datasets were identified. Observations about data capture methods and storage were noted. Some shortcomings and errors in the data were seen and noted (missing data, inconsistent values, or unresolved duplicates). This exercise of understanding technical architecture from “an end user point of view” will help in running analysis of various types. If data generation for future use is one of the top priorities for the hospital, then there should be a project plan put together and appropriate steps should be taken to plug the existing gaps.

4.2 Clinical data understanding

Sections listed below offer possible technical solutions for the shortcomings identified:

4.2.1 Visit pattern analysis

From 2011 to 2016, the number of patients visiting hospital on weekdays was less than the number of patients visiting on weekends. In-Patients were considerably less than Out-Patients. Overall number of patients coming to hospital have been increasing year on year. This information would help in employing staff across different departments from helpers, cleaners, nurses to doctors to adequately cover services for patients (Figure 3-3).

4.2.2 Vital sign dataset

The vital signs database could have an alternative presentation of one record per patient per visit in addition to the existing presentation. The vital sign parameters can be presented as distinct columns, one each for each parameter.

Table 4-1: Proposed vital sign data structure

Patient ID	Visit date	SBP	DBP	Pulse	Height	Weight
1	01-Jan-2016	xxx	xxx	xxx	xxx	xxx
1	15-Jan-2016	xxx	xxx	xxx	xxx	xxx
1	31-Jan-2016	xxx	xxx	xxx	xxx	xxx

This type of presentation would make the length of data smaller. Trends for the same patient over a period could be assessed faster. The parameter result values should be presented in numeric

form, rather than character format. This will allow the data to be used for numeric calculations. In case of age and/or gender specific analysis; normal ranges can be applied in the database and these calculations could be done in the backend without affecting the end users, here doctors, nurses to name a few.

4.2.3 Lab dataset

When a lab test is done from other pathology the data from scanned reports is not translated into hospital dataset, this results in missing information in the database, as it is not retrievable for any analysis. A single test has multiple names making it very difficult to create summaries on laboratory parameters. Would it be possible to get the pathology lab data in electronic dataset format? A few suggestions on updating the existing version:

- A standard naming convention of lab tests should be created
- A standard units look up table should be built for possible conversion from one unit to another
- Lab results values should be saved as numeric and character (when some test results come out as ordinal scale measurements) variables
- In case of cancer patients, should the National Cancer Institute, USA, proposed NCI CTC grading variable be created for specific parameters? – this could be created in the backend database, more useful for analysis [113]

4.2.4 Treatment dataset

This is one of the most important parts of data necessary for any type of analysis. A complex SQL data extraction code along with numerous merges and complex Cartesian products via the R-code had to be performed to arrive at easily readable dataset. E.g. MRD_Diagnosis, Patient_Prescription, Patient_Medicine_Prescriptions, IP_Prescription datasets had to be merged to get a complete interventional view. Treatment database could be structured in a way that components can be collected and reported in a systematic manner:

- Name of the treatment(s)
- Treatment(s) prescribed for which disease
- Treatment(s) start date
- Treatment(s) end date
- Names of medications
- Type of medications (classical formulation, proprietary, etc.)
- Dosing information
- Route of administration (Treatment procedure, oral treatment, panchakarma, etc.)
- Dose increase or decrease

Due to the complex nature of the data, the structure would be one record per patient, per visit, per disease, per treatment assigned. E.g. if a patient has 2 disease conditions and 4 treatments are assigned then for that particular visit, there should be 8 records present in the database. There are numerous medicines prescribed. These medicines are classified into following broad categories:

1. /Abhyanga
2. Aristham
3. Arka
4. Asavam
5. Avagha
6. Bhasma / Bhasma Cap / Bhasma Tab
7. Dhara
8. Ghritam and variations of Ghritam
9. Kashayam and variations
10. Kshar
11. Lehyam
12. Oil
13. Pichu
14. Rasayanam
15. Any additional classification which makes sense

Source variable for treatment will be classified into the following categories. This should allow recreation of treatment protocol as per Ayurvedic principles. Various Ayurvedic texts have defined standard treatment protocols for different ailments. Based on the table below, can we propose a sequence of treatment for various conditions and build it in our database so that an automatic re-creation of the classical treatment text can be done? This will not only serve as a support to the practicing vaidyas but also serve as a validation tool for the given treatment regime.

Figure 4-1: Treatment principles defined in different texts

Treatment	Ch	Su	AH	BP	YR	HS	BS	CD
<i>Snehana</i>	-	-	-	-	-	+	+	+
<i>Swedana</i>	-	-	-	-	-	+	-	+
<i>Vamana</i>	-	-	-	+	-	-	-	+
<i>Virechana</i>	-	-	-	+	-	-	-	+
<i>Niruha Basti</i>	+	-	-	-	-	-	-	-
<i>Anuvasana Basti</i>	+	-	+	+	+	-	+	+
<i>Siravyedha</i>	+	+	+	-	+	-	-	+
<i>Raktamokshana</i>	-	-	-	-	-	+	+	-
<i>Agnikarma</i>	+	-	+	-	+	+	-	+
<i>Shastrakarma</i>	-	-	-	-	-	-	-	+

Ch - Charaka; Su - Sushrutha; A.H.- Astanga Hrudaya; B.P. - Bhava Prakash; Y.R. - Yoga Ratnakara; H.S. - Haritha Samhitha; B.S - Bhela Samhitha; C.D. - Cakradatta

4.2.5 Medical coding

Medical coding is a robust method to simplify the variation in the data by uniformly categorizing the medical terms appropriately. This step allows us to maintain high quality database. Coded medical data is a standardized form of data, globally approved, and can aid in future machine learning and automation. The most used medical coding dictionaries for coding medical terms are MedDRA and WHO DDE [114] [115]. A few examples of medical dictionaries are:

- COSTART: Coding Symbols for Thesaurus of Adverse Reaction Terms
- ICD xx CM: International Classification of Diseases xx Revision Clinical Modification [116]
- MedDRA: Medical Dictionary for Regulatory Activities [114]
- WHO-ART: World Health Organization Adverse Reactions Terminology [115]
- WHO-DDE: World Health Organization Drug Dictionary Enhanced [115]
- ACD: Ayurvedic Classification of Diseases
- NCI: National Cancer Institute Code list [113]
- LOINC: Logical Observation Identifiers Names and Codes standards [117]
- Any other dictionaries, as recommended by AYUSH

4.2.6 Classification and Sub-classification of the Doshas / Diseases

Almost each researcher understands that research results are as good as the data using which the conclusions are drawn. Most scientists do not receive guidance in methods for controlling the quality of research data which is fundamental to clinical research. An exhaustive list of all possible diseases should be created, and a checklist of disease classification and sub-classification should be maintained so that the doctors based on their judgment can classify the dosha appropriately and use the recommended disease classification term. This should help in reducing inconsistency and disparity in reporting (Figure 3-1). The problem should be split into operational and scientific components. Identify fields which would require coding: Diagnosis codes description, Compliant, Drug description. Operational steps to be taken as follows:

- The existing data should be codified in a retrospective manner
- Business guidance document should be prepared on how to work in future
- Number of days should be predefined to have data coded from the time of patient visit
- An automatic tracking mechanism should be defined to keep track of the status:

Table 4-2: Proposed idea for clinical coding timetable

Number of days from patient visit to coded data	Number of records coded	Number of records yet to be coded
< 7 days	XX	XX
7 days to 14 days	XX	XX
14 days to 28 days	XX	XX

> 28 days	XX	XX
-----------	----	----

Temporary staff should be allocated to complete the backlog.

Scientific questions regarding Ayurvedic medical terminology should be answered by doctors at hospital. A team of 3-4 doctors for a period of 4 months or as appropriate, contributing 20% of their time, would help complete the categorization process as described above or post graduate students, under the guidance of a senior vaidya can take on this responsibility.

4.2.7 Patient profile module

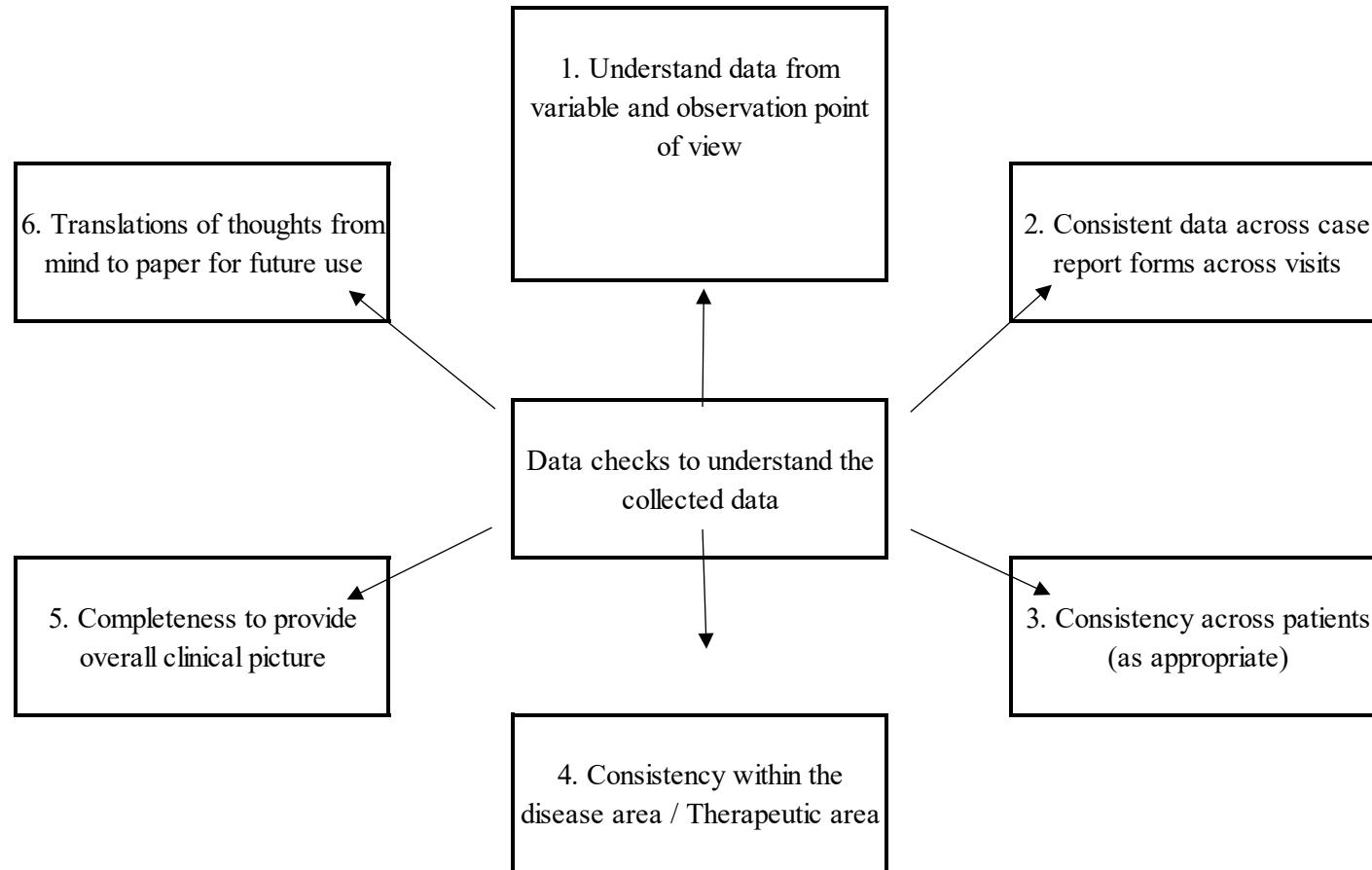
A patient profile report is a consolidation of all the data for a patient available in the database. This consolidated view at a patient level provides an easy access to the patient history (Figure 3-4, Figure 3-5). If this type of a report is electronically available for a patient then a patient's case can be handled by any doctor available. The contents of a good patient profile are outlined below:

- All the demographic characteristics of a patient: age, sex, race, religion, place of residence, etc.
- All the useful data for operational ease: policy number, health coverage status, in-patient, Out-patient, etc.
- Visit information: number of visits to the hospital, corresponding dates and day of visit. The day should be calculated based on the first visit date (visit date – first visit date + 1). This value must never be missing and must be positive.
- Background disease history: Is the patient disease history getting captured at first visit of each patient? Would it be useful to not down the background history in a systematic manner?
- Vital sign measurements: a tabular view of the collected vital sign measurements.
- Data collected for the diseases and diagnosis: details about the clinically relevant fields should be discussed. Some standard fields –
 - Complains as reported and medically coded as per section 4.2.5
 - Duration of disease or start date, end date
 - Data collected for Ayurvedic examination: variables outlined in *dash vidh pariksha* (if these variables are not captured currently then how to make provisions for the same?)
- Treatments administered:
 - Treatment start date
 - Treatment end date
 - Names of medications
 - Type of medications (classical formulation, proprietary, etc.)
 - Dosing information
 - Route of administration
- Details of lab results
- Outcomes

- Patient status still ongoing or discontinued (need an algorithm)

The pictorial representation (Figure 4-2), summarizes the cycle of understanding the hospital data so that a meaningful interpretation can be arrived at. 6 steps provide a way of generating very good quality data: (1) Understand the data from variable and observation point of view, (2) Collect consistent data across case report forms across visits, (3) Maintain consistency across patients, (4) Maintain consistency across disease areas, (5) Strive to maintain completeness to provide overall clinical picture, and (6) These steps should enable translation of thoughts from mind to data for future use.

Figure 4-2: Data understanding from an observation – patient – disease to a clinical picture



4.2.8 Improvements to the system architecture

Overall the hospital data is not captured in a standardized format as explained in the above points (Figure 3-2). Create standardized CRF pages for consistent and correct data capture. Already established standards like Clinical Data Interchange Standards Consortium (CDISC) or International Organization for Standardization (ISO) standards can be implemented [118] [119]. Appropriate drop-down menu lists with predefined inputs to be built into the system, with the help of experts, to ensure good quality data.

Usually any team in any organization sets up rules and guidelines for the implementation. Yet once the system is live, due to the lack of consistency in data entry methodology things begin to fall apart. User inputs the same data in different ways. New staff comes on board and has their own way of entering information. Inconsistent data creates inaccurate reports. Hence robust documentation and streamlined training and onboarding of the new data entry operators is a must. Building and implementing a design policy is the first step towards reinforcing the build rules. It provides documentation for Electronic Medical Record (EMR) analysts to follow which will reduce inconsistencies and improve the EMR functionality. Below are some of the aspects which if kept in check can avoid inconsistency in data

- Capitalization: Monitor the use of capitalization. Create guidelines and instruct accurately when to use caps and otherwise. In case all caps are used, ensure appropriate warning message or suggestion is generated to alert the end user.
- Abbreviations: Prepare a catalog of all allowed abbreviations along with their meanings. If possible, create inbuilt checks in the building forms to avoid incorrect abbreviations.
- Workflows: Evaluate and monitor the workflows to check the effectiveness on an ongoing basis. During a system change a workflow audit is extremely important, since non-working workflows undermines' the system functionality as the user may create smart workarounds skipping the important steps. Along with Workflow audits it is a best practice to have planned system audits.
- Naming conventions: This is the most important step. Following the appropriate naming conventions helps save time, money, and future efforts. It is easier to onboard new employees and eases future searches or any kind of analysis.
- Data Quality check plan: It is best to create data validation programs during data base setup which can be run periodically to check for the correctness of data entry.
- Well defined database maintenance plan: It is important to have a well-planned and periodically scheduled database maintenance program.
- Regular training: Regular training and refresher programs is a must to ensure that the end users are up to the mark with the processes and systems so that a healthy database can be maintained.

If any organization can follow these proposed solutions, then possible outcomes could be as follows:

- The data will be closer to analysis ready format
- The database will be useful in publishing case studies, case series, etc. in very short period. This will help us gain more visibility in scientific world

- More empirical data will be available at our disposal
- The database could become a model database for other Ayurvedic institutions to follow

Variable classification analysis: Review of the database suggested that the case report form completion was carried out by different doctors differently giving rise to differences in the way the data was captured. This lack of documentation should be addressed. Hospital management, treating doctor, researchers, and insurance companies could be the key stakeholders benefitting from these improvements.

4.3 Studying demographics and patient specific factors

A pictorial representation of data on world map is a convenient way to summarize large amounts of data. This form of data representation will help any public health official. If the individual state and city information is available, then additional drill down illustration is also possible – this supplementary graphic will allow us to identify the distribution of patients and diseases from different parts of India. More details related to diseases, treatments, additional demographic characteristics could be added to the visual analysis to efficiently recover key information as and when needed. This can form the basis of public health policies framed either by government or by private companies (Figure 3-6, Figure 3-7). The In-Patient and Out-Patient distribution suggests that the route of administration is simple and easily understood by the patients and the caregivers. The diseases may not be life threatening or fatal (Figure 3-8). Are these patients largely coming in for “second opinion”? Or if this data is to be looked at positively, are they getting benefitted and hence are not coming back for consultation beyond the first reported disease? On the other hand, a few patients could be having a lot of faith in Ayurvedic treatment, for them to continue with treatment, they could have found the underlying treatment effective (Figure 3-11). Blood group distribution for many patients is a great source of knowledge. Even though this does not help in day-to-day treatment options, there is undoubtedly epidemiological value in this presentation. There are obvious mistakes in documenting the blood groups observed via this tabulation – another secondary use of this tabulation is to build data quality related efficiencies (Figure 3-9). While finding data inconsistencies was not a primary objective of this analysis, there is this secondary usage available to the scientific community.

The empirical evidence generated by such fundamental data will be very useful for the hospital management, public health officials, treating physicians. This kind of tabulation plays a key role in evidence generation and synthesis. Is there a similar analysis available for another Ayurvedic hospital, or any other private or public hospital in public domain? This can be used to understand the use and misuse of the limited medical sources across the geographies.

Lesser duration of patient and hospital association may mean either the patients are benefitted by the treatment or are not happy and hence discontinue the treatment. Longer duration of association may mean that the patient is receiving benefit and hence is coming for regular follow-ups for the

same condition, or the disease condition could be chronic in nature. These analyses provide a useful macro level representation of data for public health policies for these non-communicable diseases. Data driven approach of optimally utilizing resources suggest strengthening the RMSD disease treating facilities from pharmacy to Vaidyas to patient (Figure 3-12). The low rate of reporting of some of the diseases may explain the natural variations or may reveal inconsistent labelling of the diseases (Figure 3-15). Boxplot representation of age provides the distribution of diseases across age and grouped by gender. It also gives a comparative view of multiple diseases thus providing an information on the disease prevalence in the age category as well as gender (Figure 3-13).

4.4 Studying diagnostics and interventions

The ACD and ICD mapping exercise shows that the current hospital data demonstrates all the types of diseases being catered to at the hospital. Large spectrum of diseases getting treated at the hospital. This provides insights into the health seeking behaviour of patients. Additionally, this data can be used by insurance companies and policy makers to strengthen ongoing efforts. If the ICD Code can be included in the data collection, then this correlation analysis can be done easily. The ICD code getting populated using the medical expertise will be more reliable than the current analysis (Figure 3-17, Figure 3-18, Figure 3-19, Figure 3-20).

The Prakriti data was not available for all patients across all visits. This points to shortcomings in the data collection methods (Figure 3-21). This analysis shows natural variations in the diseases getting treated. It should be studied by treating physicians to take a deep dive into the data. The process of data collection needs to be looked at and improved. Would it be possible to create an online tool to generate prakriti information? Can this data be collected before a patient goes in for doctor's consultation? Can this data field be made a mandatory field so that there is no missing data generated? If prakriti derivation is a complex process Vikriti or Dosha current dominance must be looked at. Tag the treatment or formulations as -kara and -hara e.g., Pippali is Kaphahara and Pittakara.

Co-morbidity analysis can be used to understand the disease clustering. Which disease(s) cause(s) the other disease(s) to manifest, which disease(s) could be precursor to subsequent disease(s). This analysis can be used to validate the existing hypothesis. This analysis could be further enriched for predictive abilities – turning this into a possible disease preventive tool. Some examples like prameha (causing many diseases for both the genders), pandu roga (mainly reported by females with many disease, and relatively low numbers reported by males), sandhigata vata (reported by more females), etc. have shown that meaning of shlokas can be shown in the modern data format. This type of exercises can be carried out with help of ayurvedic experts (Figure 3-22, Figure 3-23, Figure 3-24, Figure 3-25, and, Figure 3-26).

Treatment and disease analysis at individual patient level: This analysis at individual patient level shows life journey of each patient. This may help in understanding the severity of the disease, comorbidities and the number of medications prescribed to treat the condition. This can also provide

an overview of the practicing physician's style of treatment and may help draw parallels in treating medical conditions. If a new disease is reported and new treatments are added, then it is understood that this is a part of treatment regimen. But if a treatment is reduced then would it be considered as a part of treatment regimen or would it be considered as a removal due to side effect? This cannot be ascertained without an ayurvedic clinician's opinion. If a new disease is reported and if no new treatment is added, then also it raises some questions? Is it as per treatment protocol or are the existing treatments sufficient to cover this new imbalance? More detailed discussions with ayurvedic clinicians will help in understanding this analysis. This may give rise to better ways of collecting the data (Figure 3-27, Figure 3-28, Figure 3-29).

Area graph representation of diseases provides information about 800+ diseases in very short space. Disease patterns are interesting due to following reasons: Diseases vary seasonally, diseases are experienced differently by gender, and it gets shown easily by looking at the distributions. This view is very useful for both operational excellence as well as clinical judgment. The interactive nature of visualization allows for real time subset of diseases. One of the 4 diseases displayed has very few patients compared to other 3 diseases showing different nature of diseases. Another interpretation could be that the disease shown with very low frequency may not be treated by very regularly by Ayurvedic treatments (Figure 3-30).

Treatment and disease analysis at summary level: Mosaic plot and cross tabulation analysis: the Patient Report form or Case Report form captures diseases reported on a particular visit along with treatments and services prescribed to a patient. Due to the nature of the CRF page, multiple diseases and treatments are captured on the same visit. This creates many-to-many relationships which makes it difficult to identify the disease treatment relationship. Even though this challenge exists, the data at a summary level provides good view on treatment and disease relationship. The cross tabulations of balaristham and bhasma provide additional evidence of how these analyses can be used to validate facts and / or generate new concepts. Traditionally bhasmas of any kind are prescribed in very limited quantity and same is reflected in observed data. Naming convention and spelling correctness need to be considered while capturing data in future. The clinical utility of this analysis was shown (Figure 3-31, Figure 3-34, Figure 3-35, Figure 3-36). The t-test at 5% significance level shows statistically significant difference between duration of treatment before bhasma treatment and duration of treatment after bhasma treatment. The study was not powered to detect any specific difference in treatment duration, so the p-value and significance should be interpreted cautiously. How should one interpret ~15 days vs. ~11 days of pre and post bhasma treatment, would it be considered clinically meaningful? These discussions with experts will provide more ideas about these plain numeric observations.

Interpretation from additional Disease – treatment analysis with pre and post visit window approach are as follows: in circular data representation many green lines means that there is a greater chance of diseases reported by patients, there is a greater chance of a medicine prescribed for a disease. If there are very few lines then the combination is clinically not meaningful or if it is meaningful then it is a very rare combination which needs to be studied further (Figure 3-37,

Figure 3-38). On a single page there are multiple dimensions of the disease – disease and / or disease – treatment combinations are shown.

Distance score-based analysis reveals the following observations: More number of patients with Jaccard distance closer to 1 was seen for the Post reference day 1 period. This could be pointing to similar biological activity caused by a particular disease. This could be a very important finding from this analysis (Figure 3-39). In the medicinal display the similarity scores are lower as compared to that for the disease trajectories. Which implies that most of the prescribed treatments are dis-similar for both the periods. It is observed that around 50% of treatments could form the base of treatment regimen and could be same for the patients. The remaining part of the treatment regimen is driven by individual patient characteristics. The before and after medicine trajectories would show such underlying data. E.g., for M2.0, there are very few patients having distance above 0.5 for both genders (Figure 3-40). This analysis should be executed using other mathematical distances to understand the consistency of results. If the disease classification and treatment tagging in the underlying data is improved then we should be able to see much better results, with lesser confounding effect.

Radar plot for multiple diseases is shown next to each other. This is showing massive amounts of information immediately. Differing shapes provide differences reported in the data and an easy way of identifying differences. If there is additional data made available in a structured format, then these parameters could also be added on the radar plot. This radar + trellis combination provides a more powerful tool to visualize large amounts of data on a single page (Figure 3-41).

4.5 Use cases with in-depth illustrations

This section outlines a few use cases in-depth and how can the key stake holders make use of the information generated earlier.

4.5.1 Illustration 1: In-depth review of Visit pattern analysis

Data / observations: In a competitive world, understanding how patients plan their visits to a hospital and their social demographics can help in running an operation which would make the patient as the focus point of efficient operations. Operational efficiency allows businesses to build an edge and it is applicable in any field. Visit pattern analysis (Figure 3-3) allows insights into the same. This visualization depicts data from the very first of the hospital in 2010 on a calendar. In Feb 2011 there were more than 50 patients visit on a single calendar day. In May of 2011, there were more than 200 patients visit on a single day. Otherwise, the average number of visits was hovering around 30 – 50 patient visits. The underlying data shows that the patient inflow increasing year on year. Out of 2100+ days of data from year 2010 to 2016, there were 158 days on which more than 100 patient visit days were there, which accounts for 7.33% of all the days. Most of these 100+ patient visit days happened on Saturday, showing patients' tendency to visit hospital on a weekend. Figure 3-7: Country-wise Visualization shows that almost 98% of patients are coming from India. Analysis carried out as per Figure 3-25 for V2.0 (Vaatavyadhi) shows slightly a greater number of patients visiting in June, July months compared to other months, providing data on seasonal variations. The numbers start tapering down across other months. Figure 3-15 shows this data in terms of Indian rutes. Jwara (J1.0) in ACD is “flu” in Figure 3-25, subset for

PrimaryCode = J1.0, should show seasonal variations, as people getting with flu is seasonal in nature. But the overall number of patients reporting Jwara is low (128 females, 140 males) not allowing for these variations to be detected. If Jwara is not reported by large number of patients in the database then that would mean less patients are taking ayurveda treatment to get rid of Jwara. If patients having certain disease conditions are not represented in same proportion in hospital database, considered as a sample, as epidemiologically seen, then the underlying data will not represent disease condition appropriate, this explains relationship between sample and population.

Insights: As the sensitive information about how many doctors, how many nurses, how much money was being charged is not used in this analysis, currently there will not be any conclusions drawn w.r.to economic efficiency. As the location of the hospital is almost 4 km inside from the closest main road and the transport options were not regularly available, there were lesser number of patients seen visiting. Visit pattern analysis report can be used on a periodic basis to understand the patient patterns along with any other material hospital management must be using. Even though more than 50+ countries are represented in the database, the number of unique patients and amount of patient data is small to carry out any meaningful analysis. The visit pattern could be repeated by major disease types to get more insights into what type of doctors should be scheduled, what kind of support staff and what type of perishable pharmacy components made available in an optimal manner. Based on this information, the hospital management can have more staff working on weekends to cover patient inflow. Appropriate amount of stock of medicines in pharmacy could also be arranged. If the patient inflow is consistently lower on other days, then should hospital employ lower number of staff on these days, practically this may not be possible, but for operational efficiency this path should be explored. Some of the repairs and upgrades to the hospital infrastructure could be planned for the weekdays avoiding inconvenience to day-to-day functioning.

4.5.2 Illustration 2: In-depth review of summary statistics of number of diseases

Data / observations: Data quality is an inherent requirement for any data related exercise. Some insights based on patterns of missing data, outliers and potential scientific and medical inconsistencies can suggest methods to improve the data quality which would be of essence to hospital administration.

Analysis covering descriptive summary statistics by number of Diseases by age and gender was carried out (Figure 3-11) and explained in detail in the earlier chapter 3 section 3.3. This table summarizes descriptive statistics for age. The first column categorizes how many diseases were reported per patient going from 1, 2, ..., n diseases. The table shows 23 diseases as the maximum number of diseases reported by a patient. There is a large part of data showing “NA” = unknown number of diseases. Both observations point to potential data issues. Another key finding from the table is to have 12,884 and 14,375 female and male patients reporting only one disease. Other analysis related to duration and hospital visits (Figure 3-14) show that there is large dropout rate after one visit. The minimum and maximum age listed goes from 1 to 96 years for females, 2 to 108 years for males.

Insights: These observations should be of interest to the hospital management as well as treating doctors. At the beginning of the hospital operations the ACD coding was not implemented and that resulted in missing disease codes, giving rise to the “NA” category. Did the hospital have a patient with 23 different diseases or does this number also point a data issue or duplicate data entries for a patient? Such kind of data points should be checked on an ongoing basis.

How do hospital management as well as treating doctors view nearly 70% drop out rate after reporting first disease? This analysis will help in multiple ways. Are there operational challenges causing patients not to come back? Are the treatment mechanisms too difficult to follow for patients? What type of follow-up methods should be built to keep the patient engagement high? If this data is to be looked at positively then should we conclude that nearly 70% patients got benefitted from the treatment and hence did not need come back to the hospital. Are there truly 96- and 108-years old patients coming to hospital or are these possible data issues? Are these ages 9.6 and 10.8 years, OR 96 and 108 months / days? It is encouraging to see patients of all ages coming to the hospital. This topic should be of interest to the data managing team at hospital. If the training material is not clearly specifying an appropriate way of data entry, then this analysis helps in improving material as well as Hospital management system. Missing disease information could be understood by treating clinicians or anyone doing data entry on their behalf for having complete documentation for future use.

4.5.3 Illustration 3: In-depth review of disease table by gender

Data / observations: If we can understand the disease and underlying conditions, then the insights generated can give better understanding of science behind the disease. Disease categorization is done by the treating doctor at individual patient visit using ACD classification for documentation. One such example of subset of Prameha has been listed in Figure 3-1. This subset shows disease categories as Prameha, Prameha – Sthula, Prameha – Pidaka, Prameha – Krusha. The numbers for Prameha category are 648 and 849, and for the other categories these frequency counts are in single digits or in 20s. Is this analysis pointing to less than accurate representation of disease?

Mosaic / tile plot analysis for Prameha (Figure 3-31 subset for Metabolic: P5.0: Prameha) shows that there are 732 unique treatments prescribed, for Prameha – Sthula there are 114 unique treatments prescribed, for Prameha – Pidaka there are 48 unique treatments prescribed and, for Prameha – Krusha there are 27 unique treatments prescribed.

Figure 3-1 has data Aamavata related data represented. Aamavata – Vaataja, Kaphaja and Pittaja categories are tabulated in the analysis. The frequency counts are quite different for each category. 652 females in only Aamavata category followed by 27, 13 and 4 patients in Aamavata – Vaataja, Kaphaja and Pittaja categories. Same is the case for male category.

Insights: Should we assume that reporting just “Prameha” was a lot easier than reporting more details about it in the ACD class? The treating doctor must have treated patients as accurately as possible but thoughts have not be transferred accurately from “mind” to “paper” for future usage. Any analysis carried out using this data for which treatments were prescribed for which variation of the underlying “Prameha” could be a suboptimal approximation. This observation points to a possible shortcoming in usage of ACD and maybe a hospital level training is needed.

Is the current classification accurately expressing the underlying disease, perhaps no. There is a need to have an in-depth discussion with treating doctors to get more insights into this mislabelling. The ayurvedic experts from hospital and if needed experts from other institutions could come together and define guidance documents on how to document a disease.

Due to inaccurate representation of disease data, some of these interpretations will not be fully reliable, even though the big picture view may not be adversely impacted (this sentence should be validated by an ayurvedic vaidya). Can carefully labelling of disease at each visit be done to increase the overall quality of data and possible by products from them. This observation is not only for ayurveda but must be happening in any clinical assessment across the world. These nuances are of great importance to basic researchers. We can find similar examples for other diseases in our existing dataset. If disease classification by Vata, Pitta, Kapha by a treating doctor is not easy to be achieved at each visit to produce “close to 100% real picture of patient” then what could be possible solutions proposed? If there are existing validated tools for treating doctors to use then they should be used.

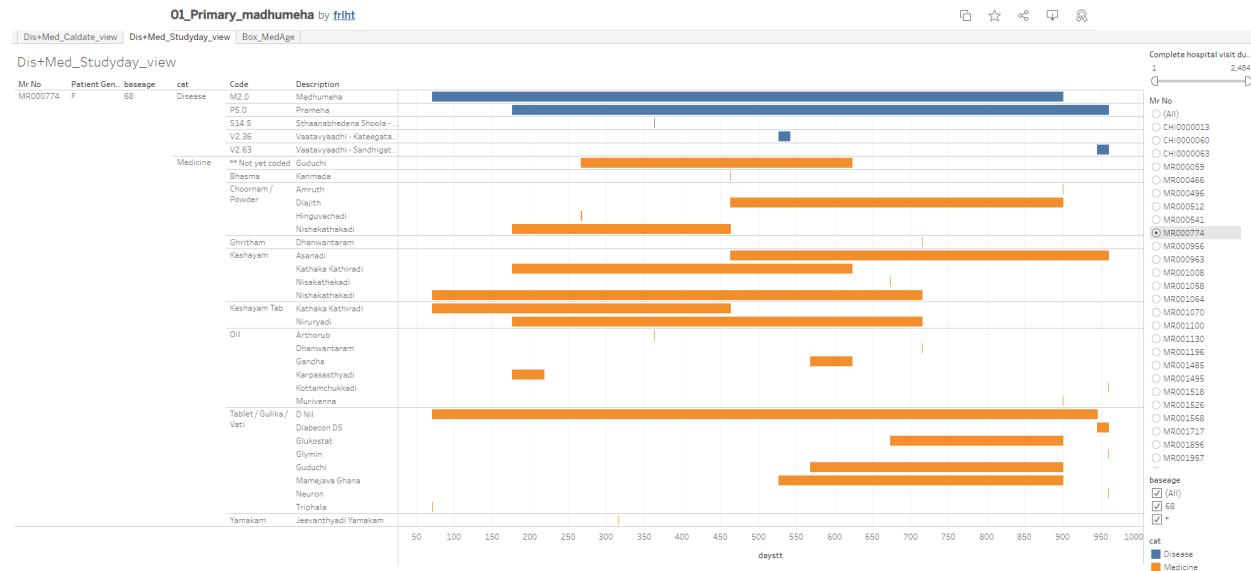
4.5.4 Illustration 4: In-depth review of individual patient disease journey

Data / observations: If we can understand the patient journey which includes, diagnoses, treatments, outcomes over time, it will allow the treating doctor to adjust and do better for the patient. The insights can as well give more understanding of the disease and the science behind it. This in-depth analysis shows us how to combine three analyses to understand individual patient journey. Figure 3-5: Patient visit profile – Vertical view, Figure 3-27: Patient Disease and Treatment administration by Study Day, and Figure 3-29: Patient Cumulative Disease and Treatment administration by Visit are combined to show how can a treating doctor use these three tools simultaneously. Subset these 3 analyses for patient MR000774. This data is for a 68-year-old female patient who has been coming to the hospital for close to 3 years (960 days). In this period, she has visited hospital for 29 times. There were 9 different diseases reported and 35 prescribed medicines in the hospital database. For a few of these diseases ACD code has not been reported, giving rise to missing data. Madhumeha and Prameha have been reported as first two diseases reported. Is this a correct representation having both Prameha and Madhumeha being reported?

Diabetes condition is treated by DNl and Nisakathakadi kashayam. Prameha was treated by Nisakathakadi, kathaka kathiradi. Nisakathakadi was prescribed as Choornam / powder and Kashayam, Nisakathakadi treatment was stopped and then Glocustat and Diabecon DS were prescribed. This line-by-line data review provides information about treatment protocol being followed.

The analysis carried out in Figure 3-29 helps in understanding first time disease reported and repeat disease representation may be used to understand the co-morbidities. 26 times diseases were reported and only 9 were unique showing a smaller number of complications, if we ignore “Not coded terms” then there are only 5 unique reported. 95 times treatments were prescribed out of which 35 were unique. There are 2 vaatavyadhis, arthritic conditions, reported after a few visits. Similar details about the treatment can be found in the medicines section.

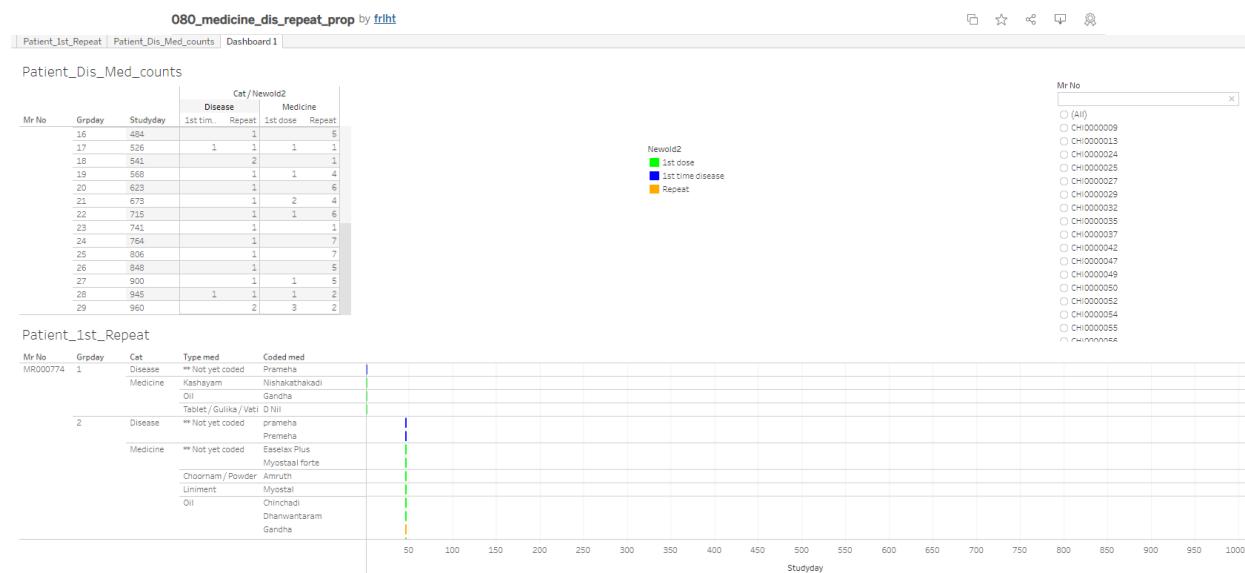
The analysis carried out in Figure 3-27 provides a tabular and line-by-line listing view at one go, providing one more variation of the same analysis. This report shows reported diseases and medicines as well as updates across timepoints. These three patient journey analyses should be good additions to existing tools to study patient status before a patient visit for any doctor.



A subset of Figure 3-5 for patient = MR000774

Patient_dis_med_Cumulative							%Patient_dis_med_Cumulative								
Mr No	Cumday2	Cat / Newold2						Mr No	Cumday2	Cat / Newold2					
		Disease	Medicine	1st time..	Reape..	1st dose	Reape..			Disease	Medicine	1st time disease	Repeat	1st dose	Repeat
MR000774	Till visit 1	1		3				MR000774	Till visit 1	100.00%		100.00%			
	Till visit 2	3		12	2				Till visit 2	100.00%	85.71%	14.29%			
	Till visit 3	4		13	5				Till visit 3	100.00%	72.22%	27.78%			
	Till visit 4	5		15	8				Till visit 4	100.00%	65.22%	34.78%			
	Till visit 5	5	1	18	9				Till visit 5	83.33%	16.67%	66.67%	33.33%		
	Till visit 6	6	1	18	14				Till visit 6	85.71%	14.29%	56.25%	43.75%		
	Till visit 7	6	2	18	19				Till visit 7	75.00%	25.00%	48.65%	51.35%		
	Till visit 8	6	3	18	22				Till visit 8	66.67%	33.33%	45.00%	55.00%		
	Till visit 9	6	4	20	22				Till visit 9	60.00%	40.00%	47.62%	52.38%		
	Till visit 10	6	5	20	26				Till visit 10	54.55%	45.45%	43.48%	56.52%		
	Till visit 11	6	6	21	26				Till visit 11	50.00%	50.00%	44.68%	55.32%		
	Till visit 12	7	7	22	26				Till visit 12	50.00%	50.00%	45.83%	54.17%		
	Till visit 13	7	8	23	30				Till visit 13	46.67%	53.33%	43.40%	56.60%		
	Till visit 14	7	9	23	35				Till visit 14	43.75%	56.25%	39.66%	60.34%		
	Till visit 15	7	10	25	39				Till visit 15	41.18%	58.82%	39.06%	60.94%		
	Till visit 16	7	11	25	44				Till visit 16	38.89%	61.11%	36.23%	63.77%		
	Till visit 17	8	12	26	45				Till visit 17	40.00%	60.00%	36.62%	63.38%		
	Till visit 18	8	14	26	46				Till visit 18	36.36%	63.64%	36.11%	63.89%		
	Till visit 19	8	15	27	50				Till visit 19	34.78%	65.22%	35.06%	64.94%		
	Till visit 20	8	16	27	56				Till visit 20	33.33%	66.67%	32.53%	67.47%		
	Till visit 21	8	17	29	60				Till visit 21	32.00%	68.00%	32.58%	67.42%		
	Till visit 22	8	18	30	66				Till visit 22	30.77%	69.23%	31.25%	68.75%		
	Till visit 23	8	19	30	67				Till visit 23	29.63%	70.37%	30.93%	69.07%		
	Till visit 24	8	20	30	74				Till visit 24	28.57%	71.43%	28.85%	71.15%		
	Till visit 25	8	21	30	81				Till visit 25	27.59%	72.41%	27.03%	72.97%		
	Till visit 26	8	22	30	86				Till visit 26	26.67%	73.33%	25.86%	74.14%		
	Till visit 27	8	23	31	91				Till visit 27	25.81%	74.19%	25.41%	74.59%		
	Till visit 28	9	24	32	93				Till visit 28	27.27%	72.73%	25.60%	74.40%		
	Till visit 29	9	26	35	95				Till visit 29	25.71%	74.29%	26.92%	73.08%		

A subset of Figure 3-29 for patient = MR000774



A subset of Figure 3-27 for patient = MR000774

Insights: The spelling was different in different prescriptions which does not change the underlying treatment but creates a perception about extra treatments prescribed to tackle the same disease. If this can be controlled by the coded medicine dictionary and type of formulation, then this will help in data analysis. The arthritic conditions reported by the patient, could be just age-related ailments reported by the patient. This elderly female patient does not have many co-morbidities reported which is a good sign from health point of view.

5 Conclusion

The introduction of this thesis outlined the need to undertake such a study, by providing perspectives on medicine, pharmacy, development of hospitals throughout the world, internet era, and the Indian context relating to modern medicine as well as Ayurveda. Insights from the thought leaders in the field of Ayurveda are profound and they call for modern methods, new approaches and innovative strategies to be attempted to take Ayurveda science forward. There is a reflection on the type of evidence generated through controlled experiments (RCTs) and life experiments (Observational, Experiential) – some evidence about how these multiple approaches could yield meaningful results. This chapter asks a few questions from diverse points of views and seeks answers – some of these answers are hidden in everyday Ayurvedic clinical practice – which is still largely untapped, prompting the following: how can data analysis of electronically captured data help in advancing our understanding of Ayurveda as a practice and science?

Next section of this thesis elaborated on the technical details of a hospital HMIS based database and the associated EMR. We highlighted technical details about the hospital database: how many source tables, how they stored in ~200+ tables, out of which ~20 to 25 tables were used to generate datasets useful for further analyses. Subsequently we displayed flowcharts outlining ~50+ steps to go from Live source to Staging data to transformed data to ~30+ source variables + ~30+ derived variables in 01adsl_met_rmsd dataset: patient level data covering treatment and disease information. This formed the basis of possible operational and clinical analyses going forward.

Clinical data understanding section showed how individual observations can be transformed into meaningful patient narratives. This section explained how the usage of operational and clinical part of the data can benefit varied stakeholders and emphasized the need to convert “a thought from a doctor’s mind” into an “actionable and consistent data point” in the database for future use. While studying both the structure and the content of the hospital database, it was observed, that standardization of database along with effective curation towards good data quality is needed. It was highlighted that this type of data could provide a gold mine of information which when summarized could lead us to many insights which could potentially increase operational efficiencies and progress the Ayurvedic practice. It laid down the foundation for “understanding demographics and patient characteristics” as a basis.

The demographic and patient characteristic analysis provided good insights into different components of the data which can feed more generally into the public health domain. It was observed that the health and healthcare requirements of a population can benefit through disease surveillance and population health insights. It also provided actionable inputs to hospital management on efficient operations, practicing doctors and for research publications.

Diagnostics and interventions section showed complex relations between diseases and interventions. Comorbidities as well as combinations of interventions showed the complex clinical decision-making process as followed by Ayurveda physicians. The disease and treatment comorbidity analyses was performed and presented using a variety of plots and heatmaps. These analyses showed how individual observations can be transformed into meaningful insights and data stories.

Day-to-day transactions at hospitals involve people from many backgrounds like, hospital administration, patients, doctors, nurses, pharmacists, pathologists, representative from insurance companies, lawyers, etc. These interactions generate a lot of information and are the primary data generators. Same set of people and a few additional professionals are the end users of the data e.g., scientists, statisticians, database developers, etc. This study has provided preliminary insights into various aspects of HMIS based EMR data generated during real time consultation at I-AIM.

A variety of analysis and summarization of the hospital data was conducted with a view to derive meaningful outcomes which confirm the Ayurvedic principles. As a final summary of all that has been said previously is represented in the figure below (Figure 5-1). First part of the diagram covers how to define the underlying question, which is followed by defining the hypothesis. Researchers should logically think about clinical context and methodological context. For converting this theoretical thinking into a real-world study, we need to have the necessary IT infrastructure which will enable data related components. Middle of the diagram shows potential stakeholders. This concise representation shows how the HMIS based EMR can shape up Real World Evidence generation.

Figure 5-1: Real World Evidence life cycle

Is the study specific to a treatment?	Is the treatment an approved one?	Is it a comparative study?		Has treatment been assigned by study protocol?		Is data available in existing sources?
Causal diagram: Specify causal relations & supporting evidence among treatment, outcome(s), & other variables to control confounding						
			All Data Sources			
Valid sample size	Data protection	Different data types	IT infrastructure	Data quality	Information governance	
Medical practitioner bias	Clinical outcome	Disease registry	Patient registry	Patient charts	Sensor data, Mobile App	Low recall bias
Methodology context	Patient reported outcome	Real World Data Individual Patient Data (pragmatic trials, cohort trials, observational) Effectiveness in wider population				Longitudinal data Co-morbidities and Cost effectiveness
	Quality of life outcome	Stakeholders: Regulatory Authorities, Policy Makers, Government and Payers				Health surveys Preference of other medicine Clinical context
Confounding and Population homogeneity	Economic outcome	Primary / Secondary data	Retrospective / Prospective study	Big data, large sample size	Social media	Hospital EHRs Real life data, clarity of treatment impact and AEs
Un-blinded treatment and Treatment switch	Operational challenges	Comparable data	Patient level data access	GDPR and Anonymization	Individual practice Incomplete data	More data available on drug and life style interaction
			Data context			

Due to the above-mentioned outcomes, the following contributions can be possible:

1. Contribution to Public health data creation based on large data at our disposal which is not marred by artificial boundaries imposed on patient disease conditions and treatments prescribed as followed in a designed randomized clinical trial.
2. Make recommendations to the practitioners for standardized way of data collection, analyses and reporting which will support future EMR based RWD studies
3. Understand the hidden wealth of data for Transdisciplinary expansion of thoughts
 - a. Sustainable treatment solutions for diseases readily available
 - b. Thought provoking work to generate new needs through unconventional use of the data
 - c. Expand the use of modern IT solutions like IT infrastructure, electronic health records, cloud, etc. within Ayurvedic area where appropriate – Ayur IT solutions.
 - d. Take advantage of freely available cutting-edge software(s) to create new approaches
 - e. Introduce statistical programming (Ayurdata analyst) as a tool to Ayurvedic area

A lot of work carried is out by health authorities, pharmaceutical companies, and nonprofit organizations. Some of these resources could be used as reference to become a world class data generator:

Clinical Data Interchange Standards Consortium (CDISC) is a global nonprofit charitable organization with administrative offices in Austin, Texas, with many people contributing across the world. CDISC brings experts together to create and advance data standards. This allows for accessibility, interoperability, and reusability of data for competent research that has greater impact on global health [118]. Many of the leading health authorities use the standards developed by the CDISC teams in various parts of drug applications.

TransCelerate BioPharma Inc. is a nonprofit organization with a mission to collaborate across the global biopharmaceutical research and development community to identify, prioritize, design, and facilitate the implementation of solutions designed to deliver high quality new medicines. They have many open-source solutions which could be used to improve delivery model [120].

Based on the 21st century act, 2016, the US FDA has created a regulatory framework for the Real-world data (RWD) and real-world evidence (RWE) which are playing increasing role in the health care decisions [121], [122]. The European Medicines Agency (EMA) has established a center to provide timely and reliable evidence from real world healthcare databases on the use, safety, and effectiveness of medicines for human use, including vaccines, across the European Union (EU). This capability is called the Data Analysis and Real-World Interrogation Network (DARWIN EU®) [123].

These resources provide a lot of material to enhance overall understanding and allows researchers to be compliant with the regulatory requirements.

This thesis outlines many tools which can be used by various stakeholders. They are free and easy to use. They allow multi-dimensional display of complex data in a very short amount of space. The tools can create evidence for multiple stakeholders. Free softwares like, R, python, Java,

tableau and many more have made it possible to harness the power of data in many ways. There is a need to have a profession of a “Statistical programmer” or a “clinical programmer” or an “Ayurdata expert”. This role can contribute to database development, data collection, data cleaning aspects, creating analyses ready datasets, and to finally analyses and reporting. This role should have capabilities related to information technology, data management techniques for generating quality data, in addition to knowing basic and advanced statistical and data science concepts. The computational advances in the world of computer science could be leveraged via appropriate software. Theoretical ideas can be converted into practical interactive visualizations and interactive analyses using multiple technologies. These will help convert individual data observations into summaries then into stories thus enabling knowledge generation.

Ayurdata expert can contribute to creating documents for medical journalism, medical education, medical marketing of healthcare products, publications, research documents, and regulatory documents by collaborating with other experts (Table 5-1). We believe that this would be a pioneering effort within ayurvedic EMR area.

Table 5-1: Different types of documents

Medical Reporting	Medical Teaching	Medical advertising of products	Publication
<ul style="list-style-type: none"> • Newspaper & magazine articles • Mostly for public • Written in simple, non-technical language 	<p>For doctors</p> <ul style="list-style-type: none"> • Textbooks, • Continued Medical Education programs, • Slide decks, • Online learning material <p>For Patients learning material</p>	<ul style="list-style-type: none"> • Promotional information for healthcare professionals • Product profiles • Brochures • Sales force training • Online learning material 	<ul style="list-style-type: none"> • Abstracts • Journal articles, case reports, review articles • Posters & presentations for scientific conferences

Research Documents	Regulatory documents #
<ul style="list-style-type: none"> • Research proposals • Clinical trial protocols • Investigators' Brochure • Informed Consent Documents • Study reports 	<ul style="list-style-type: none"> • Package Inserts • Patient Information Leaflets • Clinical study reports • Web synopses • Subject narratives <p>Aggregate safety reports such as</p> <ul style="list-style-type: none"> • Periodic Safety Update Reports

	<p>Common Technical Document (CTD) modules such as</p> <ul style="list-style-type: none"> • nonclinical and clinical overviews & summaries • expert reports • PK, Safety, Efficacy summaries 	<ul style="list-style-type: none"> • Periodic Adverse Drug Experience Reports • Annual safety reports • Policy papers
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#: Presently, some of these documents are not applicable within Ayurvedic area

Work carried out for this thesis is typically reflective of work done by a team of people. In a mid to large sized pharmaceutical organization, this type of work is carried out by (1) Clinicians and statisticians design clinical protocol, (2) Database development team creates database and data flow components, (3) Data management team reviews and cleans the data on an ongoing basis, (4) Statistical programming team and statisticians create the necessary analyses, (5) Writing team generates Clinical Study Report / Publication, and last but not the least (6) IT team handles various systems so that the data and information flow is managed appropriately.

Much more details about the database and programming done for analyses and visualization are available in the appendices.

This is not an end but just a beginning of Ayurdata experts ...

There is a lot of additional analysis carried out during PhD work which has not be written in the main text of the thesis document. This paragraph outlines some of this work and ideas about new work which can be carried out in future: (1) Work with the university and hospital management for updates to the data capture process, (2) Attempt to work with other hospitals and carry out similar analysis, (3) Use Sequential Pattern Mining library developed by Phillip Fournier-Viger, having more than 100 algorithms to discover patterns in data, (4) Use Co-morbidity package in R programming language to identify disease comorbidities using different statistical tests and metrics, (5) Use Natural Language Processing approaches using tensor flow methodologies to discover underlying patterns in the data, (6) Work with the ayurvedic physicians in the hospital on specific disease areas like Chronic Kidney Disease (CKD), and Parkinson disease data – these are the areas, hospital is working actively working on.

6 Appendix

6.1 Approval from the hospital management to carry out the retrospective study

11.1 ANNEXURE 1 –NOC FROM IAIM MEDICAL DIRECTOR.

IAIM/2020/NOC/01

Date: 29.05.2020

LETTER OF PERMISSION AND NO OBJECTION CERTIFICATE

TO WHOM IT MAY CONCERN

This is to grant permission to Mr. Vinay Mahajan to conduct the research study “Review of hospital based Ayurvedic Electronic Health Records to gain real world knowledge - a retrospective data analysis” using I-AIM anonymized Electronic Health Records as per the protocol approved by the IEC.

I am assured that Mr. Vinay Mahajan will maintain confidentiality of the data.

Further, it is also agreed that any presentation and publication of the results arising from the study will be done after due permission from the authorities of IAIM and TDU.

Dr. Prasan Shankar
Medical director
IAIM
Bangalore

6.2 Details of analysis dataset

Table 6-1: Details of the Reference Dataset “01adsl_met_rmsd”

Variable name	Description	Derivation
mr_no	Unique Patient ID	Source variable, no derivation needed E.g. MR000001, MR040237, etc.
patient_gender	Patient gender	Source variable, no derivation needed E.g. M, F
patient_id	Visit ID	Source variable, no derivation needed, the hospital database captures unique visit ID for each visit.
city_name	City name	Source variable, no derivation needed
state_name	State name	Source variable, no derivation needed
country_name	Country name	Source variable, no derivation needed
dateofbirth	Date of birth	Source variable, no derivation needed, for some patients this is missing
newdt0	Date of visit to hospital	Date of visit to hospital in numeric format All the In-Patient visits, Out-Patient visits and Service related visits are combined from source datasets into a dataset, unique visit and date combinations are created.
newdt	Date of visit to hospital	Character version of newdt0

Variable name	Description	Derivation
vis	Visit	<ol style="list-style-type: none"> Based on all the In-Patient visits, Out-Patient visits and Service related visits unique visit numbers are created. Visit numbers are numeric values from 1 to n, based on current version of data; a patient has maximum number 323 visits.
all_vis	All visits	This variable contains maximum number of visit for each patient. all_vis = max(vis) grouped by each mr_no
all_ip	All IP visits	This variable contains maximum number of visits for each patient for IP type of visits. all_vis = max(vis) grouped by each mr_no and visit type is IP.
all_op	All OP visits	This variable contains maximum number of visits for each patient for OP type of visits. all_vis = max(vis) grouped by each mr_no and visit type is OP.
studyday	Study day	<p>studyday = 1 when the visit minimum visit or first visit for a patient, else studyday is calculated as newdt0 – min(newdt0) + 1.</p> <p>Studyday is never missing and never less than 0 for the dataset created.</p>
age	Age of patient at that visit	If date of birth is non-missing for a patient, then age is calculated as round((anydate(newdt) - anydate(dateofbirth) + 1)/365.25, digits = 0)
baseage	Age of patient at the first visit	Age at vis = 1 for each patient is stored as base age

Variable name	Description	Derivation
death_date	Date of death	Source variable, no derivation needed
cstdt	Min Start date	cstdt = min(newdt)
cendt	End date	cendt = max(newdt)
cdur	Total duration in days	cdur = max(newdt) - min(newdt) + 1
stdt_IP	Start date of IP visits	Minimum visit date for IP visits for each patient
endt_IP	End date of IP visits	Maximum visit date for IP visits for each patient
dur_IP	Duration of IP visits	dur_IP = endt_IP - stdt_IP + 1
stdt_OP	Start date of OP visits	Minimum visit date for OP visits for each patient
endt_OP	End date of OP visits	Maximum visit date for OP visits for each patient
dur_OP	Duration of OP visits	dur_OP = endt_OP - stdt_OP + 1
serstdt	Service Start date	Minimum visit date for Service visits for each patient
serendt	Service End date	Maximum visit date for Service visits for each patient
Code	Code	Source variable, no derivation needed, ACD code
description	Description	Source variable, no derivation needed, description
Type	Type of visit	This variable identifies a visit either as IP or OP based on visit classification

Variable name	Description	Derivation
diag_type	Diagnosis type	Source variable, no derivation needed: Primary or Secondary
year	Year	Year part of the newdt variable
season	Indian seasons	<p>Derivation of Indian seasons based on the date variable for each visit:</p> <pre># Add Indian rutus as new variables # https://www.drikpanchang.com/seasons/season-tropical-timings.html?geoname-id=1277333&year=2010</pre> <ul style="list-style-type: none"> • 01 Vasant Rutu • 02 Grishma Rutu • 03 Varsha Rutu • 04 Sharad Rutu • 05 Hemant Rutu • 06 Shishir Rutu
C, N, P, U, X, Y	Values related to Services offered to patients	<p>Source variable, no derivation needed:</p> <ul style="list-style-type: none"> • C - Cancelled • U - Condn. Unnecessary • Y -Conducted

Variable name	Description	Derivation
		<ul style="list-style-type: none"> • N - Not Conducted • P - Partially Conducted
presc_type		Source variable, no derivation needed
medicine_name	Medicine name	<p>Source variable, no derivation needed</p> <p>Prescribed medicine names follow a certain predefined naming convention. Medicine name + Quantity + Producer's name are the details recorded for each prescribed medicine.</p>
item_name	Source value of medicine name	Source variable, no derivation needed
quantity	Quantity of prescribed medicine	Source variable, no derivation needed
med_route	Route of administration of prescribed medicine	Source variable, no derivation needed
generic_code		Source variable, no derivation needed
remarks	Notes provided by doctors for medicines	Source variable, no derivation needed
frequency	Frequency of prescribed medicine	Source variable, no derivation needed
duration	Duration of prescribed medicine	Source variable, no derivation needed

Variable name	Description	Derivation
duration_units	Unit for duration of prescribed medicine	Source variable, no derivation needed
Coded_med	Only name of medicine	Derived from medicine_name
Company	Name of the company producing the drug	Derived from medicine_name
Quantity	Quantity of prescribed medicine	Derived from medicine_name
Unit	Unit of prescribed medicine	Derived from medicine_name
Type_med	Type of medicine	<p>Derived based on medicine_name. Classified into different kinds of medicines, e.g.</p> <ul style="list-style-type: none"> • Ghritam • Kashayam • Asavam • Aristham • Bhasma • Abhyanga • Cream • Rasayanam

Variable name	Description	Derivation
		<ul style="list-style-type: none"> • Tablet / Gulika / Vati • ...
cat_id		Identification of categories
distype	Disease type	<p>Disease type as OTHER, RMSD, Metabolic</p> <ol style="list-style-type: none"> 1. If a disease code is present in Metabolic list then the value is Metabolic 2. If a disease code is present in RMSD list then the value is RMSD 3. Any other disease is classified as OTHER
Metabolic	Metabolic	<p>If a patient has reported any Metabolic disease at least once then that patient is given value Metabolic = 1, else Metabolic =0</p> <p>Metabolic disease group has 10 diseases (Refer 2.4.1.6.1)</p>
RMSD	RMSD	<p>If a patient has reported any RMSD disease at least once then that patient is given value RMSD = 1, else RMSD =0</p> <p>RMSD disease group has 97 diseases (Refer 2.4.1.6.1)</p>
combine	Metabolic RMSD Both	<ol style="list-style-type: none"> 1. If a patient is classified only as Metabolic diseased patient then combine = 1, 2. If a patient is classified only as RMSD diseased patient then combine = 2, 3. If a patient is classified as Metabolic as well as RMSD diseased patient then combine = 99

Variable name	Description	Derivation
Minday Metabolic	First day on which reported metabolic disease	First day on which any metabolic disease has been reported by a patient.
Minday RMSD	First day on which reported RMSD disease	First day on which any RMSD disease has been reported by a patient.

Table 6-2: Metabolic and RMSD disease code and de-code

Code	Description	Distype
M10.0	Medoroga	Metabolic
M10.1	Medoroga - Sthula medho roga	Metabolic
M10.2	Medoroga - Sukshma medho roga	Metabolic
M2.0	Madhumeha	Metabolic
P5.0	Prameha	Metabolic
P5.1	Prameha - Krusha	Metabolic
P5.2	Prameha - Pidaka	Metabolic
P5.3	Prameha - Sthula	Metabolic
P5.4	Prameha - Upadrava	Metabolic
S16.0	Sthaulya	Metabolic
A2.0	Aamavaata	RMSD
A2.1	Aamavaata - Kaphaja	RMSD
A2.2	Aamavaata - Pittaja	RMSD
A2.3	Aamavaata - Vaataja	RMSD
A3.0	Abhighataja Shoola	RMSD
S10.0	Stambha	RMSD
S10.1	Stambha - Baahu Stambha	RMSD
S10.10	Stambha - Prishtha Stambha	RMSD
S10.12	Stambha - Sandhi Stambha	RMSD
S10.13	Stambha - Siraa Stambha	RMSD
S10.14	Stambha - Uru Stambha	RMSD
S10.4	Stambha - Greevaa Stambha	RMSD
S10.5	Stambha - Hanu Stambha	RMSD
S10.6	Stambha - Hridaya Stambha	RMSD

S13.0	Sthaanabheden Graha	RMSD
S13.1	Sthaanabheden Graha - Anga Graha	RMSD
S13.11	Sthaanabheden Graha - Katee Graha	RMSD
S13.13	Sthaanabheden Graha - Manyaa Graha	RMSD
S13.14	Sthaanabheden Graha - Marma Graha	RMSD
S13.17	Sthaanabheden Graha - Paada Graha	RMSD
S13.18	Sthaanabheden Graha - Paarshva Graha	RMSD
S13.19	Sthaanabheden Graha - Prishtha Graha	RMSD
S13.20	Sthaanabheden Graha - Shiro Graha	RMSD
S13.22	Sthaanabheden Graha - Uro Graha	RMSD
S13.23	Sthaanabheden Graha - Vaak Graha	RMSD
S13.3	Sthaanabheden Graha - Gala Graha	RMSD
S13.5	Sthaanabheden Graha - Hanu Graha	RMSD
S13.6	Sthaanabheden Graha - Hrid Graha	RMSD
S13.7	Sthaanabheden Graha - Jaanugraha	RMSD
S13.8	Sthaanabheden Graha - Janghaa Graha	RMSD
S14.0	Sthaanabheden Shoola	RMSD
S14.11	Sthaanabheden Shoola - Guda Shoola	RMSD
S14.13	Sthaanabheden Shoola - Gulpha Shoola	RMSD
S14.14	Sthaanabheden Shoola - Hanu Shoola	RMSD
S14.15	Sthaanabheden Shoola - Hasta Shoola	RMSD
S14.16	Sthaanabheden Shoola - Hrid Shoola	RMSD
S14.17	Sthaanabheden Shoola - Jaanu Shoola	RMSD
S14.18	Sthaanabheden Shoola - Janghaa Shoola	RMSD
S14.19	Sthaanabheden Shoola - Kantha Shoola	RMSD
S14.21	Sthaanabheden Shoola - Katee Shoola	RMSD
S14.23	Sthaanabheden Shoola - Kukshi Shoola	RMSD

S14.24	Sthaanabheden Shoola - Manyaa Shoola	RMSD
S14.3	Sthaanabheden Shoola - Amsa Shoola	RMSD
S14.4	Sthaanabheden Shoola - Anga Shoola	RMSD
S14.5	Sthaanabheden Shoola - Anguli Shoola	RMSD
S14.6	Sthaanabheden Shoola - Asthi Shoola	RMSD
S14.7	Sthaanabheden Shoola - Baahu Shoola	RMSD
S15.28	Sthaanabheden Shoola - Nakha Shoola	RMSD
S15.31	Sthaanabheden Shoola - Paada Shoola	RMSD
S15.32	Sthaanabheden Shoola - Paarshni Shoola	RMSD
S15.34	Sthaanabheden Shoola - Parva Shoola	RMSD
S15.36	Sthaanabheden Shoola - Prishtha Shoola	RMSD
S15.41	Sthaanabheden Shoola - Sakthi Shoola	RMSD
S15.42	Sthaanabheden Shoola - Sandhi Shoola	RMSD
S15.43	Sthaanabheden Shoola - Skandha Shoola	RMSD
S15.44	Sthaanabheden Shoola - Snaayu Shoola	RMSD
S15.45	Sthaanabheden Shoola - Sphik Shoola	RMSD
S15.46	Sthaanabheden Shoola - Stanaanta Shoola	RMSD
S15.47	Sthaanabheden Shoola - Trika Shoola	RMSD
S15.48	Sthaanabheden Shoola - Urah Shoola	RMSD
S1A.0	Shoola	RMSD
V1.0	Vaatarakta	RMSD
V1.1	Vaatarakta - Dvandvaja	RMSD
V1.2	Vaatarakta - Gambheera	RMSD
V1.3	Vaatarakta - Kapha Vaataja	RMSD
V1.4	Vaatarakta - Kaphadhika Vaatarakta	RMSD
V1.5	Vaatarakta - Pittadhika Vaatarakta	RMSD
V1.7	Vaatarakta - Uttaana	RMSD

V1.8	Vaatarakta - Vaata Kaphaja	RMSD
V1.9	Vaatarakta - Vaataadhika Vaatarakta	RMSD
V2.0	Vaatavyaadhi	RMSD
V2.12	Vaatavyaadhi - Stabdhagaatra	RMSD
V2.16	Vaatavyaadhi - Baahugata Vaata	RMSD
V2.23	Vaatavyaadhi - Gridhrasee	RMSD
V2.30	Vaatavyaadhi - Jaanugata Vaata	RMSD
V2.31	Vaatavyaadhi - Janghaagata Vaata	RMSD
V2.36	Vaatavyaadhi - Kateegata Vaata	RMSD
V2.42	Vaatavyaadhi - Maamsagata Vaata	RMSD
V2.43	Vaatavyaadhi - Maamsamedogata Vaata	RMSD
V2.44	Vaatavyaadhi - Majjaagata Vaata	RMSD
V2.45	Vaatavyaadhi - Majjaasthigata Vaata	RMSD
V2.46	Vaatavyaadhi - Manyaagata Vaata	RMSD
V2.47	Vaatavyaadhi - Manyaastambha	RMSD
V2.48	Vaatavyaadhi - Medogata Vaata	RMSD
V2.61	Vaatavyaadhi - Prishthagata Vaata	RMSD
V2.63	Vaatavyaadhi - Sandhigata Vaata	RMSD
V2.64	Vaatavyaadhi - Sarvaangagata Vaata	RMSD
V2.65	Vaatavyaadhi - Shaakhaagata Vaata	RMSD
V2.68	Vaatavyaadhi - Siraagata Vaata	RMSD
V2.69	Vaatavyaadhi - Siraagraha	RMSD
V2.70	Vaatavyaadhi - Snaayugata Vaata	RMSD
V2.72	Vaatavyaadhi - Trikgata Vaata	RMSD
V2.73	Vaatavyaadhi - Tvaggata Vaata	RMSD
V2.74	Vaatavyaadhi - Urugata Vaata	RMSD
V2.75	Vaatavyaadhi - Vaatakantaka	RMSD

V2.77	Vaatavyaadhi - Vishvaachee	RMSD
V2.9	Vaatavyaadhi - Asthigata Vaata	RMSD

6.3 All variables in the source database

Table 6-3: All variables in the source database



6.4 Details of analysis

Figure number and analysis name	Link to visualization	Dataset(s) used, (if needed then the datasets will be made available)	R / SQL / D3js program
Figure 3-1: A snippet of disease table by gender	Link	01adsl_met_rmsd	100_adsl.R
Figure 3-2: Variable classification by categories	Link	03_typesOfassessment	03_typesOfassessment.R
Figure 3-3: Visit pattern analysis	Link	01adsl_met_rmsd	100_adsl.R
Figure 3-4: Patient visit profile – Horizontal view	Link	01adsl_met_rmsd	100_adsl.R
Figure 3-5: Patient visit profile – Vertical view	Link	01adsl_met_rmsd	100_adsl.R

Figure number and analysis name	Link to visualization	Dataset(s) used, (if needed then the datasets will be made available)	R / SQL / D3js program
Figure 3-6: Total Number of Patients	Link	04_patient_analysis_tableau_adsl	04_patients_analysis_tableau_adsl.R
Figure 3-7: Country-wise Visualization	Link	04_patient_analysis_tableau_adsl	04_patients_analysis_tableau_adsl.R
Figure 3-8: Age distribution by country, age distribution by gender	Link01 Link02	04_patient_analysis_tableau_adsl	04_patients_analysis_tableau_adsl.R
Figure 3-9: Blood-group Distribution by gender	Link	04_patient_analysis_tableau_adsl	04_patients_analysis_tableau_adsl.R
Figure 3-10: Number of Visits, and Visit Types	Link	04_patient_analysis_tableau_adsl	04_patients_analysis_tableau_adsl.R

Figure number and analysis name	Link to visualization	Dataset(s) used, (if needed then the datasets will be made available)	R / SQL / D3js program
Figure 3-11: Descriptive summary statistics by number of Diseases by Age and Gender	Link	04_patient_analysis_tableau_adsl	04_patients_analysis_tableau_adsl.R
Figure 3-12: Data tabulation for patients reporting RMSD and Metabolic diseases	Link	rmsd_met_primary_diag	rmsd_metabolic_all.R
Figure 3-13: Disease distribution by age and gender	Link	rmsd_met_primary_diag	rmsd_metabolic_all.R
Figure 3-14: Patient visit duration for	Link	rmsd_met_primary_diag	rmsd_metabolic_all.R

Figure number and analysis name	Link to visualization	Dataset(s) used, (if needed then the datasets will be made available)	R / SQL / D3js program
Disease categories by Gender			
Figure 3-15: Disease distribution by Seasonal Variations and gender	Link	rmsd_met_primary_diag	rmsd_metabolic_all.R
Figure 3-16: Pre and Post Disease Classification Analysis	Link	085_dis_1st_time_refCal_NodesEdges	085_dis_1st_time_refCal_NodesEdges.R
Figure 3-17: ICD classification by Gender	Link	060_allopathic_diag	060_allopathic_diag.R
Figure 3-18: Age distribution	Link	060_allopathic_diag	060_allopathic_diag.R

Figure number and analysis name	Link to visualization	Dataset(s) used, (if needed then the datasets will be made available)	R / SQL / D3js program
by ICD classification and Gender			
Figure 3-19: Visit distribution by ICD classification and Gender	Link	060_allopathic_diag	060_allopathic_diag.R
Figure 3-20: Duration distribution by ICD classification and Gender	Link	060_allopathic_diag	060_allopathic_diag.R
Figure 3-21: Disease classification by Prakriti and Gender	Link	Disease_by_dosha_type	Disease_by_dosha_type.R

Figure number and analysis name	Link to visualization	Dataset(s) used, (if needed then the datasets will be made available)	R / SQL / D3js program
Figure 3-22: Co-morbidity analysis approach 1 example 1: Vaatavyadhi	Link	prim_diag	diagnosis_primary.R
Figure 3-23: Co-morbidity analysis approach 1 example 2: Pandu	Link	prim_diag	diagnosis_primary.R
Figure 3-24: Co-morbidity analysis approach 1 example 3: Madhumeha	Link	prim_diag	diagnosis_primary.R
Figure 3-25: Co-morbidity	Link	prim_diag_mon	diagnosis_primary_month.R

Figure number and analysis name	Link to visualization	Dataset(s) used, (if needed then the datasets will be made available)	R / SQL / D3js program
analysis approach 2			
Figure 3-26: Co-morbidity analysis approach 3: collapsible tree view	Link	085_dis_count_edges_3rd_byPeriod_A2_bruce	085_dis_counts_bruce_java.R
Figure 3-27: Patient Disease and Treatment administration by Study Day	Link	080_disease_repeat_prop	080_medicine_dis_repeat_prop.R
Figure 3-28: Patient Disease by Study Day and Treatment administration by Study Day	Link	080_medicine_dis_all_met_rmsd_prop	080_medicine_dis_repeat_prop.R

Figure number and analysis name	Link to visualization	Dataset(s) used, (if needed then the datasets will be made available)	R / SQL / D3js program
Figure 3-29: Patient Cumulative Disease and Treatment administration by Visit	Link	080_medicine_dis_repeat_prop_cumulative	080_medicine_dis_repeat_prop.R
Figure 3-30: Area graph representation of diseases	Link	adiag	diagnosis.R
Figure 3-31: Mosaic plot: Disease and treatment representation example 1: Prameha	Link	305_medicine_duration_by_dis_xyplot	305_medicine_duration_by_dis.R
Figure 3-32: Disease and treatment	This is a part of 3-31 analysis so no other explicit link or program, use the above link		

Figure number and analysis name	Link to visualization	Dataset(s) used, (if needed then the datasets will be made available)	R / SQL / D3js program
example 2: P5.0: Prameha and Oil: Kottamchukkadi			
Figure 3-33: Disease and treatment example 3: P5.0: Prameha and Vati: Diabecon DS		This is a part of 3-31 analysis so no other explicit link or program, use the above link	
Figure 3-34: Mosaic plot Disease and treatment representation example 4: Treatment: Oil: Kottamchukkadi	Link	305_medicine_duration_by_dis_xyplot	305_medicine_duration_by_dis.R
Figure 3-35: Cross tabulation of prescribed	Link	01adsl_met_rmsd	100_adsl.R

Figure number and analysis name	Link to visualization	Dataset(s) used, (if needed then the datasets will be made available)	R / SQL / D3js program
treatments and disease group by gender Example 1			
Figure 3-36: Cross tabulation of prescribed treatments and disease group by gender Example 2	Link	01adsl_met_rmsd	100_adsl.R
Figure 3-37: Circular view: Co-occurrences of disease – disease Example 1	Link	085_dis_counts_edges_3rdbyPeriod_circular17	085_dis_counts_edges_3rdbyPeriod_circular17.R
Figure 3-38: Circular view: Co-occurrences of disease –	Link	085_dis_counts_edges_3rdbyPeriod	085_dis_counts_edges.R

Figure number and analysis name	Link to visualization	Dataset(s) used, (if needed then the datasets will be made available)	R / SQL / D3js program
treatment Example 2			
Figure 3-39: Pre and Post distance analysis for disease: M2.0: Madhumeha	Link	086time_dis_refcode_max	086time_dis_patterns_combinations_gender_Macro.R
Figure 3-40: Pre and Post distance analysis for medicines given for diseases: P5.0, V2.23, V2.63	Link	086time_dis_refcode_max	086_med_patterns_combinations.R
Figure 3-41: Radar plot	Link	300_radar_plot	300_radar_plot_tableau.R
Figure 3-42: Dynamic bubble	Link	decode_gender.csv file is converted to Json files	06_d3tree_diagram.R

Figure number and analysis name	Link to visualization	Dataset(s) used, (if needed then the datasets will be made available)	R / SQL / D3js program
plot: Example 1: Disease: A6.0: Amavaata			

6.5 Programs for the different parts of analysis

6.5.1 Data extraction from SQL database: 01adsl.sql

SQL program to get the source data from hospital database, combine major components of data in a logical manner

```
/* SQL version with UNION of data */

/*=====
/* Execute the code in following manner;                                     */
/* iaim=> \i /cygdrive/d/Hospital_data/ProgressSQL/prgm/100_adsl_sqlpart.sql; */
=====*/

drop table if exists
temp0pat_demog, temp1pat_reg, temp1doc_cons, temp2reg_cons, temp2diag, temp3pat_presc,
temp4pat_med,
temp20, temp30, temp30_1, temp30_5, temp100ip, temp350, temp100ser, temp100ser2, temp360,
base01_op0, base01_op, base01_ip, base01_ser, base_all ;

/* Country and state names */
create temp table state as
select city.city_id, city.city_name, city.state_id,
state.state_name, state.country_id
from iaim.city as city, iaim.state_master as state
where city.state_id = state.state_id;

create temp table cou as
select state.*, country.country_name
from state, iaim.country_master as country
where state.country_id = country.country_id;

/* Create demog table */
create temp table temp0pat_demog0 as
```

```

select distinct mr_no as mrno, patient_gender, patient_city, patient_state, dateofbirth,
country, /*oldmrno, remarks,*/ death_date
from iaim.patient_details;

create temp table temp0pat_demog as
select cou.city_name, cou.state_name, cou.country_name, temp0pat_demog0.*
from cou, temp0pat_demog0
where cou.city_id = temp0pat_demog0.patient_city and cou.state_id =
temp0pat_demog0.patient_state and cou.country_id = temp0pat_demog0.country;

create temp table templpat_reg as
select mr_no, patient_id, visit_type, reg_date, bed_type, dept_name, admitted_dept,
main_visit_id
from iaim.patient_registration
order by mr_no, patient_id;

create temp table templdoc_cons as
select distinct mr_no as con_mrno, patient_id as con_patient_id, consultation_id as
consult_id, doctor_name, date(visited_date) as visdate
from iaim.doctor_consultation
order by mr_no, patient_id;

create temp table temp2reg_cons as
select templpat_reg.*, templdoc_cons.*
from templpat_reg
full join templdoc_cons on
templpat_reg.mr_no = templdoc_cons.con_mrno and templpat_reg.patient_id =
templdoc_cons.con_patient_id;

/* Create diagnosis table */
create temp table temp2diag as
select distinct visit_id, id, description, icd_code, diag_type, doctor_id,
diagnosis_datetime::timestamptz::date as diagdate

```

```

from iaim.mrd_diagnosis;

/* Full join temp10 and temp2diag on temp10.patient_id and temp2diag.visit_id */
create temp table temp20 as
select temp2reg_cons.*, temp2diag.*
from temp2reg_cons
full join temp2diag on
temp2reg_cons.patient_id = temp2diag.visit_id;

/* patient_prescription = consultation_id */
/* A Subset is required for presc_type */
create temp table temp3pat_presc as
select patient_presc_id, consultation_id, presc_type, status, date(prescribed_date) as
dateonly
from iaim.patient_prescription
/*where presc_type in ('Medicine') */
order by patient_presc_id, consultation_id;

create temp table temp30 as
select temp20.*, temp0pat_demog.*
from temp20
full join temp0pat_demog on
temp20.mr_no = temp0pat_demog.mrno;

create temp table temp30_1 as
select temp30.*, temp3pat_presc.*
from temp30
full join temp3pat_presc on
temp30.consult_id = temp3pat_presc.consultation_id;

create temp table temp30_5 as
select mr_no, patient_id, patient_gender, city_name, state_name, dateofbirth,
country_name, death_date,

```

```

consult_id, description, icd_code, diag_type, diagdate, patient_presc_id
from temp30_1;

/* patient_medicine_prescriptions = medicine_id */
create temp table temp4pat_med as
select medicine_id as cat_id,
op_medicine_pres_id,
duration,
duration_units,
mod_time::timestamptz::date as prescdate,
frequency,
medicine_quantity as quantity,
medicine_remarks as remarks
from iaim.patient_medicine_prescriptions
order by medicine_id, op_medicine_pres_id;

/* BASE 1 data for the OP medication */

create temp table base01_op as
select temp30_5.*, temp4pat_med.*
from temp4pat_med
left join temp30_5 on
temp30_5.patient_presc_id = temp4pat_med.op_medicine_pres_id
order by mr_no, patient_id;

/* IP medications */
create temp table temp100ip as
select
prescription_id as consultation_id,
patient_id as ippatient_id,
doctor_id,
prescription_date::timestamptz::date as prescdate,
presc_type,

```

```

item_id as cat_id,
item_name,
med dosage as quantity,
med_route,
med_form_id,
generic_code,
remarks,
recurrence_daily_id as frequency
from iaim.ip_prescription
order by patient_id;

create temp table base01_ip as
select temp30_5.* , temp100ip.*
from temp100ip
left join temp30_5 on
temp30_5.patient_id = temp100ip.ippatient_id;

/* Services Create Base01_ser */

create temp table base01_ser as
select mr_no,
patient_id,
service_id as cat_id,
presc_date::timestamptz::date as prescdate,
conducted,
conductedby,
conducteddate::timestamptz::date as sercond_date,
prescription_id as consultation_id
from iaim.services_prescribed;

create temp table services as
select service_id as medicine_id, service_name as medicine_name
from iaim.services;

```

```

create temp table med as
select distinct medicine_name, medicine_id
from iaim.medicine_sales_view;

\copy temp30_5 TO 'd:/hospital_data/ProgressSQL/source/pat_diag_vis.csv' CSV HEADER
DELIMITER ',';
\copy base01_ip TO 'd:/hospital_data/ProgressSQL/source/base01_ip.csv' CSV HEADER
DELIMITER ',';
\copy base01_op TO 'd:/hospital_data/ProgressSQL/source/base01_op.csv' CSV HEADER
DELIMITER ',';
\copy base01_ser TO 'd:/hospital_data/ProgressSQL/source/base01_ser.csv' CSV HEADER
DELIMITER ',';

\copy services TO 'd:/hospital_data/ProgressSQL/source/services.csv' CSV HEADER DELIMITER
',';
\copy med TO 'd:/hospital_data/ProgressSQL/source/med.csv' CSV HEADER DELIMITER ',';

/*=====
/* End of program
=====

```

6.5.2 Primary dataset creation program: 100_adsl.R

This R program generates analysis dataset which is used as a primary dataset

```

#####
# Create calculations using base01_ip and base01_op
#####

#C- Cancelled
#U - Condn. Unnecessary

```

```

#Y -Conducted
#N - Not Conducted
#P - Partially Conducted

library(data.table)
library(dplyr)
library(anytime)

# Get all the data IP, OP and Service

base01_ip <- fread("D:/Hospital_data/ProgresSQL/source/base01_ip.csv")
base01_op <- fread("D:/Hospital_data/ProgresSQL/source/base01_op.csv")
base01_ser <- fread("D:/Hospital_data/ProgresSQL/source/base01_ser.csv")
pat_diag_vis <- fread("D:/Hospital_data/ProgresSQL/source/pat_diag_vis.csv")

# Get the disease category list for MCSD and Metabolic
discat <- data.table( fread ("D:/Hospital_data/ProgresSQL/analysis/discategory.csv") )

# Get the medication and service list
med <- data.table( fread ("D:/Hospital_data/ProgresSQL/source/med.csv") )
ser <- data.table( fread ("D:/Hospital_data/ProgresSQL/source/services.csv") )

medall <- rbind(med, ser, fill = TRUE)
rm(med, ser)

#####
# Work on the services data
# get the date converted to numeric date
# get the minimum and maximum date for each visit
# get the frequency count for each type of service
#####

```

```

base01_ser0 <- base01_ser [,c("mr_no", "patient_id", "prescdate", "sercond_date",
"cat_id", "conducted"), with =FALSE]
base01_ser0 <- base01_ser0 [, `:=` ( newdt = anydate(prescdate),
                                     serdt = anydate(sercond_date) ) ] [order(mr_no, newdt,
patient_id)]

base01_ser01 <- base01_ser0[, .(serstdt = min(newdt),
                                serendt = max(newdt),
                                freq = .N), by = .(mr_no, patient_id, cat_id, conducted) ]

base01_ser01t <- dcast(data = base01_ser01,
                         mr_no + patient_id + cat_id + serstdt + serendt ~ conducted,
                         value.var = c("freq"),
                         fill = "")

base01_ser01t <- merge (x = base01_ser01t,
                         y = medall,
                         by.x = "cat_id",
                         by.y = "medicine_id",
                         all.x = TRUE)

base01_ser01t <- base01_ser01t [order(mr_no, serstdt, patient_id)]
base01_ser01t <- base01_ser01t [, newdt := serstdt]

l = list(IP = base01_ip, OP = base01_op)
base01_all <- rbindlist(l, idcol = "Type", use.names = TRUE, fill = TRUE)

base01_all <- base01_all [, `:=` ( newdt = anydate(prescdate) ) ] [order(mr_no, newdt,
patient_id)]

#####
# create visit numbers and total number of visits
# Individual visits: merge the data on base01_all

```

```

# IP visits
# OP visits
# Total number of visits IP + OP
#####
vis <- unique ( rbind(base01_all [, c("mr_no", "patient_id", "newdt"), with =FALSE],
                     base01_ser01t[, c("mr_no", "patient_id", "newdt"), with =FALSE], fill=TRUE
))

vis <- vis [, Type := substr(patient_id, 1, 2)] [order (mr_no, newdt, patient_id)]
vis <- vis [, `:=` (vis =1:N,
                   all_vis = max( seq_len(.N) ) ), by = .(mr_no) ]
vis02 <- vis [, .(vistype =.N), by = .(mr_no, Type, all_vis)]
vis02t <- dcast(data = vis02,
                  mr_no +all_vis ~ paste("all_", tolower(Type), sep = ""),
                  value.var =c("vistype"),
                  fill="")
vis03 <- merge (vis [, -c("all_vis")], vis02t, by = "mr_no")

#####
# Start and end date for each type OP and IP
# Start and end date for overall visit dates
#####
base01_all01 <- vis[, .(stdt = min(newdt),
                       endt = max(newdt),
                       dur = max(newdt) - min(newdt) + 1), by = .(mr_no, Type) ]

base01_all01t <- dcast(data = base01_all01,
                        mr_no ~ Type,
                        value.var = c("stdt", "endt", "dur"),
                        fill = "")

#####

```

```

# Start for the overall study
#####
base01_all020 <- vis[, .(cstdt = min(newdt),
                           cendt = max(newdt),
                           cdur = max(newdt) - min(newdt) + 1), by = .(mr_no) ]

#####
# Create one large dataset with all the dates
#####
dates_dur <- merge (x = base01_all020,
                     y = base01_all01t,
                     by = c("mr_no"),
                     all.x = TRUE)

vis03dates_dur <- merge (x = dates_dur,
                         y = vis03,
                         by = c("mr_no"),
                         all.x = TRUE)

vis03dates_dur <- vis03dates_dur [, studyday := newdt - cstdt + 1]

#####
# Merge the Medication information
# Merge the visit information and day calculations
# Merge this information on SERVICES data as well
#####

base01_all01 <- merge (x = base01_all,
                       y = medall,
                       by.x = "cat_id",
                       by.y = "medicine_id",
                       all.x = TRUE)

```

```

base01_all011 <- merge (x = base01_all01,
                        y = vis03dates_dur [, -c("Type")],
                        by = c("mr_no", "patient_id", "newdt" ),
                        all.x = TRUE)

#####
# This should be moved after the VIS calculations
# Add the patient_info
#####
base01_ser02t <- merge (x = base01_ser01t,
                        y = vis03dates_dur,
                        by = c("mr_no", "patient_id", "newdt" ),
                        all.x = TRUE)

base01_ser02t <- merge (x = base01_ser02t,
                        y = pat_diag_vis,
                        by = c("mr_no", "patient_id"),
                        all.x = TRUE)

all <- rbind(base01_all011, base01_ser02t, fill =TRUE, use.names = TRUE)
all02 <- all [, -c("ippatient_id", "consult_id", "consultation_id", "patient_presc_id",
                   "med_form_id", "op_medicine_pres_id", "doctor_id", "diagdate",
                   "prescdate")] [order(mr_no, studyday, patient_id, newdt, vis, cat_id)]

#####
# Calculations for
# Get the disease category list for RMSD and Metabolic
#####
tmpall <- merge (x = discat[, -c("Description")], with =FALSE),
                 y = all02,
                 by.x = "Code",
                 by.y = "icd_code")

```

```

# create a dummy variable
tmpall <- tmpall[ ,val:=1]

subset2 <- tmpall [ , c("mr_no", "distype", "val"), with =FALSE]
subset2 <- unique(subset2)

subset3 <- dcast (data = subset2,
                  fill =0,
                  mr_no ~ distype,
                  value.var="val")

# Create an indicator variable to determine
# Both Metabolic and RMSD = 99
# Only Metabolic = 1
# Only RMSD = 2

subset3 <- subset3 [Metabolic == 1 & RMSD == 1, combine := "Metabolic and RMSD"]
subset3 <- subset3 [Metabolic == 1 & RMSD == 0, combine := "Metabolic"]
subset3 <- subset3 [Metabolic == 0 & RMSD == 1, combine := "RMSD"]

all_met_rmsd <- merge (x = subset3,
                        y = all02,
                        by = "mr_no",
                        all.x = TRUE)

all_met_rmsd <- merge (x = discat[, -c("Description" , "date")], with =FALSE),
                       y = all_met_rmsd,
                       all = TRUE,
                       by.x = "Code",
                       by.y = "icd_code")

all_met_rmsd$distype[is.na(all_met_rmsd$distype)] <- "OTHER"
all_met_rmsd <- all_met_rmsd [order(mr_no, studyday, patient_id, newdt, vis, cat_id)]

```

```

# Calculation of first RMSD or Metabolic disease date
minday <- all_met_rmsd[ distype != "OTHER",
                        .(minday = min(studyday)), by =.(mr_no, distype) ]
mindayt <- dcast (data = minday,
                   mr_no ~ paste("minday", distype, sep=""),
                   value.var="minday")
all_met_rmsd <- merge (all_met_rmsd, mindayt, by = "mr_no")

# Calculate the age variable for non-missing dates
all_met_rmsd <- all_met_rmsd [, `:=` ( age = ifelse ( !is.na( anydate(dateofbirth)) ,
                                                       round( (anydate(newdt) -
anydate(dateofbirth) + 1)/365.25, digits = 0 ), NA),
                                         newdt0 = anydate(newdt)), ]

# Add Indian rutus as new variables
# https://www.drikpanchang.com/seasons/season-tropical-timings.html?geoname-id=1277333&year=2010

rutus <- fread("D:/Hospital_data/ProgressSQL/analysis/rutus.csv")
rutus <- rutus [, `:=`(startdt = as.POSIXct( startdate, format="%d-%m-%Y"),
                      enddt = as.POSIXct( enddate, format="%d-%m-%Y"))]

rutus02 <- rutus[ , list(season = season, year = year,
                           newdt0 = anydate( seq(startdt, enddt, by = "day") )), by =
1:nrow(rutus)]

all_met_rmsd <- merge (x = all_met_rmsd,
                       y = rutus02 [, c("newdt0", "year", "season")],
                       by = c("newdt0"),
                       all.x = TRUE)

rm (base01_ip, base01_op, base01_ser, l)

```

```

all_met_rmsd <- all_met_rmsd [, `:=` (baseage = min(age)), by =.(mr_no) ]

#####
# Update the data by re-coded Medicine names
#####
lookup_medicine <- fread("D:/Hospital_data/ProgressSQL/analysis/lookup_medicine.txt",
sep="|")

all_met_rmsd <- merge(x = all_met_rmsd,
                      y = lookup_medicine,
                      all.x = TRUE,
                      by.x = c("medicine_name"),
                      by.y = c("medicine_name"))

fwrite(all, "D:/Hospital_data/ProgressSQL/analysis/01adsl.csv")
fwrite(all_met_rmsd, "D:/Hospital_data/ProgressSQL/analysis/01adsl_met_rmsd.csv")
saveRDS (all_met_rmsd, "D:/Hospital_data/ProgressSQL/analysis/01adsl_met_rmsd.rds")

dis_rutu <- all_met_rmsd [Code != "", .(cnt = uniqueN(mr_no)), by = .(season, Code,
description)] [order(season, -cnt, Code)]
dis_rutu_yr <- all_met_rmsd [Code != "", .(cnt = uniqueN(mr_no)), by = .(year, season,
Code, description)][order(year, season, -cnt, Code)]
dis_rutu_yr02 <- dcast(dis_rutu_yr,
                        season + Code + description ~ paste("yr", year, sep=""),
                        value.var = c("cnt"),
                        fill= " ")

fwrite(dis_rutu, "D:/Hospital_data/ProgressSQL/analysis/dis_rutu.csv")
fwrite(dis_rutu_yr02, "D:/Hospital_data/ProgressSQL/analysis/dis_rutu_yr.csv")

/*=====
*/
/* End of program
 */

```

```
/*=====*/
```

6.5.3 R and SQL programs for other datasets from SQL database: 02other_data.R

This program creates datasets for various CRFs which are not covered in the first program. This program creates 1 csv file per CRF. SQL code is added at the top of the file and then followed by R code

```
#=====
drop table if exists patient_section_details, patient_section_values;
drop table if exists patient_section_details, patient_section_values, base10_other0;

create table patient_section_details as
select mr_no, patient_id, section_id, section_detail_id, section_item_id, item_type
from iaim.patient_section_details
order by mr_no, patient_id;

create table patient_section_values as
select section_detail_id, field_id, option_id, option_remarks
from iaim.patient_section_values
order by section_detail_id;

## Not working
/*
create table base10_other0 as
select patient_section_details.*,
patient_section_values.field_id, patient_section_values.option_id,
patient_section_values.option_remarks
from patient_section_details
full join patient_section_values on
patient_section_details.section_detail_id = patient_section_values.section_detail_id and
patient_section_details.section_item_id = patient_section_values.field_id and
patient_section_details.section_id = patient_section_values.option_id;
```

```

*/
## Working:
create table base10_other11 as
select a.*,
b.field_id, b.option_id, b.option_remarks
from patient_section_details as a, patient_section_values as b where
a.section_detail_id=b.section_detail_id ;

\copy base10_other11 TO 'd:/hospital_data/ProgressSQL/data_chk/base10_other11.csv' CSV
HEADER DELIMITER ',';
\copy iaim.section_master TO 'd:/hospital_data/ProgresSQL/data_chk/section_master.csv'
CSV HEADER DELIMITER ',';
\copy iaim.section_field_options TO
'd:/hospital_data/ProgressSQL/data_chk/section_field_options.csv' CSV HEADER DELIMITER
',';
\copy iaim.section_field_desc TO
'd:/hospital_data/ProgressSQL/data_chk/section_field_desc.csv' CSV HEADER DELIMITER ',';
\copy iaim.patient_consultation_field_values TO
'd:/hospital_data/ProgressSQL/data_chk/patient_consultation_field_values.csv' CSV HEADER
DELIMITER ',';

#####
Check the _orig dataset

create table patient_section_details_orig as
select mr_no, patient_id, section_id, section_detail_id, section_item_id, item_type
from iaim.patient_section_details
order by mr_no, patient_id;

## Working:
create table base10_other11_orig as
select a.*,

```

```

b.field_id, b.option_id, b.option_remarks
from patient_section_details_orig as a, patient_section_values as b where
a.section_detail_id=b.section_detail_id ;

\copy base10_other11_orig TO
'd:/hospital_data/ProgressSQL/data_chk/base10_other11_orig.csv' CSV HEADER DELIMITER ',';

#=====
library(data.table)
library(stringi)
library(stringr)

# Read the data
base01_other <- fread("D:/Hospital_data/ProgressSQL/data_chk/base10_other11.csv")
base01_other02 <- base01_other [nchar(option_remarks)> 0]

# CRF names
section_master <- fread("D:/Hospital_data/ProgressSQL/data_chk/section_master.csv")
section_master <- section_master[, c("section_id", "section_title"), with = FALSE]

base01_other02 <- merge (x = base01_other02,
                         y = section_master,
                         by = "section_id",
                         all.x = TRUE)

# variable names
section_field_options <-
fread("D:/Hospital_data/ProgressSQL/data_chk/section_field_options.csv")

base01_other022 <- merge (x = base01_other02 [ option_id >= 0],
                           y = section_field_options ,

```

```

        by = c("option_id", "field_id"), #by = c("section_id",
"field_id"),
        all.x = TRUE)

# Keep Unique records
#base01_other022 <- unique ( base01_other02 [, c("mr_no", "patient_id", "section_id",
"option_id", "field_id", "option_remarks", "section_title", "display_order",
"option_value"), with =FALSE] )
base01_other022 <- unique ( base01_other022 [, c("mr_no", "patient_id", "section_id",
"field_id", "option_remarks", "section_title", "display_order", "option_value"), with
=FALSE] )

# Sort the data by patient and visits
base01_other022 <- base01_other022 [ order(mr_no, patient_id, section_id, field_id,
display_order) ]

section_field_desc <-
fread("D:/Hospital_data/ProgressSQL/data_chk/section_field_desc.csv")
section_field_desc <- section_field_desc[, c("section_id", "field_id", "display_order",
"field_name", "no_of_lines"), with = FALSE]

base01_other044 <- merge (x = base01_other02 [ option_id < 0],
                           y = section_field_desc,
                           by = c("section_id", "field_id"),
                           all.x = TRUE)
base01_other044 <- unique ( base01_other044 [, c("mr_no", "patient_id", "section_id",
"option_id", "field_id", "option_remarks", "section_title", "display_order",
"field_name", "no_of_lines"), with =FALSE] )

# Sort the data by patient and visits
base01_other044 <- base01_other044 [ order(mr_no, patient_id, section_id, field_id,
display_order) ]
setnames(base01_other044, "field_name", "option_value")

```

```

base01_all <- rbind(base01_other022, base01_other044, fill =TRUE)

#####
# Need to consolidate variable names and combine
# base01_other044
# base01_other022
# Create a counter variable for transposing
#####

# Create a counter variable for transpose
base01_other030 <- base01_all [, subvis := 1:.N, by = .(mr_no, patient_id, section_id,
field_id, option_value)]

fwrite(base01_other030, "D:/Hospital_data/ProgressSQL/analysis/complete_other_data.csv")

#####
# Subset for Metabolic RMSD data
#####
all_met_rmsd <- readRDS("D:/Hospital_data/ProgressSQL/analysis/01adsl_met_rmsd.rds")

subpat <- unique(all_met_rmsd [, c("mr_no", "Metabolic", "RMSD", "combine", "all_vis",
"city_name", "state_name", "dateofbirth",
"country_name",
"death_date")])

vispat <- unique(all_met_rmsd [, c("mr_no", "studyday", "patient_id", "newdt", "vis",
>Type", "Code", "distype", "description",
"all_ip", "all_op")])

# Only keep Metabolic and RMSD patients
base01_met_rmsd <- merge (x = base01_other030,

```

```

y = subpat [,c("mr_no")],
by = c("mr_no"),
all.y = TRUE)

sub <- unique( base01_met_rmsd [, c("section_id", "section_title",
                                    "field_id", "display_order", "option_value")] )
[order(section_id, field_id, display_order, option_value)]
sub <- sub [, varnum:=seq_len(.N), by =.(section_id)]
sub <- sub [, trnvar := paste("sec", str_pad(section_id, 3, side = "left", pad = 0),
                               "_var", str_pad(varnum, 3, side = "left", pad = 0),
                               "_", option_value, sep="")]
base01_met_rmsd <- merge (x = base01_met_rmsd,
                           y = sub,
                           by = c("section_id", "section_title",
                                 "field_id", "display_order", "option_value"),
                           all.x = TRUE)

# Transpose the data as per CRF pages
base01_met_rmsd_trn <- dcast(data = base01_met_rmsd,
                                mr_no + patient_id + subvis ~ trnvar,
                                value.var = c("option_remarks"))

# Add visit information and disease information:
base01_met_rmsd_trn <- merge (x = base01_met_rmsd_trn,
                               y = vispat,
                               by = c("mr_no", "patient_id"),
                               all.x = TRUE)

# Add patient demog + visit + duration information
base01_met_rmsd_trn <- merge (x = base01_met_rmsd_trn,
                               y = subpat,
                               by = c("mr_no"),

```

```

    all.x = TRUE)

# Keep variables by section

df = base01_met_rmsd_trn[, (names(base01_met_rmsd_trn) %in%
                             c("mr_no", "patient_id", "Metabolic", "RMSD", "combine",
                               "subvis",
                               "city_name", "state_name", "dateofbirth", "country_name",
                               "death_date", "Type", "Code", "distype", "description",
                               "studyday", "patient_id", "newdt", "vis", "all_vis",
                               "all_ip", "all_op"))
                           | grepl("^sec004", names(base01_met_rmsd_trn)) ), with =FALSE]

sections <- unique(sub$section_id)
for (ii in sections){

  jj <- str_pad(ii, 3, side = "left", pad = 0)
  kk <- paste0("^sec", jj, sep="")
  print(jj)
  print(kk)

  fwrite(file = paste0("D:/Hospital_data/ProgresSQL/analysis/sec",
                       jj, ".csv"),
         x = base01_met_rmsd_trn [, (names(base01_met_rmsd_trn) %in%
                                         c("mr_no", "patient_id", "Metabolic", "RMSD",
                                           "combine", "subvis", "city_name",
                                           "state_name", "dateofbirth", "country_name",
                                           "death_date", "Type", "Code",
                                           "distype", "description", "studyday",
                                           "patient_id", "newdt", "vis", "all_vis",
                                           "all_ip", "all_op") |
                                         grepl(kk, names(base01_met_rmsd_trn)) ), with
                                         =FALSE]

```

```
)  
}  
  
# dtable <- df[, fwrite(.SD, paste0("./output/"), Name, ".csv"), by = Name]  
#####  
# End of program  
#####
```

6.5.4 Analysis program for Figure 3-1

Refer to the `100_adsl.R` program

6.5.5 Analysis program for Figure 3-2

R program: `03_typesOfassessment.R`

```
library(Hmisc)  
library(data.table)  
library(stringi)  
library(stringr)  
library(sqldf)  
  
all_met_rmsd <- readRDS("D:/Hospital_data/ProgressQL/analysis/01adsl_met_rmsd.rds")  
  
#####  
# Subset for Metabolic RMSD data
```

```

#####
all_met_rmsd <- readRDS("D:/Hospital_data/ProgressQL/analysis/01adsl_met_rmsd.rds")

subpat <- unique(all_met_rmsd [, c("mr_no", "Metabolic", "RMSD", "combine", "all_vis",
"patient_gender", "baseage",
"city_name", "state_name", "dateofbirth",
"country_name",
"death_date")])

vispat <- unique(all_met_rmsd [, c("mr_no", "studyday", "patient_id", "newdt", "vis",
>Type", "Code", "distype", "description",
"all_ip", "all_op")])

#####

# Get records per visit for Treatment / Procedure
# Med start date, end date non missing and
# name non missing
#####

med_ip <- unique( na.omit( all_met_rmsd, cols = c("stdt_IP") ) )

```

```

med_ip <- unique( med_ip [Type == "IP", c("mr_no", "vis", "studyday", "Metabolic",
"RMSD", "combine", "all_vis", "patient_gender", "baseage"), ] )

med_ip <- med_ip [, cat := "Treatment - IP"]

med_op <- unique( na.omit( all_met_rmsd, cols = c("stdt_OP") ) )

med_op <- unique( med_op [Type == "OP", c("mr_no", "vis", "studyday", "Metabolic",
"RMSD", "combine", "all_vis", "patient_gender", "baseage"), ] )

med_op <- med_op [, cat := "Treatment - OP"]

ser <- unique( na.omit( all_met_rmsd, cols = c("serstdt") ) )

ser <- unique( ser [, c("mr_no", "vis", "studyday", "Metabolic", "RMSD", "combine",
"all_vis", "patient_gender", "baseage"), ] )

ser <- ser [, cat := "Treatment - Procedure"]

dis <- unique( all_met_rmsd [Code != " " | description != " ", c("mr_no", "vis",
"studyday", "Metabolic", "RMSD", "combine", "all_vis", "patient_gender", "baseage"), ] )

dis <- dis [, cat := "Disease"]

catall <- rbind(med_ip, med_op, ser, dis, fill = TRUE)

# Read the data

```

```

base01_other <- fread("D:/Hospital_data/ProgressSQL/data_chk/base10_other11.csv")
base01_other02 <- base01_other [nchar(option_remarks) > 0]

# CRF names

section_master <- fread("D:/Hospital_data/ProgressSQL/data_chk/section_master.csv")
section_master <- section_master[, c("section_id", "section_title"), with = FALSE]

base01_other02 <- merge (x = base01_other02,
                        y = section_master,
                        by = "section_id",
                        all.x = TRUE)

# variable names

section_field_options <-
fread("D:/Hospital_data/ProgressSQL/data_chk/section_field_options.csv")

base01_other022 <- merge (x = base01_other02 [ option_id >= 0 ],
                          y = section_field_options ,
                          by = c("option_id", "field_id"), #by = c("section_id",
"field_id"),
                          all.x = TRUE)

```

```

# Keep Unique records

base01_other022 <- unique ( base01_other022 [, c("mr_no", "patient_id", "section_id",
"field_id", "option_remarks", "section_title", "display_order", "option_value"), with
=FALSE] )

# Sort the data by patient and visits

base01_other022 <- base01_other022 [ order(mr_no, patient_id, section_id, field_id,
display_order) ]

section_field_desc <-
fread("D:/Hospital_data/ProgressQL/data_chk/section_field_desc.csv")

section_field_desc <- section_field_desc[, c("section_id", "field_id", "display_order",
"field_name", "no_of_lines"), with = FALSE]

base01_other044 <- merge (x = base01_other02 [ option_id < 0],
                           y = section_field_desc,
                           by = c("section_id", "field_id"),
                           all.x = TRUE)

base01_other044 <- unique ( base01_other044 [, c("mr_no", "patient_id", "section_id",
"option_id", "field_id", "option_remarks", "section_title", "display_order",
"field_name", "no_of_lines"), with =FALSE] )

```

```

# Sort the data by patient and visits

base01_other044 <- base01_other044 [ order(mr_no, patient_id, section_id, field_id,
display_order) ]

setnames(base01_other044, "field_name", "option_value")

base01_all <- rbind(base01_other022, base01_other044, fill =TRUE)

#####
# Need to consolidate variable names and combine

# base01_other044
# base01_other022
# Create a counter variable for transposing
#####

# Create a counter variable for transpose

base01_other030 <- base01_all [, subvis := 1:.N, by = .(mr_no, patient_id, section_id,
field_id, option_value)]


# Only keep Metabolic and RMSD patients

base01_met_rmsd <- merge (x = base01_other030,
                           y = subpat [,c("mr_no")],

```

```

    by = c("mr_no"),
    all.y = TRUE)

sub <- unique( base01_met_rmsd [, c("section_id", "section_title",
                                    "field_id", "display_order", "option_value")] )
[order(section_id, field_id, display_order, option_value)]
sub <- sub [, varnum:=seq_len(.N), by =.(section_id)]
sub <- sub [, trnvar := paste("sec", str_pad(section_id, 3, side = "left", pad = 0),
                               "_var", str_pad(varnum, 3, side = "left", pad = 0),
                               "_", option_value, sep="")]
base01_met_rmsd <- merge (x = base01_met_rmsd,
                           y = sub,
                           by = c("section_id", "section_title",
                                 "field_id", "display_order", "option_value"),
                           all.x = TRUE)

base01_met_rmsd02 <- unique( base01_met_rmsd [option_remarks != " ", c("mr_no",
"option_value", "patient_id", "trnvar")] )

# Add visit information and disease information:

```

```

base01_met_rmsd02 <- merge (x = base01_met_rmsd02,
                               y = unique( vispat [, c("mr_no", "patient_id", "vis",
                               "studyday")] ) ,
                               by = c("mr_no", "patient_id"),
                               all.x = TRUE,
                               allow.cartesian = TRUE)

# Add patient demog + visit + duration information
base01_met_rmsd02 <- merge (x = base01_met_rmsd02,
                               y = subpat,
                               by = c("mr_no"),
                               all.x = TRUE)

base01_met_rmsd02 <- unique( base01_met_rmsd02 )

# variable names
types <- fread("D:/Hospital_data/ProgressQL/analysis/lookup_03types.csv")

base01_met_rmsd02 <- merge (x = base01_met_rmsd02,
                               y = types [, c("trnvar", "cat")],

```

```

      by = c("trnvar"),
      all.x = TRUE)

base01_met_rmsd03 <- unique( base01_met_rmsd02 [ , -c("option_value", "patient_id",
"trnvar" )])

catal102 <- rbind(catal1, base01_met_rmsd03, fill = TRUE)
catal102 <- catal102 [, val :=1]
fwrite(catal102,
      "D:/Hospital_data/ProgressQL/analysis/03_typesOfassessent.csv")
#####
# End of program
#####

```

6.5.6 Analysis program for Figure 3-3

Refer to the 100_adsl.R program

6.5.7 Analysis program for Figure 3-4

Refer to the 100_adsl.R program

6.5.8 Analysis program for Figure 3-5

Refer to the 100_adsl.R program

6.5.9 Analysis program for Figure 3-6

R program: 04_patients_analysis_tableu_adsl.R

```
library(zoo)
```

```

setwd("C:\\\\Users\\\\mahajvi1\\\\Desktop\\\\Desktop - copied on 18August2014\\\\Backup\\\\Ayur
guidelines\\\\FRLHT\\\\01 Hospital data 30July2016\\\\")

# Create Vital sign data from 31st July 2016 version of the data

vitals <- read.csv("Vitals.csv")
vitals <- data.frame ( cbind(vitals, data="vital", type = substr(vitals$Patient.Id, 1, 2)
) )
vitals <- cbind ( data.frame ( subset (vitals, select =c(MR.No., type, data, Age, Gender,
City, Country, Blood.Group, First.Visit.Date) )), visdate = vitals$Vital.Date)

Diagnosis <- read.csv("Diagnosis.csv")
Diagnosis <- data.frame ( cbind(Diagnosis, data="diag", type =
substr(Diagnosis$Patient.Id, 1, 2) ) )
Diagnosis <- cbind ( data.frame ( subset (Diagnosis, select =c(MR.No., type, data, Age,
Gender, City, Country, Blood.Group, First.Visit.Date, Code) )), visdate =
Diagnosis$Admission.Date)

Doctor_consultation <- read.csv("Doctor_consultation.csv")
Doctor_consultation <- data.frame ( cbind(Doctor_consultation, data="Doccon", type =
substr(Doctor_consultation$Patient.Id, 1, 2) ) )

```

```

Doctor_consultation <- cbind ( data.frame ( subset (Doctor_consultation, select =c(MR.No., type, data, Age, Gender, City, Country, Blood.Group, First.Visit.Date) )), visdate = Doctor_consultation$Cons..Aptmt.Date)

Lab <- read.csv("Lab.csv")

Lab <- data.frame ( cbind(Lab, data="Lab", type = substr(Lab$Patient.Id, 1, 2) ) )

Lab <- cbind ( data.frame ( subset (Lab, select =c(MR.No., type, data, Age, Gender, City, Country, Blood.Group, First.Visit.Date) )), visdate = Lab$Conducted.Date)

# Combine all the data into 1

all0 <- rbind (vitals, subset(Diagnosis, select =-c(Code)), Doctor_consultation, Lab)
all01 <- data.frame (unique ( subset(all0, select =c(MR.No., type) ) ))
tmp01op <- data.frame( unique ( subset(all01, select =c(MR.No.), type == "OP")))
tmp01ip <- data.frame( unique ( subset(all01, select =c(MR.No.), type == "IP")))

common <- data.frame ( MR.No.= intersect(tmp01op$MR.No., tmp01ip$MR.No.) )
onlyip <- data.frame ( merge (x = tmp01op, y =tmp01ip, by ="MR.No.", all.y=TRUE) )
onlyop <- data.frame ( merge (x = tmp01ip, y =tmp01op, by ="MR.No.", all.y=TRUE) )

demog02 <- data.frame (unique ( subset (all0, select=-c(data, visdate, First.Visit.Date) ) ) )

```

```

common_demog <- cbind ( data.frame ( merge (x = demog02, y =common, by ="MR.No.",
all.y=TRUE) ), grp="Common")

onlyip_demog <- cbind ( data.frame ( merge (x = demog02, y =onlyip, by ="MR.No.",
all.y=TRUE) ), grp="OnlyIP")

onlyop_demog <- cbind ( data.frame ( merge (x = demog02, y =onlyop, by ="MR.No.",
all.y=TRUE) ), grp="OnlyOP")

all_age02 <- rbind ( common_demog, onlyip_demog, onlyop_demog)
all_age02 <- cbind (all_age02, age2= as.numeric(all_age02$Age) )

rm(list=ls(pattern="vitals"))
#rm(list=ls(pattern="Diagnosis"))
rm(list=ls(pattern="Doctor_"))
rm(list=ls(pattern="Lab"))

tmp02 <- data.frame (cbind (all0,
                               adm = gsub("-", "/", all0$visdate),
                               fdt = gsub("-", "/", all0$First.Visit.Date)
))

tmp02 <- data.frame (cbind (tmp02,

```

```

    adm2 = as.POSIXct(tmp02$adm, format="%d/%m/%Y"),
    fdt2 = as.POSIXct(tmp02$fdt, format="%d/%m/%Y")
  )

tmp03 <- data.frame (cbind (tmp02,
                            visday = difftime(tmp02$adm2, tmp02$fdt2, units="days") + 1,
                            mondt= as.yearmon(tmp02$adm2, format="%Y-%m" )
  )

tmp04 <- data.frame ( unique ( subset (tmp03, select =c (MR.No., First.Visit.Date,
visdate, adm, fdt, data) )) )

# Count the number of visits per patient
tmp05 <- data.frame (table (tmp04$MR.No.))

tmp05 <- data.frame (cbind (tmp05, MR.No. = tmp05$Var1, Novisits = tmp05$Freq))

# Count the number of diagnosis
tmp06 <- droplevels (unique (data.frame ( subset (Diagnosis, Code != "", select =
c(MR.No., Code ) ) )))
tmp07 <- subset (data.frame (table (tmp06$MR.No.)), Freq > 0)
tmp07 <- data.frame (cbind (tmp07, MR.No. = tmp07$Var1, Nodiseases = tmp07$Freq))

```

```

# Put all data into 1 with 1 record per patient

final <- data.frame (merge (x= all_age02, y =tmp05, by = "MR.No.", all=TRUE) )
final02 <- data.frame (merge (x= final, y =tmp07, by = "MR.No.", all=TRUE) )
final03 <- data.frame ( subset (final02, select =-c ( type, age2, Freq.x, Freq.y, Var1.x,
Var1.y) ) )

write.csv(final03, file="04_patient_analysis_tableu_adsl.csv")

# Create a table by one record per patient per date

tmp08 <- data.frame (unique ( subset (tmp03, select=c(MR.No., fdt2) ) ) )
tmp09 <- subset (data.frame (table (tmp08$fdt2)), Freq > 0)
tmp09 <- data.frame (cbind (tmp09, Newpatients = tmp09$Freq))
tmp09 <- data.frame ( subset (tmp09, select =-c (Freq) ) )

# Create 1 record per date for number of patients on a day

tmp10 <- data.frame (unique ( subset (tmp03, select=c(MR.No., adm2) ) ) )
tmp11 <- subset (data.frame (table (tmp10$adm2)), Freq > 0)
tmp11 <- data.frame (cbind (tmp11, Visitpatients = tmp11$Freq))
tmp11 <- data.frame ( subset (tmp11, select =-c (Freq) ) )

```

```

# Create 1 record per date per patient type for first visit date
tmp12 <- data.frame (unique ( subset (tmp03, select=c(MR.No., fdt2, type) ) ) )
tmp13 <- subset (data.frame (table (tmp12$fdt2, tmp12$type)), Freq > 0)
tmp13_tran <- reshape (tmp13,
                        direction="wide",
                        idvar= c("Var1"),
                        timevar="Var2" )

tmp13_tran <- data.frame (cbind (tmp13_tran, newIP = tmp13_tran$Freq.IP, newOP =
tmp13_tran$Freq.OP))

tmp13_tran <- data.frame ( subset (tmp13_tran, select =-c (Freq.IP, Freq.OP) ) )

# Create 1 record per date per patient type for other visit dates
tmp14 <- data.frame (unique ( subset (tmp03, select=c(MR.No., adm2, type) ) ) )
tmp15 <- subset (data.frame (table (tmp14$adm2, tmp14$type)), Freq > 0)
tmp15_tran <- reshape (tmp15,
                        direction="wide",
                        idvar= c("Var1"),
                        timevar="Var2" )

tmp15_tran <- data.frame (cbind (tmp15_tran, visitsIP = tmp15_tran$Freq.IP, visitsOP =
tmp15_tran$Freq.OP))

```

```

tmp15_tran <- data.frame ( subset (tmp15_tran, select ==c (Freq.IP, Freq.OP) ) )

# Create a table by one record per patient per date for determining what measurements
# are done on which dates

tmp16 <- data.frame (unique ( subset (tmp03, select=c(MR.No., adm2, data) ) ) )
tmp17 <- subset (data.frame (table (tmp16$adm2, tmp16$data)), Freq > 0)
tmp17_tran <- reshape (tmp17,
                       direction="wide",
                       idvar= c("Var1"),
                       timevar="Var2" )

finalcal <- data.frame (merge (x= tmp09, y =tmp11, by = "Var1", all=TRUE) )
finalcal02 <- data.frame (merge (x= finalcal, y =tmp13_tran, by = "Var1", all=TRUE) )
finalcal03 <- data.frame (merge (x= finalcal02, y =tmp15_tran, by = "Var1", all=TRUE) )
finalcal04 <- data.frame (merge (x= finalcal03, y =tmp17_tran, by = "Var1", all=TRUE) )
write.csv(finalcal04, file="04_patient_analysis_tableau_calendar.csv")

# Create 1 record per patient per disease with all other variables
# This will help us understand age group as well as other demog factors
# for different diseases

```

```

dis <- droplevels (unique (data.frame ( subset (Diagnosis, Code !="", select = c(MR.No.,
Code ) ) ) )

dis02 <- data.frame (merge (x= dis, y =all_age02, by = "MR.No.", all.x=TRUE) )

write.csv(dis02, file="04_patient_analysis_disease.csv")

# Create 1 record per patient per date per diagnosis
# Print this using the calendar display
# Display this with patient ID as a filter

dis03 <- droplevels (unique (data.frame ( subset (Diagnosis, Code !="", select =
c(MR.No., Code, visdate ) ) ) )

dis04 <- data.frame (merge (x= dis03, y =all_age02, by = "MR.No.", all.x=TRUE) )

write.csv(dis04, file="04_patient_analysis_disease_cal.csv")

#####
# End of program
#####

```

6.5.10 Analysis program for Figure 3-7

Refer to program: 04_patients_analysis_tableu_adsl.R

6.5.11 Analysis program for Figure 3-8

Refer to program: 04_patients_analysis_tableu_adsl.R

6.5.12 Analysis program for Figure 3-9

Refer to program: 04_patients_analysis_tableu_adsl.R

6.5.13 Analysis program for Figure 3-10

Refer to program: 04_patients_analysis_tableau_adsl.R

6.5.14 Analysis program for Figure 3-11

Refer to program: 04_patients_analysis_tableau_adsl.R

6.5.15 Analysis program for Figure 3-12

R program: rmsd_metabolic_all.R

```
#####
## Call all programs
#####

source("C:\\\\Users\\\\Lucky\\\\Documents\\\\Hospital
data\\\\01_31JUL2016\\\\prgm\\\\rmsd_metabolic_subset.R")

source("C:\\\\Users\\\\Lucky\\\\Documents\\\\Hospital
data\\\\01_31JUL2016\\\\prgm\\\\diagnosis_primary.R")

source("C:\\\\Users\\\\Lucky\\\\Documents\\\\Hospital
data\\\\01_31JUL2016\\\\prgm\\\\diagnosis_primary_month.R")

source("C:\\\\Users\\\\Lucky\\\\Documents\\\\Hospital data\\\\01_31JUL2016\\\\prgm\\\\diagnosis.R")

source("C:\\\\Users\\\\Lucky\\\\Documents\\\\Hospital data\\\\01_31JUL2016\\\\prgm\\\\vital_sign.R")

source("C:\\\\Users\\\\Lucky\\\\Documents\\\\Hospital data\\\\01_31JUL2016\\\\prgm\\\\lab.R")
```

```

## Calculate all the common variables from all datasets
## merge them back onto the individual datasets

keep <- c("MRNo", "Age", "AgeIn", "Gender", "City", "Country",
         "Bloodgrp", "data", "type", "visday")

# Combine all datasets
nvisall <- data.table ( rbind (diag2 [, keep, with = FALSE],
                                 vitals2[, keep, with = FALSE],
                                 lab2     [, keep, with = FALSE] [MRNo !=""] ) )

# Add a dummrly variable
nvisall <- nvisall[, cal :=1]

# Unique patient values
n1unq <- unique ( nvisall [, c("MRNo", "Age", "AgeIn", "Gender", "City", "Country"), with
= FALSE] )

# Count distinct visits for each domain based on diag2, vitals2 and lab2:
n1vis <- nvisall[ , .(novis = uniqueN(visday) ), by = .(MRNo, data) ]
n2vis <- dcast(n1vis, MRNo ~ data, value.var = "novis")

```

```

# No of diseases

n1dis <- unique ( diag2 [ , c("MRNo", "noofdis") , with = FALSE] )

# Blood group creation

n1blood <- unique( nvisall [ Bloodgrp != "", c("MRNo", "Bloodgrp") , with =FALSE] )

# OP, IP creation

n1type <- unique (nvisall [ type != "", c("MRNo", "type", "cal") , with =FALSE])
n2type <- dcast(n1type, MRNo ~ type, value.var = "cal")

# Combine the diag2 dataset and discat data and
# determine diseases which are in RMSD and Metabolic categories vs. OTHER categories

subset5 <- merge (x = discat[, -c("Description") , with =FALSE],
                   y = diag2[, -c("Code") , with =FALSE] ,
                   all = TRUE,
                   by.x = "Code",
                   by.y = "Code2")

subset5 <- subset5 [, -c("Age", "AgeIn", "Gender", "City", "Country",

```

```

    "Bloodgrp", "data", "type", "noofdis"), with =FALSE]

# Code non metabolic and non RMSD diseases as OTHER
subset5$distype[is.na(subset5$distype)] <- "OTHER"

# Count number of diseases and freq count for each patient
# ??????????????????????????????????????????????????????????
# ???? Understand why Code2 is not coming out correctly
# ??????????????????????????????????????????????????????????
subset6 <- subset5[, .(cnt = uniqueN(Code),
                      frq = .N), by =.(MRNo, distype)]

# Transpose the data and get in 1 row per patient
subset7 <- dcast(subset6,
                  MRNo ~ distype,
                  value.var = c("cnt", "frq"),
                  fill = 0)

# Combine all variables into 1 dataset ADSL
adsl <- Reduce(function(...) merge(..., all = TRUE, by = "MRNo"),

```

```

list(n1unq, n1dis, n1blood, n2type, n2vis, subset7))

setnames(adsl, "vital", "nvis_vital")
setnames(adsl, "diag", "nvis_diag")
setnames(adsl, "lab", "nvis_lab")

#####
# Create a subsetted data for RMSD and Metabolic diseases
# For analysis create a few additional variables
#####

adsl_sub <- Reduce(function(...) merge(..., all.x = TRUE, by = "MRNo"),
                     list(subset3, adsl))

# Merge this information onto diag2 dataset
diag8 <- Reduce(function(...) merge(..., all.x = TRUE, by = "MRNo"),
                 list(adsl_sub, subset5))

write.csv(diag8, file ="C:\\Users\\Lucky\\Documents\\Hospital
data\\01_31JUL2016\\analysis\\rmsd_met_diag.csv", na=" ")

```

```

# Merge this information onto vitals5 dataset

vitals8 <- Reduce(function(...) merge(..., all.x = TRUE, by = "MRNo"),
                  list(adsl_sub, vitals5))

write.csv(vitals8, file ="C:\\\\Users\\\\Lucky\\\\Documents\\\\Hospital
data\\\\01_31JUL2016\\\\analysis\\\\rmsd_met_vital.csv", na=" ")

# http://stackoverflow.com/questions/21560500/data-table-merge-based-on-date-ranges
# Version 2 of the code

#####
# Create a vertical version of diag_vital
#####

vitals5[, tempday := visday] ## Add a redundant day column to use as the end range
setkey(diag2, MRNo, min, max) ## Set the key for patient IDs ("y" table)

## Find the overlaps, remove the redundant lossDate2 column, and add the inPolicy column:
ans2 <- foverlap(vitals5,
                  diag2,
                  by.x=c("MRNo", "visday", "tempday"))[, `:=`(inPolicy=T, tempday=NULL)]

```

```

## Update rows where the claim was out of policy:
ans2[is.na(min), inPolicy:=F]

## Remove duplicates (such as policyNumber==123 & claimNumber==3),
## and add policies with no claims (policyNumber==125):
setkey(ans2, MRNo, Code2, visday, min) ## order the results
setkey(ans2, MRNo, Code2) ## set the key to identify unique values
ans2 <- rbindlist(list(
  ans2, ## select only the unique values
  diag2[! .(ans2[, unique(MRNo)])] ## policies with no claims
), fill=T)

ans20 <- ans2 [, -c("Age", "AgeIn", "City", "Country", "Bloodgrp",
  "Gender", "noofdis"), with = FALSE]

ans3 <- Reduce(function(...) merge(..., all.y = TRUE, by = "MRNo"),
  list(ans20, ads1_sub))

```

```

write.csv(ans3, file ="C:\\Users\\Lucky\\Documents\\Hospital
data\\01_31JUL2016\\analysis\\rmsd_met_vital_vertical.csv", na=" ")

#####
# Create primary disease data, combination of 1 disease
# considered as primary disease and display all other
# diseases
#####

prim_diag2 <- Reduce(function(...) merge(..., all.y = TRUE, by = "MRNo"),
list(prim_diag, adsl_sub))

write.csv(prim_diag2, file ="C:\\Users\\Lucky\\Documents\\Hospital
data\\01_31JUL2016\\analysis\\rmsd_met_primary_diag.csv", na=" ")

#####
# Create primary disease data, combination of 1 disease
# considered as primary disease and display all other
# diseases
#####

```

```

prim_diag_mon2 <- Reduce(function(...) merge(..., all.y = TRUE, by = "MRNo"),
                           list(prim_diag_mon, adsl_sub))

write.csv(prim_diag_mon2, file ="C:\\\\Users\\\\Lucky\\\\Documents\\\\Hospital
data\\\\01_31JUL2016\\\\analysis\\\\rmsd_met_primary_diag_mon.csv", na=" ")

# Create a lookup table to get the cumulative view of the patients
# Merge this onto individual datasets to create multiple records for patients
# Use vismon variable and create many to many join

dur      <- c(">=1 day", ">=1 month", ">=2 months", ">=3 months", ">=6 months",
              ">=1 year", ">=2 years", ">=3 years", ">=4 years", ">=5 years")

durlwr <- c(0,           1,           2,           3,           6,
           12,          24,          36,          48,          60)

durupr <- c(999,         999,         999,         999,         999,
            999,         999,         999,         999,         999)

ref <- data.table ( cbind.data.frame (durlwr, durupr, dur ) )

```

```

# http://stackoverflow.com/questions/21560500/data-table-merge-based-on-date-ranges
# Version 2 of the code

## The foverlaps function requires both tables to have a start and end range,
# and the "y" table to be keyed
diag8[, tempmon := vismon] ## Add a redundant day column to use as the end range
setkey(ref, durlwr, durupr) ## Set the key for patient IDs ("y" table)

## Find the overlaps, remove the redundant lossDate2 column, and add the inPolicy column:
diag8rpt <- foverlaps(diag8,
                       ref,
                       by.x=c("vismon", "tempmon")) [, `:=` (inPolicy=T, tempmon=NULL) ]

## Update rows where the claim was out of policy:
diag8rpt[is.na(durlwr), inPolicy:=F]

## Remove duplicates (such as policyNumber==123 & claimNumber==3),
## and add policies with no claims (policyNumber==125):
setkey(diag8rpt, MRNo, Code, vismon, durlwr) ## order the results

```

```

setkey(diag8rpt, MRNo, Code, dur) ## set the key to identify unique values
diag8rpt <- rbindlist(list(
  diag8rpt, ## select only the unique values
  diag8[!.(diag8rpt[, unique(MRNo))]] ## policies with no claims
), fill=T)

# Count number of unique patients, with only 1 visit, 2 visits,3 visits, etc.
diag9rpt <- diag8rpt [, unqvisit := uniqueN(dur), by = .(MRNo)] [order(MRNo, durlwr)]
diag10rpt <- diag9rpt [, .(nopat = uniqueN(MRNo)), by = .(unqvisit)] [order(unqvisit)]

# Create a file for
write.csv(diag9rpt, file ="C:\\\\Users\\\\Lucky\\\\Documents\\\\Hospital
data\\\\01_31JUL2016\\\\analysis\\\\rmsd_met_diag_repeat.csv", na=" ")

# Cumulative view on the vital signs data

vitals8[, tempmon := vismon] ## Add a redundant day column to use as the end range
setkey(ref, durlwr, durupr) ## Set the key for patient IDs ("y" table)

## Find the overlaps, remove the redundant lossDate2 column, and add the inPolicy column:

```

```

vitals8rpt <- foverlaps(vitals8 [vismon > 0],
                         ref,
                         by.x=c("vismon", "tempmon")) [, `:=` (inPolicy=T, tempmon=NULL) ]

## Update rows where the claim was out of policy:
vitals8rpt[is.na(durlwr), inPolicy:=F]

## Remove duplicates (such as policyNumber==123 & claimNumber==3),
## and add policies with no claims (policyNumber==125):
setkey(vitals8rpt, MRNo, vitalparam, vismon, durlwr) ## order the results
setkey(vitals8rpt, MRNo, vitalparam, dur) ## set the key to identify unique values
vitals8rpt <- rbindlist(list(
  vitals8rpt, ## select only the unique values
  vitals8[!.(vitals8rpt[, unique(MRNo)))] ## policies with no claims
), fill=T)

# Create a file for vital signs observations repeated for
# cumulative time point

write.csv(vitals8rpt, file ="C:\\\\Users\\\\Lucky\\\\Documents\\\\Hospital
data\\\\01_31JUL2016\\\\analysis\\\\rmsd_met_vital_vertical_repeat.csv", na=" ")

```

```

# Create primary diagnosis and all other diagnosis view by year
# This gives a view about patient having many diseases simultaneously
# along with other diseases

setkeyv (diag8rpt, c("MRNo", "Code", "Description", "dur", "durlwr"))
diag30 <- unique(diag8rpt)

diag40 <- diag30[, `:=` (primarycode = Code,
                         primarydesc = Description,
                         primarydur = dur,
                         primarydurlwr = durlwr),]

diag50 <- diag40[, c("MRNo", "Age", "AgeIn", "Gender", "City", "Country", "Bloodgrp",
                     "Code", "distype", "Description", "dur", "durlwr", "durupr",
                     "Metabolic", "RMSD", "combine"), with =FALSE]

diag60 <- diag40[, c("MRNo", "primarycode", "primarydesc",
                     "primarydur", "primarydurlwr"), with =FALSE]

```

```

# set the ON clause as keys of the tables:
setkey(diag50,MRNo, dur)
setkey(diag60,MRNo, primarydur)

# perform the join
prim_diag_dur_repeat <- data.table( merge(diag50,diag60,
                                             all=TRUE,
                                             allow.cartesian = TRUE) )

# Clean up some space
rm (list = ls( pattern = "lab*") )
rm (list = ls( pattern = "n1*") )

# Create a file for vital signs observations repeated for
# cumulative time point
write.csv(prim_diag_dur, file ="C:\\\\Users\\\\Lucky\\\\Documents\\\\Hospital
data\\\\01_31JUL2016\\\\analysis\\\\rmsd_met_primary_diag_dur_repeat.csv", na=" ")

# Find difference between 2 consecutive visits
# This may give us some idea about the data

```

```
diff <- diag8 [, c("MRNo", "visday"), with =FALSE]
setkey(diag8, MRNo, visday)
diff <- unique(diff) [order (MRNo, visday)]
diff <- diff[,diff:=c(NA,diff(visday)),by=MRNo]
summary(diff$diff)

#####
# End of program
#####
```

6.5.16 Analysis program for Figure 3-13

Refer to program: rmsd_metabolic_all.R

6.5.17 Analysis program for Figure 3-14

Refer to program: rmsd_metabolic_all.R

6.5.18 Analysis program for Figure 3-15

Refer to program: rmsd_metabolic_all.R

6.5.19 Analysis program for Figure 3-16

R program: 085_dis_1st_time_refCal_NodesEdges.R

```
library(data.table)
library(stringi)
library(stringr)
library(sqldf)
```

```

all_met_rmsd <- readRDS("D:/Hospital_data/ProgressQL/analysis/01adsl_met_rmsd.rds")

unqdis <- unique( all_met_rmsd [, c("mr_no", "studyday", "Code", "description")])
unqdis <- unqdis [!Code %in% c("", "")]
unqdis <- unqdis [, mindisday := min(studyday), by = .(mr_no, Code, description)]
unqdis <- unique( unqdis [, c("mr_no", "mindisday", "Code", "description")])

setnames(unqdis, "Code", "refcode")
setnames(unqdis, "description", "refdesc")

#####
# Create this data with min refday for each disease
#####

all_met_rmsd02 <- merge(x = all_met_rmsd,
                         y = unqdis,
                         by = c("mr_no"),
                         allow.cartesian = TRUE)

```

```

all_met_rmsd02 <- all_met_rmsd02 [, c("mr_no", "Code", "description", "combine", "RMSD",
"Metabolic",
                           "newdt0", "Type_med", "Coded_med", "studyday",
"mindisday",
                           "refcode", "refdesc", "patient_gender", "age",
"baseage",
                           "distype", "cdur"), ]

#####
# Calculate reference day for each disease as before and after
# studyday and mindisday
#####

all_met_rmsd02 <- all_met_rmsd02 [, refday := ifelse(studyday >= mindisday,
                                                       studyday - mindisday + 1,
                                                       studyday - mindisday),]

all_met_rmsd02 <- all_met_rmsd02[, refmnyr := ifelse(refday >= 1,
                                                       as.numeric( ceiling (refday /
30.4375) ),
                                                       as.numeric( floor (refday / 30.4375)
) ), ]

```

```

period01 <- fread("D:/Hospital_data/ProgressSQL/analysis/lookup_1st_nodedges.csv")
period02 <- period01[ , list(period = period, periodn = periodn,
                                refmnyr = seq(as.numeric(start), as.numeric(end)) ), by =
1:nrow(period01) ]

all_met_rmsd02 <- merge (x = all_met_rmsd02,
                           y = period02 [, c("refmnyr", "period", "periodn")],
                           by = c("refmnyr"),
                           all.x = TRUE)

#####
# Post process to get day 1 as Day 1
#####
all_met_rmsd02 <- all_met_rmsd02[, period := ifelse(refday == 1, 1, period), ]
all_met_rmsd02 <- all_met_rmsd02[, periodn := ifelse(refday == 1, "Day 1", periodn), ]

saveRDS (all_met_rmsd02, "D:/Hospital_data/ProgressSQL/analysis/all_met_rmsd02.rds")

disease <- unique(all_met_rmsd02 [ , -c("Type_med", "Coded_med"), ])
disease <- disease [ , cat :="Disease"]

```

```

meds <- unique(all_met_rmsd02 [, -c("Code", "description"), ])
meds <- meds [, cat :="Medicine"]
meds <- meds [, Coded_med := paste(Type_med, Coded_med, sep=":"), ]

setnames(meds, "Type_med", "Code")
setnames(meds, "Coded_med", "description")

all <- rbind(disease, meds)

bfraftr <- all [, .(min = min(refday), max = max(refday)), by = .(mr_no, refcode,
refdesc, Code, description) ]

bfraftr <- sqldf("select *,
case
    When min <= 0 and max <= 0 then 'Reported only before'
    When min >= 1 and max >= 1 then 'Reported on or after'
    When min <= 0 and max >= 1 then 'Reported before and after'
end as classification
from braftr")

```

```

all02 <- merge (x = all,
                 y = bfraftr ,
                 by = c("mr_no", "refcode", "refdesc", "Code", "description"),
                 all.x = TRUE)

all02 <- all02 [, -c("min", "max"),]

fwrite(all02,
       "D:/Hospital_data/ProgressSQL/analysis/085_dis_1st_time_refCal_NodesEdges.csv")

saveRDS (all02,
         "D:/Hospital_data/ProgressSQL/analysis/085_dis_1st_time_refCal_NodesEdges.rds")

#####
# Save disease and medicine version of the data
#####

all_met_rmsd02 <- merge (x = all_met_rmsd02,
                           y = bfraftr ,
                           by = c("mr_no", "refcode", "refdesc", "Code", "description"),
                           all.x = TRUE)

all_met_rmsd02 <- all_met_rmsd02 [, -c("min", "max"),]

saveRDS (all_met_rmsd02, "D:/Hospital_data/ProgressSQL/analysis/all_met_rmsd02.rds")

```

```
#####
# End of program
#####
```

6.5.20 Analysis program for Figure 3-17

R program: 060_allopathic_diag.R

```
library(dplyr)
library(data.table)
library(fuzzyjoin)
library(stringr)
library(stringi)
library(stringdist)
library(quanteda)
library(tm)
library(tidyr)
library(sqldf)

#####
# This section creates the allopathic diagnosis as per ICD 10 dictionary
#####
all_met_rmsd <- readRDS("D:/Hospital_data/ProgressQL/analysis/01adsl_met_rmsd.rds")
```

```

all_met_rmsd <- all_met_rmsd [, `:=` (baseage = min(age)), by =.(mr_no)]
all_met_rmsd <- all_met_rmsd [, `:=` (vismon = round( cdur/30.4375, digits = 0))]

# Baseline age

age01 <- unique( all_met_rmsd [, c("mr_no", "baseage", "patient_gender", "cdur")] )

lookup_allopathic_diag <-
fread("D:/Hospital_data/ProgressQL/analysis/lookup_allopathic_diag.txt", sep="|")

chkpat <- function (dname, var, dataout = "unqsec") {
  sec <- readRDS( paste("D:/Hospital_data/ProgressQL/analysis/", noquote(dname) , ".rds",
sep=""))
}

sec011 <- sec [, `:=` (orig = get(var),
                        all_diag = toupper( get( var))), ]

#####
# Replace multiple diseases in 1 row to multiple rows,
# Seperate_rows allows: keeping all other rows as is

```

```

#####
sec011_1 <- separate_rows(sec011, all_diag, sep =",|\r\n|\\?|\\bAND\\b|;" )
#sec011_1 <- sec011_1 [, all_diag := trimws(all_diag), ]
#sec011_1 <- sec011_1 [, dname := paste(var, sep = ""), ]

sec011_1 [, all_diag := trimws(all_diag)]
sec011_1 [, dname := paste(var, sep = "")]

#####
# Create unique row per disease, this will be matched against ICD 10
#####
#unqsec <- unique( sec011_1 [, c("all_diag", "dname"), ] )
tmp <- sec011_1

assign(dataout, tmp, envir=.GlobalEnv)
}

chkpat(dname = "sec011", var= "sec011_var001_Allopathic Diagnosis", dataout = "dsec011")
chkpat(dname = "sec082", var= "sec082_var001_Allopathic Diagnosis", dataout = "dsec082")
chkpat(dname = "sec122", var= "sec122_var001_Allopathic Diagnosis", dataout = "dsec122")

```

```

chkpat(dname = "sec123", var= "sec123_var001_Allopathic Diagnosis", dataout = "dsec123")

dislist <- lapply(ls(pattern="dsec*"), get)
dis_all <- data.table( rbindlist (dislist))

dis_all02 <- merge(x = dis_all,
                     y = lookup_allopathic_diag,
                     all.x = TRUE,
                     allow.cartesian=TRUE,
                     by = c("all_diag", "dname") )

#####
# Subset for coded records
#####
dis_pat <- dis_all02 [ nchar(code01) > 0 ]
dis_pat <- dis_pat[ code01 != c("** Can not be coded") ]

dis_pat02 <- merge (x = dis_pat,
                     y = age01,
                     by = c("mr_no"))

```

```

unqpat <- dis_pat02 [, .(npat = uniqueN (mr_no)), by = .(combine)]
unqpat_gender <- dis_pat02 [, .(npat = uniqueN (mr_no)), by = .(combine, patient_gender)]

chk01 <- unique( dis_pat02 [, c("mr_no", "code01", "text01", "baseage",
                                "patient_gender", "combine", "Metabolic", "RMSD", "cdur",
                                "all_vis")])

chk01 <- chk01 [, high := substr(code01, 1, 3)]

#####
# ICD dictionary
#####

icd10 <- fread("D:/Hospital_data/ProgresSQL/analysis/icd10cm_order_2018.csv", header=
FALSE)

cats <- data.table( expand.grid( cat1 = LETTERS,
                                 cat2 = seq (0, 99) ) )

cats <- cats [, high := paste( cat1, str_pad(cat2, 2, side = "left", pad = 0), sep="") , ]

cats <- sqldf("select *,

```

case

When cat1 == 'A' OR cat1 == 'B' then 'Certain infectious and parasitic diseases'

When (cat1 == 'C' OR (cat1 == 'D' AND cat2 < 50)) then 'Neoplasms'

When (cat1 == 'D' AND cat2 >=50) then 'Diseases of the blood and blood-forming organs and certain disorders involving the immune mechanism'

When (cat1 == 'E') then 'Endocrine, nutritional and metabolic diseases'

When (cat1 == 'F') then 'Mental and behavioural disorders'

When (cat1 == 'G') then 'Diseases of the nervous system'

When (cat1 == 'H' and cat2 <= 59) then 'Diseases of the eye and adnexa'

When (cat1 == 'H' and cat2 > 59) then 'Diseases of the ear and mastoid process'

When (cat1 == 'I') then 'Diseases of the circulatory system'

When (cat1 == 'J') then 'Diseases of the respiratory system'

When (cat1 == 'K') then 'Diseases of the digestive system'

When (cat1 == 'L') then 'Diseases of the skin and subcutaneous tissue'

When (cat1 == 'M') then 'Diseases of the musculoskeletal system and connective tissue'

When (cat1 == 'N') then 'Diseases of the genitourinary system'

When (cat1 == 'O') then 'Pregnancy, childbirth and the puerperium'

When (cat1 == 'P') then 'Certain conditions originating in the perinatal period'

When (cat1 == 'Q') then 'Congenital malformations, deformations and chromosomal abnormalities'

When (cat1 == 'R') then 'Symptoms, signs and abnormal clinical and laboratory findings, not elsewhere classified'

When (cat1 == 'S' OR cat1 == 'T') then 'Injury, poisoning and certain other consequences of external causes'

When (cat1 == 'V' OR cat1 == 'W' OR cat1 == 'X' OR cat1 == 'Y') then 'Injury, poisoning and certain other consequences of external causes'

When (cat1 == 'Z') then 'Factors influencing health status and contact with health services'

When (cat1 == 'U') then 'Codes for special purposes'

end as icd

from cats")

```
#####
# Get the 2nd level terms from ICD dictionary
#####
icd_sub <- icd10 [ v2 %in% unique (chk01$high) ]

#####
# Merge the high level terms and 2nd level terms with the data
#####
```

```

chk02 <- merge (x = chk01,
                 y = cats,
                 all.x = TRUE,
                 by = c("high"))

chk02 <- merge (x = chk02,
                 y = icd_sub [, c("V2", "V5")],
                 all.x = TRUE,
                 by.x = c("high"),
                 by.y = c("V2"))

fwrite(chk02,
       "D:/Hospital_data/ProgresSQL/analysis/060_allopathic_diag.csv")
#####
# End of program
#####

```

6.5.21 Analysis program for Figure 3-18

Refer to R program: 060_allopathic_diag.R

6.5.22 Analysis program for Figure 3-19

Refer to R program: 060_allopathic_diag.R

6.5.23 Analysis program for Figure 3-20

Refer to R program: 060_allelomorphic_diag.R

6.5.24 Analysis program for Figure 3-21

Refer to R program

6.5.25 Analysis program for Figure 3-22

R program: diagnosis_primary.R

```
#####
# Code to generate DIAGNOSIS data
#####
library(data.table)
setwd ("C:\\\\Users\\\\Lucky\\\\Documents\\\\Hospital data\\\\01_31JUL2016\\\\source")

diag <- fread("Diagnosis.csv", check.names = FALSE)
diag2 <- diag[, c(1, 8, 9), with=FALSE ]
setnames(diag2, "MR No.", "MRNo")

# Code ** NOT YET CODED for the missing code values
# Sort the data by patient and day
diag2 <- diag2[, Code2 := ifelse(Code == "", "ZZZ999", Code), ] [order(MRNo, Code2) ]
setkeyv (diag2, c("MRNo", "Code2", "Description"))
diag3 <- unique(diag2)
```

```

diag4 <- diag3[, `:=`(primarycode = Code2,
                     primarydesc = Description),]

diag3 <- diag3[, c(1, 3, 4), with =FALSE]
diag4 <- diag4[, c(1, 5, 6), with =FALSE]

# set the ON clause as keys of the tables:
setkey(diag3,MRNo)
setkey(diag4,MRNo)

# perform the join
prim_diag <- merge(diag3,diag4, all=TRUE, allow.cartesian = TRUE)
#####
# End of program
#####

```

6.5.26 Analysis program for Figure 3-23

Refer to R program: diagnosis_primary.R

6.5.27 Analysis program for Figure 3-24

Refer to R program: diagnosis_primary.R

6.5.28 Analysis program for Figure 3-25

R program: diagnosis_primary_mon.R

```
#####
# Code to generate DIAGNOSIS data
#####

library(data.table)
setwd ("C:\\\\Users\\\\Lucky\\\\Documents\\\\Hospital data\\\\01_31JUL2016\\\\source")

diag <- fread("Diagnosis.csv", check.names = FALSE)
diag2 <- diag[, c(1, 8, 9, 10), with=FALSE ]
setnames(diag2, "MR No.", "MRNo")
setnames(diag2, "Admission Date", "visdate")

# Code ** NOT YET CODED for the missing code values
# Sort the data by patient and day
# Create date variables and find the difference
diag2 <- diag2[, visdate := as.POSIXct( gsub("-", "/", visdate), format="%d/%m/%Y") ]
diag2 <- diag2[, Code2 := ifelse(Code == "", "ZZZ999", Code), ] [order(MRNo, Code2)]
```

```

# Only extract month part
diag2 <- diag2[, month := format(as.Date(visdate), "%m"), ]

setkeyv (diag2, c("MRNo", "Code2", "Description", "month"))

diag3 <- unique(diag2)

diag4 <- diag3[, `:=`(primarycode = Code2,
                     primarydesc = Description,
                     primarymon = month),]

diag5 <- diag4[, c(1, 3, 5, 6), with =FALSE]
diag6 <- diag4[, c(1, 7, 8, 9), with =FALSE]

# set the ON clause as keys of the tables:
setkey(diag5,MRNo, month)
setkey(diag6,MRNo, primarymon)

# perform the join
prim_diag_mon <- merge(diag5,diag6, all=TRUE, allow.cartesian = TRUE)
#####

```

```
# End of program  
#####
```

6.5.29 Analysis program for Figure 3-26

R program: 085_dis_counts_bruce_java.R

```
#####
```

```
# This is used for 085_dis_count_edges_3rd_byPeriod Tableau display
```

```
#####
```

```
library(data.table)
```

```
library(stringi)
```

```
library(stringr)
```

```
library(sqldf)
```

```
library(tidyr)
```

```
library(rjson)
```

```
library(jsonlite)
```

```
library(dplyr)
```

```
#####
```

```
# These 2 are created using 085_dis_1st_time_refCal_NodeEdges.R program
```

```

#####
all_met_rmsd02 <- readRDS ("D:/Hospital_data/ProgressSQL/analysis/all_met_rmsd02.rds")
all_met_rmsd02 <- all_met_rmsd02 [, Coded_med := paste(Type_med, Coded_med, sep=":"),]

all_met_rmsd02 <- all_met_rmsd02 [, Coded_med := str_replace_all(Coded_med, "\\"", "") ,]

chk01 <- all_met_rmsd02 [, .(cnt = uniqueN(mr_no)),
                           by = .(refcode, refdesc, Code, description, Type_med, Coded_med)
] ]

chk01 <- chk01[Code != "" & Coded_med != ""]

chk01 <- chk01 [, `:=` (Code02 = paste(Code, ":", description, "->", Coded_med, sep = ""),
                      name = paste(refcode, refdesc, sep =","),
                      key = paste(Code, description, sep=",") ), ]

med <- unique( chk01 [Coded_med != c("", " "), c("Coded_med"), ] )
setnames(med, "Coded_med", "name")

dis <- unique( chk01 [name != c("", " "), c("name"), ] )
meddis <- rbind(med, dis)

meddis <- meddis [, nrow := .I,]

```

```

#####
# Create a version of data as follows:
# Fixed nodes as relation between
# (1) Period + Reference disease <--> other diseases
# (2) other diseases <--> Medicine
# Use the other diseases section for creating the moving nodes
#####
part01 <- chk01 [, c("name", "key", "Code02", "cnt", "refdesc", "refcode"), ]

part02 <- chk01 [, c("Coded_med", "key", "Code02", "cnt", "refdesc", "refcode"), ]
setnames(part02, "Coded_med", "name")

part03 <- rbind (part01, part02)
part03 <- merge(part03,
                 meddis,
                 by = c("name"),
                 all = TRUE)

part03 <- part03 [, num := .N, by =.(refdesc, key)]
```

```

part03 <- part03 [, maxnum := max(num), by =.(refdesc) ]
part03 <- part03 [, pernum := (num / maxnum) * 100,]

#####
# Create the Json file
#
#[{
#  "name": "addons",
#  "count": 1,
#  "key": "addons",
#  "pages": [
#    {
#      "name": "A year in apps script and my bucket list",
#      "key": "4478459723408930641",
#      "title": "A year in apps script and my bucket list",
#      "url": "http://excelramblings.blogspot.com/2015/01/a-year-in-apps-script-and-my-
#bucket-list.html"
#    }
#  ]
#}
#
# "name" : use key

```

```

# "count" : use num
# "key" : use key
# "pages" :
#   "names" : use name
#   "key" : use nrow
#   "title" : use name
#   "url" : Code02
#####
part04 <- part03 [, frstprt := paste('{"name" :"', key, '", "count" :', pernum, ', "key" :"', key, '",', sep ="" ), ]
part04 <- part04 [, scndprt := paste('{"name" :"', name, '", "key" :', nrow, ', "title" :"', name, '", "url" :"', Code02, '"}', sep = "" ), ]
#####

# Combine the scndprt variable into 1 row per refdesc + key combination
#####
part05 <- part04 [, .(scndprt02 = paste(scndprt, collapse = ",", sep = " " )),
                  by = .(refcode, refdesc, frstprt)]
part05 <- part05 [ order(refcode, refdesc, frstprt) ]
part05 <- part05 [, rowrecal := .I, by = .(refcode, refdesc) ]

```

```

part05 <- part05 [, scndprt03 := paste('"pages": [', scndprt02, "]},", sep=""), ]

chk02 <- part05 [ refcode == "A2.0"]

fwrite(chk02 [ scndprt02 != "...", c("frstp", "scndprt03"), ],
       "D:/Hospital_data/ProgressSQL/analysis/085d3concept.json",
       col.names = FALSE,
       quote = FALSE,
       sep = " ")

chk02 <- part05 [ refcode == "P5.0"]

fwrite(chk02 [ scndprt02 != "...", c("frstp", "scndprt03"), ],
       "D:/Hospital_data/ProgressSQL/analysis/085d3concept_P5_0.json",
       col.names = FALSE,
       quote = FALSE,
       sep = " ")

#####
# End of program
#####

```

```

chk02 <- chk02 [, `:=` (name = paste(period, periodn, refcode, refdesc, sep =","),
                      count = cnt,
                      key = paste(Code, description, sep =","),
                      pages = Coded_med,
                      url = Code02,
                      title = Code02),]

chk03 <- chk02 [, c("name", "count", "key", "pages", "url", "title", "nrow"), ]

write_json(chk03,
           "D:/Hospital_data/ProgressQL/misc/bruce_approach/085d3concept.json")

# Validate Json using https://jsonlint.com/

fwrite(chk01,
       "D:/Hospital_data/ProgressQL/analysis/085_dis_count_edges_3rd_byPeriod_.csv")

chk01 <- all_met_rmsd02 [, .(cnt = uniqueN(mr_no)),
```

```

        by = .(refcode, refdesc, Code, description, Type_med, Coded_med
) ]

chk01 <- chk01[Code != "" & Coded_med != ""]

chk01 <- chk01 [, Code02 := paste(Code, ":", description, "->", Coded_med, sep = "") ,]

chk02 <- chk01 [ refcode == "A2.0"]

fwrite(chk02,
"D:/Hospital_data/ProgressQL/analysis/085_dis_count_edges_3rd_byPeriod_A2_bruce.csv")
#####
# End of program
#####

6.5.30 Analysis program for Figure 3-27
R program: 080_medicine_repeat_prop.R
```

```

library(data.table)
library(stringi)
library(stringr)
library(sqldf)
library(scales)
```

```
all_met_rmsd <- readRDS("D:/Hospital_data/ProgressQL/analysis/01adsl_met_rmsd.rds")
```

```

#substr(cat_id, 1, 3) != "SER"

#c("mr_no", "medicine_name", "studyday", "remarks", "frequency", "duration",
"duration_units", "Coded_med", "Type_med", "quantity", "patient_id", "cat_id") )

#####
# Data related to medicines
#####

meds0 <- unique( all_met_rmsd [medicine_name != " ",
                                c("mr_no", "studyday", "Coded_med", "Type_med")] )

#####
# Get the minimum day (minday) for any medicine and
# Get the minimum day (minmedday) for individual medicine
#####

meds0 <- meds0 [order(mr_no, studyday) ]

meds0 <- meds0 [, minday := min(studyday), by = .(mr_no) ]
meds0 <- meds0 [, minmedday := min(studyday), by = .(mr_no, Type_med, Coded_med) ]

#####

```

```

# Get group (each day of treatment) as a grouping variable
# Get individual sequential rows within each group
#####
time <- unique(all_met_rmsd [, c("mr_no", "studyday")] )
time <- time [order(mr_no, studyday) ]
time <- time [, grpday := 1:.N, by = .(mr_no) ]
time <- time [, grpmaxday := max(grpday), by = .(mr_no) ]

#####
# Merge the grouping variables for further calculations
# Sort the data
#####
meds0 <- merge (x = meds0, y = time, by = c("mr_no", "studyday") )
meds0 <- meds0[order(mr_no, studyday, grpday) ]

#####
# Sort the data to get prescription number for each medicine
# If the prescription number is > 1 then that medicine is given more than once
#
# There are 2 sequence variables: one for day and one for medicine

```

```

#####
cum01 <- meds0 [, presc := 1:.N, by = .(mr_no, Type_med, Coded_med) ]
cum01 <- cum01 [order(mr_no, studyday, minday, Type_med, Coded_med, presc )]
cum01 <- cum01 [, grpall := 1:.N, by = .(mr_no) ]

#####
# If the prescription = 1 and studyday = minmedday then Start
# If prescription > 1 then Old (already given and not a medicine)
# If prescription group number is > 1 then Start
#####
cum01 <- cum01 [, newold := ifelse (studyday == minmedday, "1st dose", ""), ]
cum02 <- cum01 [, newold2 := ifelse(presc > 1 & grpday > 1 & studyday > minmedday &
newold != "1st dose", "Repeat", newold), by =.(mr_no) ]
cum02 <- cum02 [, cat := "Medicine", ]

#####
# Duplicate the medication and see which medications are given multiple times
# This gives a cumulative view of what has been prescribed till a certain
# Visit, how many medicines are 1st time given and how many are Repeated
#####

```

```

cum03 <- cum02 [, (list( cumday = (grpday: grpmaxday) ) ),
  by = .(mr_no, presc, Type_med, Coded_med,
  studyday, grpday, grpmaxday, minmedday, newold2, cat) ]

cum03 <- cum03 [, cumday2 := paste("Till visit", cumday, sep = " "), ]

#####
# Execute similarly for the diseases area
# check if it is easy to combine disease and medicine like 01_Primary_madhumeha
# display
#####
#substr(cat_id, 1, 3) != "SER"
# nchar(Code) > 0

#####
# Data related to diseases
#####

meds0 <- unique( all_met_rmsd [, c("mr_no", "Code", "studyday", "description")] )

```

```

meds0 <- data.table(meds0 [, Code := ifelse (Code == " " | Code == "", "*** Not yet
coded", Code),])

meds0 <- data.table(meds0 [, description:= ifelse (description == "" | description ==" ",
"** Not yet coded", description),])

#####
# Get the minimum day (minday) for any medicine and
# Get the minimum day (minmedday) for individual medicine
#####

meds0 <- meds0 [order(mr_no, studyday, Code, description )]

meds0 <- meds0 [, minday := min(studyday), by = .(mr_no)]
meds0 <- meds0 [, minmedday := min(studyday), by = .(mr_no, Code, description)]

#####
# Merge the grouping variables for further calculations
# Sort the data
#####

meds0 <- merge (x = meds0, y = time, by = c("mr_no", "studyday") )

meds0 <- meds0[order(mr_no, studyday, grpday)]


#####

```

```

# Sort the data to get prescription number for each medicine
# If the prescription number is > 1 then that medicine is given more than once
#
# There are 2 sequence variables: one for day and one for medicine
#####
cum01 <- meds0 [, presc := 1:.N, by = .(mr_no, Code, description)]
cum01 <- cum01 [order(mr_no, studyday, minday, presc )]
cum01 <- cum01 [, grpall := 1:.N, by = .(mr_no) ]

#####
# If the prescription = 1 and studyday = minmedday then Start
# If prescription > 1 then Old (already given and not a medicine)
# If prescription group number is > 1 then Start
#####
cum01 <- cum01 [, newold := ifelse (studyday == minmedday, "1st time disease", "") , ]
cum02dis <- cum01 [, newold2 := ifelse(presc > 1 & grpday > 1 & studyday > minmedday &
newold != "1st time dose", "Repeat", newold), by =.(mr_no) ]
cum02dis <- cum02dis [, cat := "Disease", ]

setnames (cum02dis, "Code", "Type_med")

```

```

setnames (cum02dis, "description", "Coded_med")

#####
# Duplicate the medication and see which medications are given multiple times
# This gives a cumulative view of what has been prescribed till a certain
# Visit, how many medicines are 1st time given and how many are Repeated
#####

cum03dis <- cum02dis [, (list( cumday = (grpday: grpmaxday) ) ),
                      by = .(mr_no, Type_med, presc, Coded_med,
                            studyday, grpday, grpmaxday, minmedday, newold2, cat) ]

cum03dis <- cum03dis [, cumday2 := paste("Till visit", cumday, sep = " ") , ]

#####

# Combine all disease and medicine information
# for individual visits as well as cumulative visit data
#####

cum02all <- rbind (cum02, cum02dis, fill = TRUE)
cum02all <- cum02all[, -c("newold"),]
cum03all <- rbind (cum03, cum03dis, fill = TRUE)

```

```

fwrite(cum02all,
      "D:/Hospital_data/ProgressQL/analysis/080_medicine_dis_repeat_prop.csv")
fwrite(cum03all,
      "D:/Hospital_data/ProgressQL/analysis/080_medicine_dis_repeat_prop_cumulative.csv")

all_met_rmsd0 <- data.table(all_met_rmsd [, Code := ifelse (Code == " " | Code == "", "***  
Not yet coded", Code),])
all_met_rmsd0 <- data.table(all_met_rmsd0 [, description:= ifelse (description == "" |  
description == " ", "** Not yet coded", description),])
keep <- c("mr_no", "studyday", "patient_gender", "baseage", "age", "Code", "description",
         "Coded_med", "Type_med", "combine", "Metabolic", "RMSD", "vis", "season",
         "newdt0", "distype")

all_met_rmsd_unq <- unique( all_met_rmsd0 [, ..keep, ])
all_met_rmsd_unq02 <- merge(x = all_met_rmsd_unq,
                            y = cum02 [, -c("newold", "cat"), ],
                            by = c("mr_no", "studyday", "Coded_med", "Type_med"),
                            all.x = TRUE)

```

```

#####
# Should look at this syntax for these 2 variables
#####
setnames (cum02dis, "Type_med", "Code")
setnames (cum02dis, "Coded_med", "description")

setnames (cum02dis, "presc", "prescdis")
setnames (cum02dis, "newold2", "newold2dis")
setnames (cum02dis, "grpday", "grpdaydis")

all_met_rmsd_unq03 <- merge(x = all_met_rmsd_unq02,
                               y = cum02dis [, -c("newold", "cat", "grpall", "minday",
                               "minmedday", "grpmaxday"), ],
                               by = c("mr_no", "studyday", "Code", "description"),
                               all.x = TRUE)

fwrite(all_met_rmsd_unq03,
      "D:/Hospital_data/ProgressQL/analysis/080_medicine_dis_all_met_rmsd_prop.csv")

```

```

all_met_rmsd_unq04 <- all_met_rmsd_unq03 [grpday > 0, `:=` (cumday = grpmaxday,
                                                    cumday3 = max(studyday),
                                                    cumday2 = paste("Till visit",
grpmaxday, sep = " ") ),
                                                    by = .(mr_no) ]

#####
# Duplicate the medication and see which medications are given multiple times
# This gives a cumulative view of what has been prescribed till a certain
# Visit, how many medicines are 1st time given and how many are Repeated
#####

all_met_rmsd_unq05 <- all_met_rmsd_unq03 [grpday > 0, (list( cumday = (grpday: grpmaxday)
) ),
                                                    by = .(mr_no, presc, prescdis, Type_med,
Coded_med,
                                                    Code, description, baseage, age,
combine, Metabolic, RMSD,
                                                    studyday, grpday, grpmaxday, minmedday,
newold2, newold2dis) ]

all_met_rmsd_unq05 <- all_met_rmsd_unq05 [, cumday2 := paste("Till visit", cumday, sep =
" "), ]

```

```

all_met_rmsd_unq05 <- all_met_rmsd_unq05 [, cumday3 := max(studyday), by = .(mr_no,
cumday2)]



#####
# Count number of 1st and repeat diseases
# for individual patient
#
# Count number of 1st and repeat doses
# for individual patient
#
# Transpose the
#####

a0dis <- all_met_rmsd_unq04 [, .(cntdis = uniqueN(paste(Code, description, sep=" "))),
                                by = .(mr_no, grpday, cumday, cumday2, cumday3, newold2dis)]
a0dis_t <- dcast(data = a0dis,
                  mr_no + grpday + cumday + cumday2 + cumday3 ~ newold2dis,
                  value.var = c("cntdis"),
                  fill = 0)

```

```

setnames(a0dis_t, "Repeat", "Repeatdis")

a0dose <- all_met_rmsd_unq04 [, .(cntdose = uniqueN( paste(Type_med, Coded_med, sep=""))),
                                by = .(mr_no, grpday, cumday, cumday2, cumday3, newold2)]
a0dose_t <- dcast(data = a0dose,
                     mr_no + grpday + cumday + cumday2 + cumday3 ~ newold2,
                     value.var = c("cntdose"),
                     fill = 0)
setnames(a0dose_t, "Repeat", "Repeatdose")

#####
# Count total number of diseases and doses for individual patients
#####

a0distot <- all_met_rmsd_unq05 [, .(totdis = uniqueN( paste(Code, description, sep=""))),
                                    by = .(mr_no, cumday, cumday2, cumday3)]
a0dosetot <- all_met_rmsd_unq05 [, .(totdose = uniqueN( paste(Type_med, Coded_med, sep=""))),
                                    by = .(mr_no, cumday, cumday2, cumday3)]

```

```

a01small <- Reduce(function(...) merge(..., all.y = TRUE, by = c("mr_no", "grpday",
"cumday", "cumday2", "cumday3") ),
                      list(a0dis_t, a0dose_t))

a01cap <- Reduce(function(...) merge(..., all.y = TRUE, by = c("mr_no", "cumday",
"cumday2", "cumday3") ),
                      list(a0distot, a0dosetot))

a01all <- merge(x = a01small [, -c("cumday", "cumday2", "cumday3")], ,
                  y = a01cap,
                  by.x = c("mr_no", "grpday"),
                  by.y = c("mr_no", "cumday"))

a01all <- a01all [, `:=` (percldis = percent(`1st time disease` / totdis),
                           percrepdis = percent(`Repeatdis` / totdis),
                           percldose = percent(`1st dose` / totdose),
                           percrepdose = percent(`Repeatdose` / totdose)) , ]

#####
# Get the diseases and doses collapsed into 1 row
#####

```

```

dis <- unique(all_met_rmsd_unq03 [grpday > 0,
                                     c("mr_no", "grpday", "Code", "description", "distype",
                                       "studyday", "newold2dis"), ])
dis <- dis [, `:=` (disall = paste(distype, Code, sep= ":"),  

                   desall = paste(distype, description, sep= ":"))]

discomb <- dis [grpday > 0,  

                .(discomb = paste(disall, collapse = ";", sep = " " ),  

                  descomb = paste(desall, collapse = ";", sep = " " )),  

                by = .(mr_no, grpday, newold2dis)]
discomb_t <- dcast(data = discomb,  

                     mr_no + grpday ~ newold2dis,  

                     value.var = c("discomb", "descomb"))

dose <- unique(all_met_rmsd_unq03 [grpday > 0,  

                                         c("mr_no", "grpday", "Type_med", "Coded_med",
                                           "studyday", "newold2"), ])
dose <- dose [, doseall := paste(Type_med, Coded_med, sep= ":" )]
doscomb <- dose [grpday > 0,  

                  .(dosecomb = paste(doseall, collapse = ";", sep = " " )),  

                  by = .(mr_no, grpday, newold2)]
```

```

doscomb_t <- dcast(data = doscomb,
                     mr_no + grpday ~ trimws(paste("Combine", newold2, sep="")),
                     value.var = c("dosecomb"))

adsl <- unique( all_met_rmsd_unq03 [grpday >0, c("mr_no", "patient_gender", "grpday",
"season",
"age", "baseage", "combine", "Metabolic",
"RMSD"), ] )

a01all <- Reduce(function(...) merge(..., all.y = TRUE, by = c("mr_no", "grpday") ),
                  list(a01all, discomb_t, doscomb_t))

a01all <- merge(x = a01all,
                 y = adsl,
                 by = c("mr_no", "grpday"))

fwrite(a01all,

"D:/Hospital_data/ProgressQL/analysis/080_medicine_repeat_prop_cumulative_Rcal.csv")
saveRDS (a01all,
"D:/Hospital_data/ProgressQL/analysis/080_medicine_repeat_prop_cumulative_Rcal.rds")

```

```

#####
# Create disease and medicine combination
# by patient
#####

dismed <- all_met_rmsd_unq04 [, .(cntdismed = .N),
                                by = .(mr_no,
                                       Code, description, Type_med, Coded_med) ]

dis100 <- all_met_rmsd_unq04 [, .(cntdis = .N),
                                 by = .(mr_no,
                                       Code, description) ]

med100 <- all_met_rmsd_unq04 [, .(cntmed = .N),
                                 by = .(mr_no,
                                       Type_med, Coded_med) ]

dismed01 <- merge(x = dismed,
                    y = dis100,
                    by = c("mr_no", "Code", "description"),
                    all = TRUE)

dismed02 <- merge(x = dismed01,
                    y = med100,

```

```

by = c("mr_no", "Type_med", "Coded_med"),
all = TRUE)

fwrite(dismed02,
      "D:/Hospital_data/ProgressSQL/analysis/080_medicine_bymr_no_dismed_comb_Rcal.csv")
saveRDS (dismed02,
"D:/Hospital_data/ProgressSQL/analysis/080_medicine_bymr_no_dismed_comb_Rcal.rds")

#####
# Create disease and medicine combination
# by medicine and disease
# count number of combinations and number of
# patients
#####

a_dismed <- all_met_rmsd_unq04 [, .(cntdismed = .N,
                                    unqdismedpat = uniqueN(mr_no)),
                                by = .(Code, description, Type_med, Coded_med)]

a_dis100 <- all_met_rmsd_unq04 [, .(cntdis = .N, unqdispat = uniqueN(mr_no)),
                                 by = .(Code, description)]

```

```

a_med100 <- all_met_rmsd_unq04 [, .(cntmed = .N, unqmedpat = uniqueN(mr_no)) ,
                                by = .(Type_med, Coded_med) ]

a_dismed01 <- merge(x = a_dismed,
                     y = a_dis100,
                     by = c("Code", "description"),
                     all = TRUE)

a_dismed02 <- merge(x = a_dismed01,
                     y = a_med100,
                     by = c("Type_med", "Coded_med"),
                     all = TRUE)

fwrite(a_dismed02,
       "D:/Hospital_data/ProgressSQL/analysis/080_medicine_byoverall_dismed_comb_Rcal.csv")
saveRDS (a_dismed02,
       "D:/Hospital_data/ProgressSQL/analysis/080_medicine_byoverall_dismed_comb.rds")
#####
# End of program
#####

```

6.5.31 Analysis program for Figure 3-28

Refer to R program: 080_medicine_repeat_prop.R

6.5.32 Analysis program for Figure 3-29

Refer to R program: 080_medicine_repeat_prop.R

6.5.33 Analysis program for Figure 3-30

R program: diagnosis.R

```
#####
# Code to generate DIAGNOSIS data
#####

library(data.table)
setwd ("C:\\\\Users\\\\Lucky\\\\Documents\\\\Hospital data\\\\01_31JUL2016\\\\source")

diag <- fread("Diagnosis.csv", check.names = FALSE)

diag <- diag[, `:=` (data = "diag",
                     type = substr(`Patient Id`, 1, 2) ), ]

diag2 <- diag[, c(1, 4, 5, 6, 8, 9, 10, 23, 29, 34, 44, 118, 119), with=FALSE ]
```

```

setnames(diag2, "MR No.", "MRNo")
setnames(diag2, "Admission Date", "visdate")
setnames(diag2, "Blood Group", "Bloodgrp")
setnames(diag2, "Age In", "AgeIn")
setnames(diag2, "First Visit Date", "fvisdate")

#setnames(diag2, "Diagnosis Type", "diagtype")
# Create date variables and find the difference
diag2 <- diag2[, visdate := as.POSIXct( gsub("-", "/", visdate), format="%d/%m/%Y") ]
diag2 <- diag2[, fvisdate := as.POSIXct( gsub("-", "/", fvisdate), format="%d/%m/%Y") ]
diag2 <- diag2[, visday := as.Date(visdate) - as.Date(fvisdate) + 1]
diag2 <- diag2[, vismon := round(visday /30.4375, 1)]
diag2 <- diag2[, Age := ifelse(AgeIn =="M", Age/12, Age), ]
diag2 <- diag2[, AgeIn := ifelse(AgeIn =="M", "Y", AgeIn), ]

# Code ** NOT YET CODED for the missing code values
# Sort the data by patient and day
diag2 <- diag2[, Code2 := ifelse(Code =="", "ZZZ999", Code), ] [order(MRNo, visday,
Code2) ]

```

```

# Create number of diagnosis per patient and a counter for each diagnosis
diag2 <- diag2[ , noofdis := uniqueN(Code2), by = .(MRNo) ]

# Count number of unique diagnosis per patient per day
# Sort the data by patient and day
diag2 <- diag2[ , `:=` (IDX = 1: .N), by = .(MRNo, visdate, visday) ] [order(MRNo,
visday, IDX, Code2) ]

# Get the first date of the diagnosis by each code
diag2 <- diag2 [ , min := min(visday), by = .(MRNo, Code2) ]

# Get the maximum date of the diagnosis (end date for each patient)
# Use this data with vital sign data to get diagnosis attached to vital sign measurements
diag2 <- diag2 [ , max := max(visday), by = MRNo]

setkeyv (diag2, c("MRNo", "Code2", "Description", "min", "max", "type", "IDX",
"noofdis"))

diag2 <- unique(diag2)

write.csv(diag2, file ="C:\\\\Users\\\\mahajvi1\\\\Desktop\\\\adiag.csv", na=" ")

#####

```

```
# End of program  
#####
```

6.5.34 Analysis program for Figure 3-31

R program: 305_medicine_duration_by_dis.R

```
#####
```

```
# Medicine duration
```

```
# Medicine duration by disease
```

```
# Summary statistics should show the most frequently used medicines
```

```
# Indirect relationship building
```

```
# More usage stronger the relationship
```

```
# Less usage may be no relationship or rare usage
```

```
#####
```

```
library(data.table)
```

```
library(tidyverse)
```

```
library(sqldf)
```

```
all_met_rmsd <- readRDS("D:/Hospital_data/ProgressSQL/analysis/01adsl_met_rmsd.rds")
```

```
all_met_rmsd <- all_met_rmsd [, Code := ifelse (Code == " " | Code == "", "** Not yet coded", Code), ]
```

```

all_met_rmsd <- all_met_rmsd [, description:= ifelse (description == "" | description =="",
"** Not yet coded", description),]

all_met_rmsd <- all_met_rmsd [, Code02 := paste(distype, ":", Code, ":", description, sep = ""),
]

all_met_rmsd <- all_met_rmsd [, Med02 := paste(Type_med, ":", Coded_med, sep = "")], ]

med01 <- unique( all_met_rmsd [Med02 != "NA:NA" ,
c("mr_no", "Med02", "Type_med", "Coded_med", "studyday",
"frequency", "duration", "duration_units", "cat_id",
"patient_gender"),])

med01 <- med01 [ duration > 0]

med01 <- med01 [, duration := as.numeric(duration),]

med01 <- med01 [, numdays := case_when( duration_units == "D" ~ duration,
duration_units == "W" ~ duration * 7,
duration_units == "M" ~ duration * 30),]

# Create 1 record per patient per medication with sum of durations

med011 <- med01 [, .(numdays = sum(numdays)), by =.(mr_no, Med02, Type_med, Coded_med,
patient_gender)] 

med02 <- med011 [, .(n=uniqueN(mr_no),
mean = round( mean(numdays, na.rm = TRUE), digits =1),

```

```

median= round( median(numdays, na.rm = TRUE), digits =2),
SD = round( sd(numdays, na.rm = TRUE), digits =2),
min = round( min(numdays, na.rm = TRUE), digits =0),
max = round( max(numdays, na.rm = TRUE), digits =0),
sum = round( sum(numdays, na.rm = TRUE), digits =0)),
by = .(Type_med) ]

med02_med <- med011 [, .(n=uniqueN(mr_no),
mean = round( mean(numdays, na.rm = TRUE), digits =1),
median= round( median(numdays, na.rm = TRUE), digits =2),
SD = round( sd(numdays, na.rm = TRUE), digits =2),
min = round( min(numdays, na.rm = TRUE), digits =0),
max = round( max(numdays, na.rm = TRUE), digits =0),
sum = round( sum(numdays, na.rm = TRUE), digits =0)),
by = .(Type_med, Med02) ]

dismed01 <- unique( all_met_rmsd [Med02 != "NA:NA" ,
c("mr_no", "Med02", "Type_med", "Coded_med",
"studyday",
"Code02",

```

```

        "frequency", "duration", "duration_units", "cat_id",
        "patient_gender"), ])

dismed01 <- dismed01 [ duration > 0]

dismed01 <- dismed01 [, duration := as.numeric(duration),]

dismed01 <- dismed01 [, numdays := case_when( duration_units == "D" ~ duration,
                                              duration_units == "W" ~ duration * 7,
                                              duration_units == "M" ~ duration * 30), ]

# Create 1 record per patient per medication with sum of durations

dismed011 <- dismed01 [, .(numdays = sum(numdays)), by =.(mr_no, Code02, Med02, Type_med,
Coded_med, patient_gender) ]

# Create count of patients with
# totpatdis: total patients having the disease
# totpatmed: total patients having the medicine prescribed

dismed011 <- dismed01 [, totpatdis := uniqueN(mr_no), by =.(Code02) ]
dismed011 <- dismed01 [, totpatmed := uniqueN(mr_no), by =.(Med02) ]
dismed02 <- dismed011 [, .(n=uniqueN(mr_no),
                           mean = round( mean(numdays, na.rm = TRUE), digits =1),

```

```

median= round( median(numdays, na.rm = TRUE), digits =2),
SD = round( sd(numdays, na.rm = TRUE), digits =2),
min = round( min(numdays, na.rm = TRUE), digits =0),
max = round( max(numdays, na.rm = TRUE), digits =0),
sum = round( sum(numdays, na.rm = TRUE), digits =0)),
by = .(Type_med, Code02, totpatdis, totpatmed)

dismed02_med <- dismed011 [ , .(n=uniqueN(mr_no),
mean = round( mean(numdays, na.rm = TRUE), digits =1),
median= round( median(numdays, na.rm = TRUE), digits =2),
SD = round( sd(numdays, na.rm = TRUE), digits =2),
min = round( min(numdays, na.rm = TRUE), digits =0),
max = round( max(numdays, na.rm = TRUE), digits =0),
sum = round( sum(numdays, na.rm = TRUE), digits =0)),
by = .(Code02, totpatdis, Type_med, Med02, totpatmed)]

# n: total number of patients having the disease and medicine prescribed
# So n and totpatmed: calculate the %
dismed02_med <- dismed02_med [ , perc := round ( n / totpatmed * 100, digits = 2),]
#####

```

```
# End of program  
#####
```

6.5.35 Analysis program for Figure 3-32

Refer to R program: 305_medicine_duration_by_dis.R

6.5.36 Analysis program for Figure 3-33

Refer to R program: 305_medicine_duration_by_dis.R

6.5.37 Analysis program for Figure 3-34

Refer to R program: 305_medicine_duration_by_dis.R

6.5.38 Analysis program for Figure 3-35

Refer to R program: 100_adsl.R

6.5.39 Analysis program for Figure 3-36

Refer to R program: 100_adsl.R

6.5.40 Analysis program for Figure 3-37

R program: 085_dis_counts_edges_3rdbyPeriod.R

```
#####  
# This is used for 085_dis_count_edges_3rd_byPeriod Tableau display  
#####
```

```
library(data.table)  
library(stringi)  
library(stringr)
```

```

library(sqldf)
library(tidyr)

#####
# These 2 are created using 085_dis_1st_time_refCal_NodeEdges.R program
#####

all_met_rmsd02 <- readRDS ("D:/Hospital_data/ProgressSQL/analysis/all_met_rmsd02.rds")
all_met_rmsd02 <- all_met_rmsd02 [, Coded_med := paste(Type_med, Coded_med, sep=":"),]

edges <-
readRDS ("D:/Hospital_data/ProgressSQL/analysis/085_dis_1st_time_refCal_NodesEdges.rds")
#####

# Get unique diseases in RMSD and Metabolic
# Keep refcode from these 2 areas 107 unique values
#####

discat <- unique( all_met_rmsd02 [distype %in% c("RMSD", "Metabolic"), c("Code",
"description") , ])

#####

# Get the unique number of reference diseases and medicines

```

```

# Create this for each of the periods before and after 1st
# occurrence of the disease
#####
unqref <- unique( edges [ , c("period", "periodn")] )

dismed <- unique( edges [ , c("cat", "refcode", "refdesc", "Code", "description")])
dismed <- dismed [nchar(Code) > 0] [order(cat, refcode, refdesc, Code, description)]
dismed <- dismed [, `:=` (npoints = 1:N, tot = .N), by = .(cat, refcode, refdesc)]
dismed <- dismed [, `:=` (radius = ifelse (cat == "Disease", 20, 40),
                        angle = 360 / tot), ]
dismed <- dismed [ , cumulative := cumsum(angle), by = .(cat, refcode, refdesc) ]

#####
# Function for the degrees and radian conversion
#####
deg2rad <- function(deg) { (deg * pi) / (180) }

dismed <- dismed [ , radian := deg2rad(cumulative), ]
dismed <- dismed [, `:=` (xaxis = cos(radian)*radius,
                         yaxis = sin(radian)*radius), ]

```

```

#dismed <- dismed [, Code02 := paste(Code, ":", description), ]
#dismed <- dismed [, cnt := 0,]

#####
# create a complete dataset
# this is to ensure, circle is displayed all the time
# Combine with the individual period for replication
#####

dismed_all <- crossing(unqref, dismed)

chk01 <- all_met_rmsd02 [, .(cnt = uniqueN(mr_no)),
                           by = .(period, periodn, refcode, refdesc, Code, description,
Type_med, Coded_med )]
chk01 <- chk01[Code != "" & Coded_med != ""]
chk01 <- chk01 [, Code02 := paste(Code, ":", description, "->", Coded_med, sep = "") ,]

# Merge the x and y coordiantes

chk02dis <- unique(chk01 [, c("period", "periodn", "refcode", "refdesc", "Code",
"description", "cnt", "Code02")] )

```

```

chk02dis <- chk02dis [, cat := "Disease"]

chk02med <- unique(chk01 [, c("period", "periodn", "refcode", "refdesc", "Type_med",
"coded_med", "cnt", "Code02")])

setnames (chk02med, "Type_med", "Code")
setnames (chk02med, "coded_med", "description")
chk02med <- chk02med [, cat := "Medicine"]

chk02all <- rbind(chk02dis, chk02med)
chk02all <- chk02all [nchar(Code) > 0 & nchar(description) > 0]

path01 <- merge (x = chk02all,
                  y = dismed_all,
                  by = c("cat", "period", "periodn", "refcode", "refdesc", "Code",
"Description"),
                  all = TRUE)

path01 <- path01 [, `:=` (cat = "DiseaseMedicine", Code = Code02),]
path01 <- path01 [, c("TabCode", "TabMed") := tstrsplit(Code, "->", fixed = TRUE),]

chk03all <- rbind(path01, dismed_all, fill = TRUE)
chk04all <- chk03all [ refcode %in% discat$Code]

```

```
fwrite(chk04all,  
      "D:/Hospital_data/ProgressSQL/analysis/085_dis_count_edges_3rd_byPeriod.csv")  
#####
```

6.5.41 Analysis program for Figure 3-38

Refer to R program: 085_dis_counts_edges_3rdbyPeriod.R

6.5.42 Analysis program for Figure 3-39

R program: 086time_dis_patterns_combinations_gender_Macro.R

```
#####  
# 086time_dis_patterns_combinations_gender_Macro.R  
#####  
  
library(tidyverse)  
library(tidytext)  
#library(stringr)  
library(stringi)  
library(data.table)  
library(stringdist)  
library(scales)
```

```

# https://stackoverflow.com/questions/43706729/expand-dates-in-data-table
dis <- fread("D:/Hospital_data/ProgressSQL/analysis/discategory.csv")
setnames (dis, "Code", "refcode")

all_met_rmsd <- readRDS ("D:/Hospital_data/ProgressSQL/analysis/all_met_rmsd02.rds")

#####
# Find patients with only the disease
# same as reference disease
# 1 = patients with only disease
# 99 = patients with more than 1 disease in
# a reference disease category
#####

addmr <- unique( all_met_rmsd [!Code %in% c(" ", ""), c("mr_no", "refcode", "Code",
"distype"),])
addmr <- addmr [, cnt := uniqueN(refcode), by = .(mr_no)]
addmr <- addmr [, dis := ifelse(refcode == Code, 1, 0),]
addmr <- addmr [, calc := ifelse(cnt == 1 & dis == 1, 1, 99),]

```

```

addmr02 <- addmr [, .(cntr = uniqueN(mr_no)), by = .(distype, refcode, Code, calc)]
addmr03 <- addmr [, .(cntot = uniqueN(mr_no)), by = .(refcode)]
addmr04 <- merge(addmr02, addmr03, by = c("refcode"))
addmr04 <- addmr04 [, perc := percent(cntr / cntot),]
addmr05 <- addmr04 [ refcode == Code]
addmr06 <- merge (addmr05, dis, by = c("refcode"), all.y = TRUE)

unq <- unique(addmr06 [cntot > 5, c("refcode"),])
unqdis <- unique(unq$refcode)

count <- 1

for ( dis in unqdis[1:uniqueN(unqdis)])
{ print (dis)
  print (count)

  a2 <- all_met_rmsd [ !Code %in% c("", " ", dis) & refcode == dis]
  a2 <- a2 [, Code := paste(period, Code, sep="_"),]

```

```

#a2med <- a2 [, description := paste(Type_med, Coded_med), ]
#a2med <- a2med [ order(description) ]
#a2med <- a2med [, Code := paste("M", str_pad(.N, width =4, pad="0"), sep =""), by =
.(description) ]

#a2all <- rbind(a2 [, c("mr_no", "studyday", "refday", "Code", "description",
"refcode", "refdesc", "patient_gender")],
#                  a2med [, c("mr_no", "studyday", "refday", "Code", "description",
"refcode", "refdesc", "patient_gender")] )

# Change a2 to a2all
dis <- unique(a2[, c("mr_no", "studyday", "refday", "Code", "description", "refcode",
"refdesc", "patient_gender")])

dis <- dis [, `:=` (refday2 = ifelse(refday >=1, "After", "Before"),
                   Code = str_replace_all (Code, " ", ""),
                   description = str_replace_all(description, " ", "")),]

dis <- dis [ order(mr_no, studyday, Code, refcode, refdesc) ]

dis <- dis [, `:=` (alldis = uniqueN(Code),
                   nrow = seq_len(.N),
                   nrowend = seq_len(.N) + 4,
                   totrow = .N), by = .(mr_no, refcode, refdesc) ]

```

```

dis <- dis [, `:=` (alldisbрафtr = uniqueN(Code),
                    nrowbрафtr = seq_len(.N) ), by = .(mr_no, refcode, refdesc,
refday2, patient_gender) ]

dis <- dis [, `:=` (total = uniqueN(mr_no) ), by = .(refcode, refdesc, refday2,
patient_gender) ]

dis <- dis [, `:=` (allcapn = uniqueN(mr_no) ), by = .(refcode, refdesc,
patient_gender) ]

dis02 <- dis [, .(combdis = paste(unique(Code), collapse = ",",
sep = " " ),
                combdesc = paste(unique(description), collapse = ",",
sep = " " )),
by = .(mr_no, refcode, refdesc, refday2, patient_gender, alldis, totrow,
total, allcapn) ]

unq01comb <- unique( dis02 [, c("mr_no", "refcode", "refdesc", "alldis",
"refday2", "patient_gender",
"totrow", "combdis", "combdesc", "total", "allcapn"),
])

unq01comb <- unq01comb [, x := 1, ]

# create a copy
unq02comb <- copy(unq01comb)
setnames(unq02comb, "mr_no", "mr_no2")

```

```

setnames(unq02comb, "combdis", "combdis2")

unq01comb <- unq01comb [, combdis := str_replace_all(combdis, ",", "|"), ]

# Merge the datasets on x to get all the combinations

unq03comb <- merge(x = unq01comb,
                     y = unq02comb [, -c("refcode", "refdesc", "totrow", "alldis",
                     "total", "allcapn", "combdesc"), ],
                     by = c("x", "refday2", "patient_gender"),
                     allow.cartesian = TRUE)

#####
# Using str_count function to count the common diseases
# Create tempdis and tempdis2
#
# Consider mr_no as the reference patient
# tempdis: should be lookup
# a: common in both the strings
# b: only present in reference patient (mr_no)

```

```

# c: only present in other patient (mr_no2)
# d: complete absence -- not sure how to calculate this
#####
##### unq03comb <- unq03comb [, `:=` (tempdis = str_replace_all(combdis, ",", "|"),
#                                     tempdis2 = str_replace_all(combdis2, ",", "|))), ]
#####

unq03comb <- unq03comb [, `:=` (cntdis = str_count(tempdis, "\\|") + 1,
#                               cntdis2 = str_count(tempdis2, "\\|") + 1), ]

unq03comb <- unq03comb[, `:=` (a = str_count(combdis2, tempdis)),]

unq03comb <- unq03comb[, `:=` (b = cntdis - a,
#                               c = cntdis2 - a),]

unq03comb <- unq03comb[, `:=` (a01jac = (a / (a + b + c)),
#                               a02dice = (2 * a / (2 * a + b + c) ),
#                               a03CZEKANOWSKI = (2 * a / (2 * a + b + c) ),
#                               a04jac3w = (3 * a / (3 * a + b + c) ),
#                               a05nei_li = (2 * a / (a + b + a + c) ),]

```

```

a06sokalsneath1 = (a / (a + 2 * b + 2 * c)) ,]

unq03comb <- unq03comb [ mr_no != mr_no2]

maxscr <- unq03comb[, .(maxscr = max(a01jac) ), by = .(mr_no, refcode, total, allcapn,
totrow, alldis, refday2, patient_gender, combdis, combdesc) ]

maxscr_t <- dcast (data = maxscr,
                     mr_no + patient_gender + refcode + totrow + alldis ~ refday2,
                     value.var = c("maxscr", "combdis", "combdesc"))

maxscr02 <- maxscr [, .(scr = uniqueN(mr_no)), by = .(refcode, total, allcapn, refday2,
patient_gender, cut(maxscr,
                     seq(0, 1, .25),

include.lowest = TRUE,
                     ordered_result = TRUE))]

maxscr02_t <- dcast(data = maxscr02,
                     refcode + patient_gender + allcapn + cut ~ refday2,
                     value.var = c("scr", "total"))

```

```

maxscr03 <- maxscr [, .(scr = uniqueN(mr_no)), by = .(refcode, total, allcapn, maxscr,
combdis, combdesc, refday2, patient_gender)]

maxscr03_t <- dcast(data = maxscr03,
                     refcode + patient_gender + allcapn + combdis + combdesc + maxscr ~
refday2,
                     value.var = c("scr", "total"))

maxscr04_t <- unq03comb [, .(scr = .N), by = .(mr_no, refcode, total, allcapn, refday2,
patient_gender, cut(a01jac,
                     seq(0, 1, .25),
                     include.lowest = TRUE,
                     ordered_result = TRUE))]

maxscr04_t <- maxscr04_t [, numrow := .N, by = . (mr_no, refcode, refday2,
patient_gender)]


totscr <- unq03comb [, .( rowcnt = .N), by = .(refcode, total, allcapn, refday2,
patient_gender, cut(a01jac,
                     seq(0, 1, .25),
                     include.lowest = TRUE,

```

```

ordered_result = TRUE) )]

totscr02 <- unq03comb [, .(totn = .N), by = .(refcode, refday2, patient_gender, total,
allcapn )]

totscr02 <- merge (totscr, totscr02, by = c("refcode", "refday2", "patient_gender",
"total", "allcapn"))

totscr02 <- totscr02 [, perc := percent( rowcnt / totn),]

totscr02_t <- dcast(data = totscr02,
                      refcode + patient_gender + allcapn + cut ~ refday2,
                      value.var = c("perc", "totn", "rowcnt", "total"))

assign ( paste("D01maxscr_t", count, sep="") , maxscr_t)
assign ( paste("D02maxscr02_t", count, sep="") , maxscr02_t)
assign ( paste("D03maxscr03_t", count, sep="") , maxscr03_t)
assign ( paste("D03maxscr04_t", count, sep="") , maxscr04_t)
assign ( paste("t02totscr02_t", count, sep="") , totscr02_t)

count = count + 1

}

```

```

allD01maxscr_t <- rbindlist(mget(ls(pattern = "D01maxscr_t*")), fill = TRUE)
allD02maxscr02_t <- rbindlist(mget(ls(pattern = "D02maxscr02_t*")), fill = TRUE)
allD03maxscr03_t <- rbindlist(mget(ls(pattern = "D03maxscr03_t*")), fill = TRUE)
allD03maxscr04_t <- rbindlist(mget(ls(pattern = "D03maxscr04_t*")), fill = TRUE)

allt02maxscr02_t <- rbindlist(mget(ls(pattern = "t02totscr02_t*")), fill = TRUE)

rm(list = ls( pattern='^D01maxscr_t*'))
rm(list = ls( pattern='^D02maxscr02_t*'))
rm(list = ls( pattern='^D03maxscr03_t*'))
rm(list = ls( pattern='^D03maxscr04_t*'))
rm(list = ls( pattern='^t02totscr02_t*'))

fwrite(allD01maxscr_t, "D:/Hospital_data/ProgressQL/analysis/086time_dis_indPat_max.csv")
fwrite(allD02maxscr02_t,
"D:/Hospital_data/ProgressQL/analysis/086time_dis_refcode_max.csv")
fwrite(allD03maxscr03_t,
"D:/Hospital_data/ProgressQL/analysis/086time_dis_indtrajectory.csv")
fwrite(allD03maxscr04_t,
"D:/Hospital_data/ProgressQL/analysis/086time_dis_indPat_freqcat.csv")

```

```
fwrite(allt02maxscr02_t,
"D:/Hospital_data/ProgressQL/analysis/086time_dis_refcode_allfreq_max.csv")
#####
# End of program
#####
```

6.5.43 Analysis program for Figure 3-40

R program: 086_med_patterns_combinations.R

```
#####
# 086_med_patterns_combinations
#####

library(tidyverse)
library(tidytext)
library(stringr)
library(stringi)
library(data.table)
library(stringdist)

all_met_rmsd <- readRDS ("D:/Hospital_data/ProgressQL/analysis/all_met_rmsd02.rds")
a2 <- all_met_rmsd [ refcode == "A2.0" & Coded_med != " "]
```

```

a2 <- a2 [, description := paste(Type_med, Coded_med), ]
a2 <- a2 [ order(description) ]
a2 <- a2 [, Code := paste("M", str_pad(.N, width =4, pad="0"), sep =""), by =
.(description) ]

dis <- unique(a2[!Code %in% c("", " ", "A2.0") & refcode == "A2.0", c("mr_no",
"studyday", "refday", "Code", "description", "refcode", "refdesc")])
dis <- dis [, `:=` (refday2 = ifelse(refday >=1, "After", "Before"),
                  Code = str_replace_all (Code, " ", ""),
                  description = str_replace_all(description, " ", "")),]
dis <- dis [ order(mr_no, studyday, Code, refcode, refdesc) ]
dis <- dis [, `:=` (alldis = uniqueN(Code),
                  nrow = seq_len(.N),
                  nrowend = seq_len(.N) + 4,
                  totrow = .N), by = .(mr_no, refcode, refdesc)]
dis <- dis [, `:=` (alldisbрафtr = uniqueN(Code),
                  nrowbрафtr = seq_len(.N) ), by = .(mr_no, refcode, refdesc,
refday2) ]

dis02 <- dis [, .(combdis = paste(unique(Code), collapse = ",",
sep = " " )), by = .(mr_no, refcode, refdesc, refday2, alldis, totrow) ]

```

```

unq01comb <- unique( dis02 [, c("mr_no", "refcode", "refdesc", "alldis", "refday2",
                           "totrow", "combdis"), ])

unq01comb <- unq01comb [, x := 1, ]

# create a copy
unq02comb <- copy(unq01comb)
setnames(unq02comb, "mr_no", "mr_no2")
setnames(unq02comb, "combdis", "combdis2")

unq01comb <- unq01comb [, combdis := str_replace_all(combdis, ", ", "|"), ]

# Merge the datasets on x to get all the combinations

unq03comb <- merge(x = unq01comb,
                     y = unq02comb [, -c("refcode", "refdesc", "totrow", "alldis"), ],
                     by = c("x", "refday2"),
                     allow.cartesian = TRUE)

#####

```

```

# Using str_count function to count the common diseases
# Create tempdis and tempdis2
#
# Consider mr_no as the reference patient
# tempdis: should be lookup
# a: common in both the strings
# b: only present in reference patient (mr_no)
# c: only present in other patient (mr_no2)
# d: complete absence -- not sure how to calculate this
#####
unq03comb <- unq03comb [, `:=` (tempdis = str_replace_all(combdis, ",", "|"),
                                tempdis2 = str_replace_all(combdis2, ",", "|")), ]
unq03comb <- unq03comb [, `:=` (cntdis = str_count(tempdis, "\\|") + 1,
                                cntdis2 = str_count(tempdis2, "\\|") + 1), ]
unq03comb <- unq03comb[, `:=` (a = str_count(combdis2, tempdis)),]

unq03comb <- unq03comb [, `:=` (b = cntdis - a,
                                c = cntdis2 - a), ]

```

```

unq03comb <- unq03comb[, a01jac := (a / (a + b + c)),]

distraj <- unique(unq03comb [tempdis != tempdis2 , c("tempdis", "tempdis2", "a01jac",
"refday2"),])

distraj01 <- distradj [, .(distradj = .N), by = .(refday2, a01jac)]

common <- unq03comb [, .(cmn = (.N / nrow(unq03comb)) * 100), by = .(a)]

#####
# End of program
#####

```

6.5.44 Analysis program for Figure 3-41

R program: 300_radar_plot_tableau.R

```

# Tableau help

# Use https://www.tableau.com/about/blog/2015/7/use-radar-charts-compare-dimensions-over-
several-metrics-41592

library(data.table)
library(tidyverse)
library(sqldf)

# Install the ggradar library
#devtools::install_github("ricardo-bion/ggradar", dependencies = TRUE)

```

```

library(ggradar)

all_met_rmsd <- readRDS("D:/Hospital_data/ProgressQL/analysis/01adsl_met_rmsd.rds")
all_met_rmsd <- all_met_rmsd [, Code := ifelse (Code == " " | Code == "", "** Not yet
coded", Code), ]
all_met_rmsd <- all_met_rmsd [, description:= ifelse (description == "" | description =="",
"** Not yet coded", description), ]
all_met_rmsd <- all_met_rmsd [, Code02 := paste(distype, ":", Code, ":" , description, sep
=""), ]
all_met_rmsd <- all_met_rmsd [, Med02 := paste(Type_med, ":", Coded_med, sep =""), ]

all_met_rmsd02 <- readRDS("D:/Hospital_data/ProgressQL/analysis/all_met_rmsd02.rds")
all_met_rmsd02 <- all_met_rmsd02 [, Code := ifelse (Code == " " | Code == "", "** Not yet
coded", Code), ]
all_met_rmsd02 <- all_met_rmsd02 [, description:= ifelse (description == "" | description ==
" ", "** Not yet coded", description), ]
all_met_rmsd02 <- all_met_rmsd02 [, Code02 := paste(distype, ":", Code, ":" , description, sep
=""), ]
all_met_rmsd02 <- all_met_rmsd02 [, Med02 := paste(Type_med, ":", Coded_med, sep =""), ]

# Disease:
# (1) Distinct number of patients

```

```

t10 <- all_met_rmsd02 [, .(cal10 = uniqueN(mr_no)), by =.(refcode, refdesc) ]
t10 <- t10 [, perc10 := as.numeric( ntile(cal10, 100) ), ]

# (2) Number of times a disease is reported

totdis <- unique( all_met_rmsd [ , c("Code", "description", "patient_id"), ] )

t20 <- totdis [, .(cal20 = .N), by =.(Code, description) ]
t20 <- t20 [, perc20 := as.numeric( ntile(cal20, 100) ), ]

# (3) Number for a specific disease (chronological number of disease reported by a patient)

# Calculate median number of disease reported for each disease

# Then calculate the percentile for each disease

numdis <- unique( all_met_rmsd [ , c("mr_no", "Code", "description", "studyday"), ] )
numdis <- numdis [ order(mr_no, studyday, Code) ]
numdis <- numdis [ , `:=`( COUNT = .N , ndis = 1:.N ),
                    by = .(mr_no, Code, description) ]

t30 <- numdis [, .(cal30 = median(ndis)), by =.(Code, description) ]

```

```

t30 <- t30 [, perc30 := as.numeric( ntile(cal30, 100) ), ]

# (4) Number of diseases before and after the specific disease
banumdis <- unique( all_met_rmsd02 [, c("mr_no", "Code", "description", "period",
"periodn", "refcode", "refdesc"),])
banumdis <- banumdis [, classification := ifelse (period >=1 , "After", "Before"), ]
banumdis <- banumdis [ order(mr_no, refcode, refdesc, classification) ]
banumdis <- banumdis [ , `:=`( ndis = uniqueN(Code) ),
                           by = .(mr_no, refcode, refdesc, classification) ]

t40 <- banumdis [ , .(cal40 = median(ndis)), by =.(refcode, refdesc, classification)]
t40 <- t40 [, perc40 := as.numeric( ntile(cal40, 100) ), ]
t40_trn <- dcast(data = t40,
                   refcode + refdesc ~ classification,
                   value.var = c("cal40", "perc40"),
                   fill ="0")

# (5) Number of treatments before and after the specific disease
banummed <- unique( all_met_rmsd02 [, c("mr_no", "Med02", "period", "periodn", "refcode",
"refdesc"),])
banummed <- banummed [, classification := ifelse (period >=1 , "After", "Before"), ]

```

```

banummed <- banummed [ order(mr_no, refcode, refdesc, classification) ]
banummed <- banummed [ , `:=` ( nmed = uniqueN(Med02)) ,
                           by = .(mr_no, refcode, refdesc, classification) ]

t50 <- banummed [ , .(cal50 = median(nmed)), by =.(refcode, refdesc, classification) ]
t50 <- t50 [ , perc50 := as.numeric( ntile(cal50, 100) ), ]
t50_trn <- dcast(data = t50,
                   refcode + refdesc ~ classification,
                   value.var = c("cal50", "perc50"),
                   fill ="0")

#setnames(t10, "Code", "refcode")
setnames(t20, "Code", "refcode")
setnames(t30, "Code", "refcode")
#setnames(t10, "description", "refdesc")
setnames(t20, "description", "refdesc")
setnames(t30, "description", "refdesc")

all01 <- Reduce(function(...) merge(..., all.x = TRUE, by = c("refcode", "refdesc")),
                  list(t40_trn, t10, t20, t30, t50_trn))

```

```

all01 <- all01 [ refcode != "sandhigata vaa"]

all01_trn <- melt (data = all01,
                     id.vars = c("refcode", "refdesc"),
                     measure.vars = c("perc10", "perc20", "perc30",
                                     "perc40_After", "perc40_Before",
                                     "perc50_After", "perc50_Before") )

all01_trn <- as.data.table ( sqldf("select *,
                                         case
                                             When variable == 'perc10' then '1 Unique patients'
                                             when variable == 'perc20' then '2 no of times disease
reported'
                                             when variable == 'perc30' then '3 disease chronology'
                                             when variable == 'perc40_After' then '4 no of diseases
before'
                                             when variable == 'perc40_Before' then '5 no of
diseases after'
                                             when variable == 'perc50_After' then '6 no of
medicines before'
                                         end
                                         from all01_trn")
)

```

```

when variable == 'perc50_Before' then '7 no of
medicines after'

end as category
from all01_trn"))
}

# Possible background creation within Tableau
all01_trn <- all01_trn [, valuedumm := 100,]

# Used for the tableau visual
fwrite(all01_trn, file="D:/Hospital_data/ProgresSQL/analysis/300_radar_plot.csv")
#####
# End of program
#####

```

6.5.45 Analysis program for Figure 3-42

R program: 06_d3tree_diagram.R

```

#####
# This version is for m / f
# Use 04dis_gender_csv folder
#####

all_met_rmsd <- readRDS("D:/Hospital_data/ProgresSQL/analysis/01adsl_met_rmsd.rds")
```

```

all_met_rmsd <- all_met_rmsd [, Code := str_replace_all(Code, "\\.\\.", "_")]
cnt<- unique( all_met_rmsd [patient_gender != "" & Code != "", 
                           c("mr_no", "studyday", "Code", "description", "distype",
                             "patient_gender"), ])
cnt <- cnt [, `:=` (mnth = round( studyday /30.25, digits = 0),
                     description = paste("[", trimws(distype), ":", trimws(description),
                     "]", sep = "")),
                     Code = paste("[", trimws(Code), "]", sep=""))
cntrow <- cnt [, .(permnth = uniqueN(Code) ), by =.(mr_no, mnth)]
cnt <- cnt [order(mr_no, studyday, Code, description, patient_gender)]
cnt2 <- unique(cnt [, c("mr_no", "Code", "description", "patient_gender", "distype"), ])

# Combinations for each patient
# Do these calculations for first rows
cnt3 <- cnt2[, `:=` (numcomb = seq_len(.N),
                      descomb = description,
                      discomb = Code,
                      grpcomb = paste(trimws(Code), collapse = " ", sep=)),
                      by = .(mr_no, patient_gender)]

```

```

cnt30 <- cnt3 [numcomb > 1, `:=` (discomb = sapply(seq_len(.N), function(x)
paste(Code[seq_len(x)], collapse = ">")) ,
                           descomb = sapply(seq_len(.N), function(x)
paste(description[seq_len(x)], collapse = ">")) ),
               by = .(mr_no, patient_gender) ]

cnt31 <- rbind(cnt3 [numcomb ==1], cnt30 [numcomb > 1])

# Starting disease sttdis

stt <- cnt3 [ numcomb == 1, .(sttdis = paste(descomb, ">", patient_gender, sep="")), by
=.(mr_no, patient_gender, Code, description) ]

cnt3disprgs <- merge(cnt31, stt [, c("mr_no", "sttdis"), ], by = c("mr_no"))

cnt3disprgs <- cnt3disprgs [, .(npt = uniqueN(mr_no)), by = .(discomb, descomb, numcomb,
grpcomb, sttdis, patient_gender) ]

cnt3disprgs <- cnt3disprgs [order(sttdis, patient_gender, numcomb, discomb, grpcomb) ]
cnt3disprgs <- cnt3disprgs [, node := 1:.N, by =.(sttdis, patient_gender, grpcomb, npt) ]
cnt3disprgs <- cnt3disprgs [, treecomb := paste(sttdis, ">", descomb, " (N=", npt, ")",
sep="")]

cnt3disprgs <- cnt3disprgs [order(sttdis, grpcomb, node) ]
cnt3disprgs02 <- cnt3disprgs [numcomb > 1]

```

```

# These 2 subsets are for the CSV for D3js

sttdis <- unique(stt [, c("description"), ])
sttdisgen <- unique(stt [ sttdis != "", c("sttdis"), ])
frow <- data.table ( treecomb = "id,value")

# Rename to the same variable

setnames(sttdis, "description", "treecomb")
setnames(sttdisgen, "sttdis", "treecomb")

cnt3disprgs03 <- rbind(cnt3disprgs02 [, c("treecomb")], sttdis, sttdisgen)
[order(treecomb) ]

cnt3disprgs03 <- cnt3disprgs03[, treecomb := paste("Disease>", treecomb, sep="")]

# No subset

fwrite(unique(cnt3disprgs03),
       col.names = FALSE,
       quote = FALSE,
       "D:\\Hospital_data\\ProgressSQL\\misc\\jsfolder\\999temp\\decode_gender.csv")
#####

```

```
# End of program
#####
#
# Create Json file using the following commands:
#
# This is the working directory path.
SimpleJar=Hospital_data/ProgressQL/misc/jsfolder/999temp
java -classpath `cygpath -wp /cygdrive/d/${SimpleJar}:./json-simple-1.1.1.jar` D3Taxonomy
decode_gender.csv ">"
#####
# End of program
#####
```

7 References

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