outlined above. For the casual data browser, HTML output is ideal. For printing, PDF is preferred. And for the additional analysis, Excel is a popular option. With ODS, we can meet all of these needs. **Methods:** Because ODS permits opening multiple output destinations simultaneously, a single procedure can be used to generate data in HTML, PDF, and Excel at once. The presentation will demonstrate the following: o- basic ODS syntax for HTML, PDF, and Excel output o- custom HTML table of contents o- using the ExcelXP tagset for multi-tab spreadsheets o- a custom macro for managing multiple ODS destinations simultaneously o- simple PROC Template code for easy customization o- techniques for consistent output from multiple platforms. **Results:** The techniques outlined here have been well-received in a variety of business reporting environments. **Conclusions:** The SAS ODS provides a wide array of reporting options. Don't limit yourself to just one type of output.

Keywords: SAS Output Delivery System, Reporting options, Output Delivery System destinations

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PS3-04:

Cultivating an Environment and Attitudes Where Data Quality Improvement of the Virtual Data Warehouse Can Occur

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Background and Aims: The Virtual Data Warehouse (VDW) at the Institute for Health Research (IHR) at Kaiser Permanente Colorado (KPCO) is the data source of choice for the IHR analytic team. This research ready data source is important for efficient use of analytic team resources. Our aims are to 1) describe the attitudes, methods and processes that lead to high data quality in the VDW at KPCO, and 2) provide examples of improvement successes. **Methods:** The methods used to pursue VDW improvement include the following: 1) we gathered support from all local interested parties and provided avenues for all interested parties to participate in setting VDW file improvement priorities along with the allocation of available resources to support the process; 2) we worked to develop relationships with experts in data content areas throughout KPCO's clinical delivery system and those overseeing legacy source data systems; 3) we stayed informed of issues concerning the VDW by participating at the national level in committees concerned with VDW development; 4) we encouraged programmer networking at both the local and national levels; 5) we created an environment that encouraged detailed file documentation; 6) we encouraged two way communications between those using data files and those creating data files. **Results:** We found that nurturing a collaborative team spirit encouraged 1) the identification of key individuals best suited to improve specific files, 2) realistic estimates of time necessary to complete the improvement tasks, and 3) the freeing of time for those key individuals to perform these tasks. Engaging content experts outside of the IHR allowed for better understanding of legacy data files and allowed for lead time to respond to data system changes. Engaging programmer networks allowed for the development and sharing of best practices. Enhanced VDW file documentation lessened the chance of misinterpretation or misuse of data. Enhanced communication between those creating the VDW files and those using the files assure continued improvement. **Conclusions:** Good communication among many different parties and a supportive team spirit from local interested parties are necessary to facilitate the building and maintenance of a high quality research data structure.

Keywords: Virtual Data Warehouse, High quality research data, Quality data best practices

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Genetics

PS1-08:

Genetic Service Providers Identify Barriers Related to Referral, Counseling and Testing for Familial Cancer

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Background and Aims: Little of what we know about the use of family history and genetic risk assessment services has been gathered from those engaged in counseling. To fill this gap, we conducted a survey to understand the processes of identifying and referring high-risk patients for genetic counseling and testing for familial cancer from the perspective of genetic service providers. **Methods:** Genetics professionals (genetic counselors and physician geneticists) from eight CRN sites were surveyed. The survey, administered via Survey Monkey, included questions regarding sources of referrals, steps to get an appointment, use of electronic medical records, perceived barriers to referral, strategies employed to improve identification and referral of high-risk patients, and ways to increase awareness among providers of the value of obtaining family history of cancer. Analyses involved computing frequencies of categorical responses and means of continuous responses (performed in SAS v9.1). **Results:** Of the 40 invited, twenty-eight individuals responded to the survey (70%). Referrals were predominantly from providers (89% on average) versus self-referrals (10% on average). Barriers that may prevent patients who are referred for counseling services from being seen included the following: genetic risk evaluation was not a priority for patients (72%, 18 of 25 responding to this item), concerns about insurance (52%, 13 of 25), distance to appointments (48%, 12 of 25), lack of patient and/or provider knowledge (36%, 9 of 25), discouragement by family members (28%, 7 of 25), and fear (20%, 5 of 25). Attending meetings was the most frequently (57%, 16 of 28) reported strategy to increase awareness among and referrals from providers. Provider education was mentioned most frequently (70%, 14 of 20 responding to this item) to improve understanding of the value of family history documentation and increasing referrals. **Conclusions:** Our survey identified several areas in the identification and referral process for cancer genetic services where opportunities for improvement exist including increasing awareness of the importance of genetic risk assessment among general practitioners, creating a simple standard for collecting genetic information and referring patients, and promoting the value of family history and the importance of determining genetic susceptibility, when appropriate, among patients and providers.

Keywords: Genetic risk assessments, Genetic counseling, Testing for familial cancer

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PS1-09:

Public Opinion of Family History and Genetic Testing for Common Diseases: Results from Focus Groups with Kaiser Permanente Colorado Members

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Background and Aims: With the advent of personalized medicine, consumers are routinely exposed to information about new gene discoveries, family history, and direct-to-consumer (DTC) advertising of genetic tests. Since 2008, the BRACAnalsysis® test for breast cancer risk has been steadily advertised directly to consumers in different markets across the US, and at least 3 companies now offer DTC genetic screening for $300 - $1000, with more companies entering this burgeoning market. The specific aims of this project are to: 1) determine how individuals understand the issue of family history and DTC genetic tests, and 2) to determine how individual perspectives about issue salience and issue frames differ by population group.

Methods: As part of a CRN pilot project, focus groups were conducted with Kaiser Permanente Colorado members in 2009 to determine individual perspectives and public opinion about the importance and value of family history, DTC genetic testing, and DTC advertising and other media representations of DTC genetic tests. Focus groups were conducted by concordant population groups: General population KPCO members, members who self-identify as African American, members who self-identify as Hispanic/Latino, women with a recent referral for BRCA1/2 testing, KPCO primary care providers, and KPCO specialty care providers. **Results:** Results on focus group demographics, media use, trust in information, and most trusted information sources are presented. Additional results include coding focus group transcripts for value and polarity (positive/negative) of opinion on family history and genetic testing. Additional coding for how different population groups frame opinion on the issue (progressive, deterministic, caution) include results on whether frames are similar or different across population groups. Finally, information on the impact of media presentations on member opinion and decision-making were assessed. **Conclusions:** Individual opinions about the value of family history and genetic testing for disease risk vary greatly. Salience of themes related to genetic testing and DTC genetic tests specifically may vary across concordant population groups.

Keywords: Direct-to-consumer genetic testing, Health and family history, CRN pilot project

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PS1-10:

Response to Metformin and Genetic Variants of Organic Cation and Multidrug and Toxin Extrusion Transporters

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Background and Aims: Metformin is the most widely-used anti-diabetic drug in the United States. However, medication management fails to achieve therapeutic goals in ~20% of patients. This study attempted to identify genetic polymorphisms associated with metformin treatment failure. We studied the associations between polymorphisms in two liver and kidney organic cation transporter genes (OCT1 & OCT2) and two kidney multidrug and toxin extrusion transporter genes, (MATE1 & MATE2K) and response to metformin monotherapy. **Methods:** At Kaiser Permanente Southeast and Marshfield Clinic Research Foundation we identified 304 type 2 diabetes (T2DM) patients on metformin monotherapy who: were enrolled for >=6 months prior to initiation; remained on metformin >= 90 days following initiation; and had a HgbA1c measured prior to first metformin prescription and then after initiation. From this group we selected 171 patients who had not received metformin or other anti-diabetics previously, and had baseline HbA1c levels >7.0% prior to metformin initiation. We genotyped 10 SNPs, and assessed response by measuring absolute and relative change in HbA1c after after metformin initiation. **Results:** Three SNPs were identified that were significantly associated with reduced response to metformin, after adjustment for baseline HbA1c, dose, and ethnicity. In a dominant model, heterozygosity or homozygosity for minor A allele in the MATE1 intronic SNP, rs2289669, resulted in a smaller absolute change in HbA1c (mean of 0.45% less reduction in absolute change in HbA1c; 95% CI 0.17 to 0.74%) compared to individuals homozygous for major G allele. In a recessive model, homozygosity for minor A allele in MATE2K 5'-UTR SNP, rs12943590, resulted in smaller absolute change in HbA1c (mean of 0.43% less reduction in absolute change in HbA1c, 95% CI 0.053 to 0.86%). The reduced function SNPs in OCT1 & OCT2 were not associated with metformin response, except for rs34059508 (G465R). This SNP showed a positive (but not statistically significant) association with smaller absolute change in HbA1c (mean of 0.49%; 95% CI -0.06354 to 1.045%). **Conclusions:** These three variants of metformin transporter genes may be important for personalizing treatment for patients with T2DM. A replication study in a larger population is currently being planned.

Keywords: Genetic polymorphisms, Metformin transporter genes, Metformin treatment

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PS1-11:

Specimen Collection Within the Cancer Research Network: A Critical Appraisal

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Background and Aims: The Genomics Working Group (of the Cancer Research Network (CRN) Pharmacovigilance Project) explored single-site experiences with genomic studies to understand challenges and opportunities for collecting and using biological specimens. Its specific aims were to: (i) describe the availability of existing biospecimens; (ii) document successful past specimen collection strategies; (iii) identify potential barriers to selected recruitment strategies; and (iv) develop standardized study documents for future genomic research. **Methods:** We distributed a survey on existing biospecimen availability to principal investigators at all CRN Pharmacovigilance sites. Information collected included the number of specimens, storage methods, and type of specimens available. Investigators were also asked to identify past and current studies at their institutions in order to collect information on successful specimen collection strategies. A literature review was conducted both to identify potential barriers to participation and to understand the feasibility of various recruitment procedures. Benefits and limitations of 'opt-out' and 'opt-in' specimen collection methods were examined. Lastly, we developed study documents, including recruitment letters and informed consent forms, for future saliva and blood specimen collection efforts. **Results:** Two of the CRN HMOs currently have large-scale banked blood or saliva specimens (>20,000) within existing repositories. One site has two large-scale studies (>20,000 participants each) with banked specimens able to provide DNA for future research. Whole blood or blood components are the most commonly collected specimen types, and multiple CRN sites have access to banked tumor blocks. There were 33 past or current studies that included biospecimen collection. There was a trade-off between intensive data collection requirements and recruitment yield, cost, and participation burden. **Conclusions:** There is great potential for collection, storage, and use of biospecimen samples for research within the CRN. For future collection efforts, 'opt-out' models allow fast sample accrual, but impact data de-identification requirements. 'Opt-in' models allow for broad data collection, but are resource and time intensive. Pathology time and support may be a barrier to future use of stored samples.

Keywords: Genomics Working Group, Specimen collection strategies, Genomic research

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PS1-12:

Use of Tumor Registry to Obtain Family History Information

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Background: The Human Genome project has revolutionized the field of medicine to move toward personalized medicine. The family history is a screening tool to identify families at risk for common conditions allowing for personalized care. For breast cancer syndromes, genetic testing, counseling and prophylactic treatment are available. While there are data about the efficacy and clinical utility of the family history, there are areas that still need investigation. Does obtaining the family history lead to patient