distributions of "true" physician scores (means of 73, 88, 95% satisfaction and standard deviations of log odds = 0.5, 1.0 and 1.5), we simulated 5,000 physicians and assigned each a true score and rank within these distributions. We then tested various patient sample sizes (N) from 10-100, and repeated 1,000 simulations under each scenario to calculate 95% inner ranges of observed ratings and ranks for each physician. True and observed ranks were compared and examined as a function of underlying distribution and N. **Results:** The precision of an individual physician's percentile rank increases dramatically with 3 factors: increase in N; increase in variance of true physician scores; and decrease in overall mean physician score. Precision is also greatest for the best and worst physicians and less precise in the mid-range. In the best case scenario tested (mean 73%, log odds SD = 1.5, N = 100), physicians with an observed rank as low as the 68th percentile were likely to be equivalent to physicians with an observed rank above the 90th percentile. In the worst case scenario (95% mean, log odds SD = 0.5, N = 10), physicians with a "true" 90th percentile rank were likely to receive a ranking as low as the 18th percentile. **Conclusions:** If physician rankings based on patient satisfaction scores are used to measure and incentivize quality, rankings should ether be based on a measure with maximal variation among physicians, or incentives should be based on ranges that reflect uncertainty rather than absolute rankings.

Keywords: Patient satisfaction; Quality metrics

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Vaccine/Infectious Diseases

PS1-36:

Developing Rapid Molecular E.coli Clonal Diagnostics for Community Laboratory Settings

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Background/Aims: E.coli infections of the urinary tract (UTI) are among the most common infections worldwide. U.S. costs of UTI care are >$1B annually. Recently, there has been rapid worldwide emergence of resistant E.coli, which increases the percentage of serious events and the difficulty of care. One contributing factor may be that usual care typically involves presumptive antibiotic treatment, with antimicrobial sensitivity results available only after 1-2 days. Inappropriate treatment during that interval is suboptimal for the patient and facilitates E.coli resistance. We conducted a 1-year pilot of a potential new diagnostic technology to test for E.coli infection at the clonal level by: 1) optimizing PCR methods to directly and rapidly test urine samples for two E.coli sub-strains (clones) in a community lab setting (Group Health [GH]); 2) using this method to identify two highly-resistant sub-strains in GH samples; and 3) comparing usual care prescribing patterns to potential prescribing based on sub-strain results, focusing on the "drug-bug mismatch". **Methods:** A research strategy developed at the University of Washington to diagnose E.coli sub-strains was adapted to a commercial PCR platform for two selected sub-strains: ST131 and ST69. We tested 653 urine samples for presence of ST131 and ST69 and reviewed EMRs to collect the clinical diagnoses and antibiotics prescribed at the visit. **Results:** In the GH lab, the PCR-based diagnostic test required about 1.5 hrs. Prevalence (UW-confirmed) was 10% (65/653) for ST131 and 5% (33/653) for ST69. Of 200 EMR reviews to date, these two clones represent 65% (17/26) of fluoroquinolone and 17% (5/29) of trimethoprim/sulfa resistant isolates. Five percent (9/200) of patients were empirically prescribed therapy for which the isolate was resistant. Adjustment of the original prescribed antibiotic based on the E.coli clonal identity would reduce the drug-bug mismatch by 55%. **Conclusions:** These methods delivered accurate, economical results, at the clonal level, faster than usual lab methods. The two E.coli sub-strains are found in a sizable percentage of the isolates that are resistant to the main E.coli therapies. Clonal-based diagnostic strategies can offer opportunities to improve antibiotic prescribing and to impact the continued spread of antimicrobial resistance.

Keywords: Rapid diagnosis; Antibiotic resistance

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Virtual Data Warehouse

A4-1:

Validating Electronic Health Record Demographic Data Using Self-reported Data from the Autism Registry Survey

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Background/Aims: The use of administrative patient data via the electronic health record (EHR) is very important in research. It's critical we have a sense of the validity and relative accuracy of key data in this widely available data source. The HMORN Virtual Data Warehouse (VDW) is an example of a large repository of administrative data used in numerous studies. The recent Mental Health Research Network (MHRN) Autism Spectrum Disorder (ASD) Registry Survey was hosted by four HMORN sites inviting Kaiser Permanente members to complete a Web-based questionnaire on behalf of their child identified as having an ASD diagnosis in the EHR. **Methods:** In addition to an extensive battery of questions regarding ASD, the survey collected data on a number of demographic data elements also available in the VDW. These are: age, gender, race/ethnicity (child), income (household) and education (household adult). A total of 1155 adults responded to the ASD Registry Survey. These records were matched with demographic data from the VDW for the same child. **Results:** Preliminary examination of race-ethnicity and gender data shows that there's a good to excellent level of agreement between the two sources when data are non-missing in both data sources. A total of 992 records had non-missing race/ethnicity data from both data sources. In 81.1% (805/992) of the cases, both data sources agreed (kappa = 0.68, CI = 0.64-0.72). The categories that had the highest level of agreement are White, Black, and Asian, while the Hispanic and multi-racial groupings had a comparatively much lower level of agreement (46.9%). For gender, level of agreement was very high (99.0%, 1118/1129, kappa = 0.97, CI = 0.95-0.99). **Conclusions:** In this study, race in the electronic health record was a very accurate measure for major race categories but was far less accurate when reporting the emergent and important multi-racial category and Hispanic ethnicity. Gender had an excellent level of agreement between the two sources. Age, gender, and race-ethnicity are key covariates for many studies analyzing EHR data. Income and education can serve to illuminate socioeconomic factors very relevant to health care research. Having a sense of the validity and accuracy of these data is crucial to the research process.

Keywords: Data validation; Demographic data

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A4-2:

ICD-10 CM Transition across Three Research Centers

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Background/Aims: The United State currently uses version nine (ICD-9) for diagnosis and procedure coding. Federal regulations require that the US adopt the next version (ICD-10) by 10/1/2014. The new version expands the number of diagnosis codes from about 13,000 to 68,000, providing more granularity to classify diseases. Challenges in moving to ICD-10 include: (a) the crosswalk between versions is a many-to-many match; (b) the relationship between the old and the new codes will sometimes be complex; and (c) it will encompass system-level changes such as expanded field sizes and support for alphanumeric characters. Our challenge is to implement the transition across three research centers at Kaiser Permanente Northwest, Southeast and Hawaii. **Methods:** The three research centers need to account for the new ICD-10 code set and any new data structures introduced by either the EMR or Research Data Warehouse. A smooth transition between coding systems requires working with researchers across the three regions. This includes identifying corresponding ICD-10 codes that correctly identify the research cohort members and remediating the existing programing logic. Kaiser Permanente's Center for Health Research (CHR) has developed a detailed plan to accomplish these two goals. CHR staff are partnering with the Kaiser