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# Access in action

## Google Scholar

The screenshot shows a Google Scholar search interface. At the top, the Google logo is on the left, and a search bar contains the text "New generations: sequencing machines and their computational challenges". To the right of the search bar is a magnifying glass icon. Below the search bar, the word "Scholar" is displayed in red, followed by "About 20,200 results (0.12 sec)". To the right of this information are three buttons: "Any time" with a dropdown arrow, a notification bell icon with the number "0", and another dropdown arrow.



The first search result is titled "New generations: Sequencing machines and their computational challenges" in purple, with a "[HTML]" link to the right. The author information is "DC Schwartz, MS Waterman - Journal of computer science and technology, 2010 - Springer". The abstract text reads: "Schwartz DC, Waterman MS. **New generations: Sequencing machines and their computational challenges**. JOURNAL OF COMPUTER SCIENCE AND TECHNOLOGY 25(1): 3-9 Jan. 2010 ... **New Generations: Sequencing Machines and Their Computational**". Below the abstract are the links "Cited by 13", "Related articles", "All 14 versions", and "Cite".

The second search result is titled "Evolutionary computation: toward a new philosophy of machine intelligence" in blue, with a "[BOOK]" icon to the left. The author information is "DB Fogel - 2006 - books.google.com". The abstract text reads: "... If the process is understood, methods for **its generation** should converge functionally and become fundamentally identical, relying on ... of computing, we have envisioned **machines** that could go beyond our own ability to solve problems—intelligent **machines**. ... This is nothing **new**. ...". Below the abstract are the links "Cited by 2874", "Related articles", "All 14 versions", "Cite", and "More" with a dropdown arrow.

The third search result is titled "How to map billions of short reads onto genomes" in blue, with a "[HTML]" icon to the left. The author information is "C Trapnell, SL Salzberg - Nature biotechnology, 2009 - ncbi.nlm.nih.gov". The abstract text reads: "... As a practical matter, the task of mapping billions of **sequences** to a mammalian-sized ... To reduce the computing cost of analysis for **sequencing**-based assays and to make them available to all investigators, we and others have created a **new generation** of alignment ...". Below the abstract are the links "Cited by 142", "Related articles", "All 26 versions", and "Cite".

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### Abstract

New generation sequencing systems are changing how molecular biology is practiced. The widely promoted \$1000 genome will be a reality with attendant changes for healthcare, including personalized medicine. More broadly the genomes of many new organisms with large samplings from populations will be commonplace. What is less appreciated is the explosive demands on computation, both for CPU cycles and storage as well as the need for new computational methods. In this article we will survey some of these developments and demands.

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The screenshot shows the PubMed website interface. At the top, there are navigation links for 'NCBI Resources' and 'How To', and a 'Sign In to NCBI' link. The main header includes the PubMed logo, a search bar containing the text 'new generations: sequencing machines and their computational challenges', and buttons for 'RSS', 'Save search', and 'Advanced'. A blue banner below the header contains a notice: 'PubMed is open, however it is being maintained with minimal staffing due to the lapse in government funding. Information will be updated to the extent possible, and the agency will attempt to respond to urgent operational inquiries. For updates regarding government operating status see USA.gov.' The article title 'New Generations: Sequencing Machines and Their Computational Challenges.' is displayed, along with the author 'Schwartz DG, Waldman MS' and their affiliation 'Laboratory for Molecular and Computational Genomics, Department of Chemistry and Laboratory of Genetics, University of Wisconsin-Madison, WI 53706 USA.' An abstract follows, discussing the impact of new generation sequencing systems on molecular biology and personalized medicine. Below the abstract are links for 'Grant Support' and 'LinkOut - more resources'. On the right side, there are sections for 'Send to', 'Save Items' (with an 'Add to Favorites' button), 'PubMed' (with a 'Click here to read article using PubMed' link), and 'Related citations in PubMed' (listing several related articles with their titles and journal information).

# Access in action

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J Dent Res. 2013 Jan;92(1):32-7. doi: 10.1177/0022034512463241. Epub 2012 Oct 11.

### Clustering tooth surfaces into biologically informative caries outcomes.

Shaffer JR, Feingold E, Wang X, Weeks DE, Wevart RJ, Crout B, McNeil DW, Marazita ML.  
Department of Human Genetics, Graduate School of Public Health, University of Pittsburgh, Pittsburgh, PA 15261, USA. jr@pitt.edu

#### Abstract

Dental caries affects most adults worldwide; however, the risk factors for dental caries do not necessarily exert their effects uniformly across all tooth surfaces. Instead, the actions of some risk factors may be limited to a subset of teeth/surfaces. Therefore, we used hierarchical clustering on tooth surface-level caries data for 1,068 Appalachian adults (ages 18-75 yrs) to group surfaces based on co-occurrence of caries. Our cluster analysis yielded evidence of 5 distinct groups of tooth surfaces that differ with respect to caries: (C1) pit and fissure molar surfaces, (C2) mandibular anterior surfaces, (C3) posterior non-pit and fissure surfaces, (C4) maxillary anterior surfaces, and (C5) mid-dentition surfaces. These clusters were replicated in a national dataset (NHANES 1999-2000, N = 3,123). We created new caries outcomes defined as the number of carious tooth surfaces within each cluster. We show that some cluster-based caries outcomes are heritable (i.e., under genetic regulation;  $p < 0.05$ ), whereas others are not. Likewise, we demonstrate the association between some cluster-based caries outcomes and potential risk factors such as age, sex, educational attainment, and toothbrushing habits. Together, these results suggest that the permanent dentition can be subdivided into groups of tooth surfaces that are useful for understanding the factors influencing cariogenesis. Abbreviations: COHRA, Center for Oral Health in Appalachia, the principal study sample; C1-5, clusters 1-5, groups of similarly behaving tooth surfaces identified through hierarchical clustering; DMFS index, decayed, missing, or filled surfaces, a traditional caries measure representing the number of affected surfaces across the entire dentition; DMFS1-5, partial DMFS indices representing the number of affected surfaces within a hierarchical cluster; and NHANES, National Health and Nutrition Examination Survey, the secondary study sample.

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J.R. Shaffer<sup>1,2\*</sup>, E. Feingold<sup>1,3</sup>,  
X. Wang<sup>2,4,5</sup>, D.E. Weeks<sup>1,3</sup>,  
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J Dent Res 92(1):32-37, 2013

## ABSTRACT

Dental caries affects most adults worldwide; however, the risk factors for dental caries do not necessarily meet their effects uniformly across all tooth surfaces. Instead, the extent of some risk factors may be a subset of tooth/human. Therefore, we used hierarchical clustering on tooth surface categories from 1,068 Appalachian adults (ages 18-75 yrs) to group surfaces based on co-occurrence of caries. Our cluster analysis yielded evidence of 5 distinct groups of tooth surfaces that differ with respect to caries (C1) pit and fissure molar surfaces, (C2) mesial-labial anterior surfaces, (C3) posterior non-pit and fissure anterior, (C4) maxillary anterior surfaces, and (C5) mid-distal anterior. These clusters were replicated in a national dataset (NHANES 1999-2004, N = 3,123), the overall mean caries outcomes defined as the number of carious tooth surfaces within each cluster. We show that some cluster-based caries outcomes are heritable (i.e., under genetic regulation;  $p < 0.05$ ), whereas others are not. Likewise, we demonstrate the association between some cluster-based caries outcomes and potential risk factors such as age, sex, educational attainment, and breastfeeding habits. Together, these results suggest that the permanent dentition can be subdivided into some clusters of tooth surfaces that are useful for understanding the factors influencing caries etiology. Abbreviations: COHRA, Center for Oral Health in Appalachia; the principal study samples C1-5, cluster 1-5, groups of similarly behaving tooth surfaces identified through hierarchical clustering; DMFS index, decayed, missing, or filled surface, a traditional caries measure representing the number of affected surfaces across the entire dentition; DMFTS-5, partial DMFS index representing the number of affected surfaces within a hierarchical cluster; and NHANES, National Health and Nutrition Examination Survey, the secondary study sample.

**KEY WORDS:** dental caries, permanent dentition, white spots, hierarchical clustering, cluster analysis, heritability.

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## Clustering Tooth Surfaces into Biologically Informative Caries Outcomes

## INTRODUCTION

Dental caries, which affects the great majority of adolescents and adults throughout the world, is a multi-factorial disease caused by the effects of numerous environmental, behavioral, and genetic factors. Many risk factors have been identified, such as: host genetics (Horowitz et al., 1958); environmental exposures, including fluoride, cariogenic bacteria, and pH-altering agents; behavioral factors, including diet and oral hygiene; characteristics of the dentition, including enamel composition and position and morphology of teeth; characteristics of the oral environment, including saliva composition, flow rate, and pH buffering capacity; and demographic factors, including age, sex, race, ethnicity, socio-economic status, and access to oral health care (Hunter, 1988). This complexity is further compounded by the disease phenotype, which may manifest as innumerable combinations of caries lesions across tooth surfaces of the full dentition. Because caries risk factors may exert differential effects across tooth surfaces of the permanent dentition, measurable caries experience may be modeled as the cumulative result of multiple superimposed patterns of decay due to the various risk factors (Batchelor and Sheiham, 2004; Shaffer et al., 2012a).

In epidemiological studies, however, caries experience is typically reduced to a single measure of decay, such as the widely used DMFTS index (calculated as the sum of decayed, missing due to decay, or filled/restored teeth/surfaces). Such global measures of caries experience ignore the fact that categories of tooth surfaces exhibit differences in susceptibility to decay and are differentially affected by risk factors. Because they ignore the patterns of dental caries across the dentition, global measures of decay such as DMFTS index may be limited in their ability to identify caries risk factors that exert their effects on specific categories of tooth surfaces. Indeed, previous studies have demonstrated that modeling the patterns of tooth decay is beneficial for epidemiological (Pester et al., 2003, 2009) and genetic studies (Shaffer et al., 2012a, 2012b). We used hierarchical clustering analysis to group tooth surfaces into categories based on co-occurrence of caries lesions. We then generated novel caries outcomes reflecting these tooth-surface categories, and explored their utility for studying caries etiology.

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### Clustering tooth surfaces

Shaffer JR, Feinold E, Department of Human & Biomedical Sciences, University of Wisconsin-Madison

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## RESEARCH REPORTS

### Clinical

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### APPENDIX

#### COHRA Population Characteristics

Descriptive characteristics of the COHRA sample are shown in the Appendix Table. Compared with the general US population, this Appalachian sample from rural West Virginia and Pennsylvania is poorer, less educated, and underserved with respect to oral health care.

#### Cross-validation and Defining Separate Clusters

Determining the number of separate clusters is the principal challenge in the field of cluster analysis, and there is currently very little statistical theory in this area. Defining *a priori* minimum distances between clusters is arbitrary and may lead to over-fitting. Therefore, we instead performed two-fold cross-validation (e.g., Salvador and Chan, 2004), a commonly used approach for determining the number of clusters. Cross-validation allows us to determine the sensitivity of our clusters to perturbations of the input data and to identify what level of within-cluster similarity and between-cluster dissimilarity defines stable clusters. We randomly divided our sample into two halves and performed hierarchical clustering on each half. This process was repeated for 10 random halves. By comparing dendrograms, we determined the maximum number of separate clusters that were consistently observed across all random halves. Overall, tooth surfaces were distributed across 5 very stable clusters. Example cluster results for two complementary halves (which total to the full sample) are shown in Appendix

## Clustering Tooth Surfaces into Biologically Informative Caries Outcomes

Fig. 1. Similarly, to assess any effects of the inclusion of biological relatives in our sample, we repeated hierarchical clustering in the maximal subset of unrelated individuals (see Appendix Fig. 2), which were newly identical to the total COHRA and NHANES 1999-2000 samples.

In both the total COHRA sample and in the NHANES 1999-2000 sample, the fifth cluster was subdivided into maxillary and mandibular components (indicating possibly 6 instead of 5 clusters). However, these subdivisions were not consistently observed *via* cross-validation of the COHRA sample. That is, in some randomly chosen halves of the COHRA sample, the sixth cluster did not distinguish maxillary and mandibular components of the fifth cluster. Therefore, we have conservatively shown results for the 5 stable clusters, as well as the maxillary and mandibular subdivisions of the fifth cluster.

Overwhelmingly, the cluster results were stable within the COHRA sample, and consistent between the COHRA sample and NHANES 1999-2000 sample. That being stated, there were subtle differences observed among cluster results. For example, left-right asymmetry was observed, albeit rarely, in the random halves (e.g., Appendix Fig. 1A, tooth #20 and tooth #29). Likewise, some tooth surfaces physically positioned on the border between two adjacent clusters shifted membership (e.g., Appendix Figs. 1A and 2, tooth #21 and tooth #28). In many cases, the result of such shifts in cluster membership echoed the subtle differences between COHRA and NHANES 1999-2000. We speculate that the all-or-nothing nature of our clustering approach represents an oversimplification of the relationships among tooth surfaces with respect to dental caries risk factors

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