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Short title: Genome-wide Association Studies of the Human Gut Microbiota

Emily R. Davenport, Darren A. Cusanovich, Katelyn Michelini, Luis B. Barreiro, Carole Ober, and Yoav Gilad

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Abstract

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Introduction

Humans have complex interactions with the bacteria that live in and on their bodies, referred to as the microbiota[1]. Alterations in the microbiota, particularly in the gut, have been linked to variation in risk for obesity[2-4], celiac disease[5], Crohn's disease[6, 7], ulcerative colitis[8-11], gastroenteritis[12], asthma[13], and inflammatory bowel disease[14, 15].
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- User experience testing with live users on dummy manuscripts
  - Volunteer researchers acting as authors and submitting to the journal sites
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We have also been actively engaging our researcher community

• User experience testing with live users on dummy manuscripts
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  • Submit feedback button
  • Journal office contact in case stuck
  • UX shadowing and screen sharing
  • Debriefs and final feedback interviews
An improved test for detecting multiplicative homeostatic synaptic scaling

Jimok Kim1,2*, Richard W. Tsien2* and Bradley E. Alger3

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Funding: This work was supported by grants R01AG036704 to J.K., B37MH071760 to R.W.T. and R01DA014625 to B.E.A. from the National Institutes of Health. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

ABSTRACT

Homeostatic scaling of synaptic strengths is essential for maintenance of network “gain”, but also poses a risk of losing the distinctions among relative synaptic weights, which are possibly cellular correlates of memory storage. Multiplicative scaling of all synapses has been proposed as a mechanism that would preserve the relative weights among them, because they would all be proportionately adjusted. It is crucial for this hypothesis that all synapses be affected identically, but whether or not this actually occurs is difficult to determine directly. Mathematical tests for multiplicative synaptic scaling are presently carried out on distributions of miniature synaptic current amplitudes, but the accuracy of the test procedure has not been fully validated. We now show that the existence of an amplitude threshold for empirical detection of miniature synaptic...
Is “Huh?” a Universal Word? Conversational Infrastructure and the Convergent Evolution of Linguistic Items

Abstract

A word like Huh?—used as a repair initiator when, for example, one has not clearly heard what someone just said—is found in roughly the same form and function in spoken languages across the globe. We investigate it in naturally occurring conversations in ten languages and present evidence and arguments for two distinct claims: that Huh? is universal, and that it is a word. In support of the first, we show that the similarities in form and function of this interjection across languages are much greater than expected by chance. In support of the second claim we show that it is a lexical, conventionalised form that has to be learnt, unlike grunts or emotional cries. We discuss possible reasons for the cross-linguistic similarity and propose an account in terms of convergent evolution. Huh? is a universal word not because it is innate but because it is shaped by selective pressures in an interactional environment that all languages share: that of other-initiated repair. Our proposal enhances evolutionary models of language change by suggesting that conversational infrastructure can drive the convergent cultural evolution of linguistic items.

Introduction

A fundamental tenet of linguistic science is that the sound of a word has a purely arbitrary connection to the word’s meaning [1], [2]. Thus, the sound of the word dog in English is connected to the concept ‘dog’ by historical accident and not by any natural connection; roughly the same concept is just as well denoted in French by chien, in German by hund, and in Japanese by imo. But it is not that a word can have just any vocal sound. While the possibility space for sound systems of the world’s language is enormous, any given language makes use of only a restricted portion of the possible sounds [3], [4]. It follows from these two basic principles—the ‘arbitrariness of the sign’, and the ‘selectiveness of particular sound systems’—that the words that exist in the world’s languages should sound quite different from each other, and that the likelihood that there are universal words is extremely small. But in this study we present a striking
...and very little

Short title: Genome-wide Association Studies of the Human Gut Microbiota

Emily R. Davenport¹✉, Darren A. Cusanovich¹✉, Katelyn Michelin³, Luis B. Barreiro², Carole Ober³✉, and Yoav Gilad³✉

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