ASJP World Language Tree of Lexical Similarity: Version 2 (April 2009)

by

André Müller, Viveka Velupillai, Søren Wichmann, Cecil H. Brown, Pamela Brown, Eric W. Holman, Dik Bakker, Oleg Belyaev, Dmitri Egorov, Robert Mailhammer, Anthony Grant, and Kofi Yakpo

The World Language Tree graphically illustrates relative degrees of lexical similarity holding among 3384 of the world's languages and dialects (henceforth, languages) currently found in the ASJP database (ASJP stands for Automated Similarity Judgment Program). Languages branched more closely together on the ASJP tree are lexically more similar than those branched less closely together. While most lexical resemblance charted in the tree almost certainly is related to genetic affiliation, closely branched languages cannot routinely be assumed to be closely genetically associated since lexical resemblance among languages can be due to factors other than genetic relatedness (see below).

The tree is generated through use of the neighbour-joining computer algorithm originally designed to depict phylogenetic relationships in biology (Saitou & Nei 1987). This is implemented in MEGA 4 (Kumar et al. 2008), the software that we use. The algorithm is applied to a matrix of lexical similarity scores based on Levenshtein (or edit) distances holding between all possible pairs of the 3384 languages (for details about this, including how we modify the Levenshtein distances for our purposes, see Bakker et al. 2009: 169). All languages of the database are compared to one another with respect to lexical similarity relating to their words for 40 referents determined statistically in Holman et al. (2008) to be most stable among core vocabulary items commonly used in lexicostatistical analysis. The tree is unrooted, but organized around a midpoint, i.e., the point which is equidistant between the two most lexically dissimilar languages in the network. Finally, the tree is annotated to show how it corresponds to the classification used in the latest version of the online World Atlas of Language Structures (Haspelmath et al. 2008), with some updates from Dryer (personal communication). This annotation is presented for ease of orientation, not necessarily because ASJP agrees with it. The language names used are normally simply those

¹ http://www.megasoftware.net/

http://wals.info/

of the sources consulted. The sources, as well as corresponding language names of *Ethnologue*, are provided in a continuously updated wiki.³

Four factors influence lexical similarity registered in the tree: (1) genetic or genealogical relationship of languages, (2) diffusion (language borrowing), (3) universal tendencies for lexical similarity such as onomatopoeia, and (4) random variation (chance).

Languages branched closely together on the tree may be so because of strong lexical similarity produced by any one or a combination of the four factors. Genetic relationship would appear to be the most dominant factor accounting for close branching, followed next by diffusion. Universal tendencies and chance are less significant contributors to close branching than either genetic relationship or diffusion, but nonetheless clearly contribute to the overall structure of the tree.

Typically, all languages of non-controversial language families such as Austro-Asiatic, Uralic, or Mayan, are respectively branched together on the tree. When some languages of a non-controversial family are not found branched together, this is because they are substantially lexically different from other members of their family despite unambiguously belonging to that family. Occasionally, a language can be so lexically different from co-members of its family that it is found branched more closely with some language or languages with which it is not genetically related at all, usually because of chance lexical similarity or similarity due to borrowing. (When such languages are geographically remote from one another, chance usually explains close branching.)

Typically, branching accords closely with genetic subgroups recognized by experts within non-controversial language families. When branching is not isomorphic with genealogical subgrouping, this often reflects diffusion among languages of the family promoted by language contact. Thus, when used in conjunction with expert classifications of non-controversial language families, the tree can be helpful in calling attention to historical relationships (contact) among genetically related languages that sometimes might not be otherwise apparent.

The tree may also suggest relationships heretofore not noticed among languages that may be profitably investigated. For example, if two languages not known to be related in any way are found together on a terminal branch, this may indicate a relationship between them entailing either inheritance or contact, especially if they are not geographically remote from one another. If the two languages are geographically distant, their close lexical similarity is

http://lingweb.eva.mpg.de/asjp/index.php/ASJP

more likely explained by chance than by either inheritance or diffusion. Also, language isolates may join one another on a terminal branch because they have nowhere else to go in the tree, creating the illusion that exciting, new far-flung relations may be in evidence. One should be cautious in the interpretation of these cases.

References

- Bakker, Dik, André Müller, Viveka Velupillai, Søren Wichmann, Cecil H. Brown, Pamela Brown, Dmitry Egorov, Robert Mailhammer, Anthony Grant, and Eric W. Holman. 2009. Adding typology to lexicostatistics: a combined approach to language classification. *Linguistic Typology* 13: 167-179.
- Holman, Eric W., Søren Wichmann, Cecil H. Brown, Viveka Velupillai, André Müller, and Dik Bakker. 2008. Explorations in automated lexicostatistics. *Folia Linguistica* 42.2: 331-354.
- Haspelmath, Martin, Matthew S. Dryer, David Gil and Bernard Comrie. 2008. *The World Atlas of Language Structures Online*. Munich: Max Planck Digital Library.
- Kumar S., J. Dudley, M. Nei, and K. Tamura K. 2008. MEGA: A biologist-centric software for evolutionary analysis of DNA and protein sequences. *Briefings in Bioinformatics* 9: 299-306.
- Saitou, Naruya and Masatoshi Nei. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* 4: 406-425.

Language family abbreviations

AA Afro-Asiatic Chu Chumash

Aik Aikana CK Chukotko-Kamchatkan

Ain Ainu Cmu Chimúan Alacalufan CN Cacua-Nukak Ala Algic Cnd Candoshi Alg Alt Altaic Cof Cofán

AM Amto-Musan Com Comecrudan An Austronesian Cre Creoles&Pidgins

AP Awin-Pare Cui Cuitlatec

Arc Araucanian CW Chapacura-Wanhan

Art Arutani Dos Doso Arauan Dra Dravidian Aru Arawakan EA Eskimo-Aleut Arw Atakapa EB East Bougainville Ata AuA Austro-Asiatic EBH East Bird's Head **EGB** East Geelvink Bay Aus Australian

Aym Aymaran Ela Elamite Ban Bangi Me Ele Eleman

Bar Barbacoan ES East Strickland
Bas Basque GA Great Andamanese

Beo Beothuk Gcu Guaicuruan Bil Bilua GS Gogodala-Suki Bor Border Gua Guahiban Bos Bosavi Had Hadza

Haida Brs Burushaski Hai Bulaka River Bul Har Harakmbet Bur Burmeso HM Hmong-Mien Cad Caddoan Hok Hokan

Cah Cahuapanan Hua Huavean Cam Camsá Hui Huitotoan Cariban ΙE Car Indo-European IG Inland Gulf Cay Cayuvava Chi Chibchan Ira Irantxe Chimila Chm Iro Iroquoian Ito Chn Chon Itonama

ChoChocoJabJabutiChtChitimachaJapJapanese

JivJivaroanMosMosetenanKadKadugliMovMovimaKapKapixanaMrwMorwap

Kar Karok MUM Morehead and Upper Maro Rivers

Kat Katukinan Mur Mura

Kau Kaure Mus Muskogean Kay Kayagar MZMixe-Zoque Kaz Kazukuru Nam Nambikuaran KF Kwomtari-Fas Nat Natchez Kho Khoisan NC Niger-Congo

Kib Kibiri NDa Nakh-Daghestanian

Kiw NDe Na-Dene Kiwaian Kol Kolopom Nih Nihali Kor Korean Nim Nimboran Krt Kartvelian NS Nilo-Saharan

KT Kiowa Tanoan NWC Northwest Caucasian

Ktn Kutenai OC Oregon Coast

KunKunzaOdiOdiaiKusKusundaOksOksapminKutKutoOMOto-Manguean

Kwa Kwalean Pae Paezan Kwe Kwerba Pan Panoan Kwz Kwaza Pat Pataxo KY Karkar-Yuri Pau Pauwasi Lavukaleve Pen Penutian Lav LeM Left May Pui Puinave PY Len Lencan Peba-Yaguan LP Lakes Plain Que Quechuan LS Leonhard Schultze Sal Salishan

LSR Lower Sepik-Ramu SAn South Andamanese

Marind Mar Sav Savosavo Mas Mascoian Sen Senagi Mat Matacoan Sep Sepik Sho Shom Peng May Mayan MGe Macro-Ge Sio Siouan Mis Misumalpan Sko Sko Mom Mombum Sln Salinan Mon Monumbo Slv Sáliban Mor Mor Snt Sentani

ST	Sino-Tibetan
Sum	Sumerian
Tac	Tacanan
Tar	Tarascan
Tau	Taushiro
Teb	Teberan-Pawaian
Teq	Tequistlatecan
Tic	Ticuna
Tim	Timucua

ΤK Tai-Kadai Trans-New Guinea **TNG**

TO Tor-Orya Tol Tol Ton Tonkawa Tor Torricelli Tot Totonacan Tou Touo Tru Trumai

Tucanoan TuK Turama-Kikorian

Tup **Tupian** UA Uto-Aztecan UC Uru-Chipaya

Ura Uralic Urarina Urr Usk Usku

Tuc

UY Upper Yuat VJ Vaupés-Japurá Wak Wakashan Wao Waorani War Warao Was Wasi

WBg West Bougainville WBm West Bomberai WF Western Fly WP West Papuan

Wsh Washo

WY Wappo-Yukian

Xin Xincan

Yal Yale Yam Yamana Yanomam Yan Yaw Yawa Yel Yele Yen Yeniseian Yka Yukaghir Yrb Yareban Yrr Yaruro Yuc Yuchi Yuw Yuwana Zam Zamucoan Zap Zaparoan Zun Zuni























































































