

Quelques publications récentes

Lord E, Le Cam M, Bapteste É, Méheust R, Makarenkov V, Lapointe FJ. BRIDES: A New Fast Algorithm and Software for Characterizing Evolving Similarity Networks Using Breakthroughs, Roadblocks, Impasses, Detours, Equals and Shortcuts. PLoS One. 2016 Aug 31;11(8):e0161474. doi: 10.1371/journal.pone.0161474.

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Jaffe AL, Corel E, Pathmanathan JS, Lopez P, Bapteste E. Bipartite graph analyses reveal interdomain LGT involving ultrasmall prokaryotes and their divergent, membrane-related proteins. Environ Microbiol. 2016 Aug 3. doi: 10.1111/1462-2920.13477.

Méheust R, Zelzion E, Bhattacharya D, Lopez P, Bapteste E. Protein networks identify novel symbiogenetic genes resulting from plastid endosymbiosis. Proc Natl Acad Sci U S A. 2016 Mar 29;113(13):3579-84. doi: 10.1073/pnas.1517551113.

Corel E, Lopez P, Méheust R, Bapteste E. Network-Thinking: Graphs to Analyze Microbial Complexity and Evolution. Trends Microbiol. 2016 Mar;24(3):224-37. doi: 10.1016/j.tim.2015.12.003.

Lopez P, Halary S, Bapteste E. Highly divergent ancient gene families in metagenomic samples are compatible with additional divisions of life. Biol Direct. 2015 Oct 26;10:64. doi: 10.1186/s13062-015-0092-3.

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genes and the construction of high-level composite lineages of life. Trends in Ecology & Evolution. doi:10.1016/j.tree.2015.01.001

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Bapteste E. The origins of microbial adaptations: how introgressive descent, egalitarian evolutionary transitions and expanded kin selection shape the network of life. Front. Microbiol. 2014. 5:83

Bapteste E. Les gènes voyageurs: l'odyssée de l'évolution. Belin. 2013. 192 pages.

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1: Lord E, Le Cam M, Bapteste É, Méheust R, Makarenkov V, Lapointe FJ. BRIDES: A New Fast Algorithm and Software for Characterizing Evolving Similarity Networks Using Breakthroughs, Roadblocks, Impasses, Detours, Equals and Shortcuts. *PLoS One*. 2016 Aug 31;11(8):e0161474. doi: 10.1371/journal.pone.0161474. PubMed PMID: 27580188; PubMed Central PMCID: PMC5007014. 2: List JM, Pathmanathan JS, Lopez P, Bapteste E. Unity and disunity in evolutionary sciences: process-based analogies open common research avenues for biology and linguistics. *Biol Direct*. 2016 Aug 20;11:39. doi: 10.1186/s13062-016-0145-2. Review. PubMed PMID: 27544206; PubMed Central PMCID: PMC4992195. 3: Jaffe AL, Corel E, Pathmanathan JS, Lopez P, Bapteste E. Bipartite graph analyses reveal interdomain LGT involving ultrasmall prokaryotes and their divergent, membrane-related proteins. *Environ Microbiol*. 2016 Aug 3. doi: 10.1111/1462-2920.13477. [Epub ahead of print] PubMed PMID: 27485833. 4: Méheust R, Zelzion E, Bhattacharya D, Lopez P, Bapteste E. Protein networks identify novel symbiogenetic genes resulting from plastid endosymbiosis. *Proc Natl Acad Sci U S A*. 2016 Mar 29;113(13):3579-84. doi: 10.1073/pnas.1517551113. PubMed PMID: 26976593; PubMed Central PMCID: PMC4822624. 5: Corel E, Lopez P, Méheust R, Bapteste E. Network-Thinking: Graphs to Analyze Microbial Complexity and Evolution. *Trends Microbiol*. 2016 Mar;24(3):224-37. doi: 10.1016/j.tim.2015.12.003. Review. PubMed PMID: 26774999; PubMed Central PMCID: PMC4766943. 6: Lopez P, Halary S, Bapteste E. Highly divergent ancient gene families in metagenomic samples are compatible with additional divisions of life. *Biol Direct*. 2015 Oct 26;10:64. doi: 10.1186/s13062-015-0092-3. PubMed PMID: 26502935; PubMed Central PMCID: PMC4624368. 7: Méheust R, Lopez P, Bapteste E. Metabolic bacterial genes and the construction of high-level composite lineages of life. *Trends Ecol Evol*. 2015 Mar;30(3):127-9. doi: 10.1016/j.tree.2015.01.001. PubMed PMID: 25601290; PubMed Central PMCID: PMC4359277.