

## Preprints

Grytten, I., Rand, K. D., **Nederbragt, A. J.**, Storvik, G. O., Glad, I. K., & Sandve, G. K. (2018). Graph Peak Caller: Calling ChIP-Seq Peaks on Graph-based Reference Genomes. *bioRxiv*, 286823. <https://doi.org/10.1101/286823>

Khelik, K., **Nederbragt, A. J.**, Sandve, G. K., & Rognes, T. (2018). NucMerge: Genome assembly quality improvement assisted by alternative assemblies and paired-end Illumina reads. *bioRxiv*, 483701. <https://doi.org/10.1101/483701>

NucBreak: Location of structural errors in a genome assembly by using paired-end Illumina reads *bioRxiv*. (n.d.). Retrieved from <https://www.biorxiv.org/content/early/2018/11/29/393488>

## Peer-reviewed publications

Jørgensen, T. E., Karlsen, B. O., Emblem, Å., Breines, R., Andreassen, M., Rounge, T. B., **Nederbragt, A. J.**, Jakobsen, K. S., Nymark, M., Ursvik, A., Coucheron, D. H., Jakt, L. M., Nordeide, J. T., Moum, T., & Johansen, S. D. (2018). Mitochondrial genome variation of Atlantic cod. *BMC Research Notes*, 11, 397. <https://doi.org/10.1186/s13104-018-3506-3>

Lie, K. K., Tørresen, O. K., Solbakken, M. H., Rønnestad, I., Tooming-Klunderud, A., **Nederbragt, A. J.**, Jentoft, S., & Sæle, Ø. (2018). Loss of stomach, loss of appetite? Sequencing of the ballan wrasse (*Labrus bergylta*) genome and intestinal transcriptomic profiling illuminate the evolution of loss of stomach function in fish. *BMC Genomics*, 19, 186. <https://doi.org/10.1186/s12864-018-4570-8>

Varadharajan, S., Sandve, S. R., Gillard, G. B., Tørresen, O. K., Mulugeta, T. D., Hvidsten, T. R., Lien, S., Asbjørn Vøllestad, L., Jentoft, S., **Nederbragt, A. J.**, & Jakobsen, K. S. (2018). The Grayling Genome Reveals Selection on Gene Expression Regulation after Whole-Genome Duplication. *Genome Biology and Evolution*, 10(10), 2785–2800. <https://doi.org/10.1093/gbe/evy201>

Elgvin, T. O., Trier, C. N., Tørresen, O. K., Hagen, I. J., Lien, S., **Nederbragt, A. J.**, Ravinet, M., Jensen, H., & Sætre, G.-P. (2017). The genomic mosaicism of hybrid speciation. *Science Advances*, 3(6), e1602996. <https://doi.org/10.1126/sciadv.1602996>

Khelik, K., Lagesen, K., Sandve, G. K., Rognes, T., & **Nederbragt, A. J.** (2017). NucDiff: In-depth characterization and annotation of differences between two sets of DNA sequences. *BMC Bioinformatics*, 18, 338. <https://doi.org/10.1186/s12859-017-1748-z>

Rand, K. D., Grytten, I., **Nederbragt, A. J.**, Storvik, G. O., Glad, I. K., & Sandve, G. K. (2017). Coordinates and intervals in graph-based reference genomes. *BMC Bioinformatics*, 18, 263. <https://doi.org/10.1186/s12859-017-1678-9>

Simovski, B., Vodak, D., Gundersen, S., Domanska, D., Abdulrahman Azab, Holden, L., Holden, M., Grytten, I., Rand, K., Drablos, F., Johansen, M., Mora, A., Lund-Andersen, C., Fromm, B., Eskeland, R., Gabrielsen, O. S., Ferkingstad, E., Sigve Nakken, Bengtsen, M., **Nederbragt, A. J.**,

Thorarensen, H. S., Akse, J. A., Glad, I., Hovig, E., & Sandve, G. K. (2017a). Gsuite HyperBrowser version2.0b. GigaScience Database. <https://doi.org/10.5524/100292>

Simovski, B., Vodák, D., Gundersen, S., Domanska, D., Azab, A., Holden, L., Holden, M., Grytten, I., Rand, K., Drabløs, F., Johansen, M., Mora, A., Lund-Andersen, C., Fromm, B., Eskeland, R., Gabrielsen, O. S., Ferkingstad, E., Nakken, S., Bengtsen, M., **Nederbragt, A. J.**, Sif Thorarensen, H., Andreas Akse, J., Glad, I., Hovig, E., & Sandve, G. K. (2017b). GSuite HyperBrowser: Integrative analysis of dataset collections across the genome and epigenome. GigaScience. <https://doi.org/10.1093/gigascience/gix032>

Tørresen, O. K., Star, B., Jentoft, S., Reinart, W. B., Grove, H., Miller, J. R., Walenz, B. P., Knight, J., Ekholm, J. M., Peluso, P., Edvardsen, R. B., Tooming-Klunderud, A., Skage, M., Lien, S., Jakobsen, K. S., & **Nederbragt, A. J.** (2017). An improved genome assembly uncovers prolific tandem repeats in Atlantic cod. *BMC Genomics*, 18(1), 95. <https://doi.org/10.1186/s12864-016-3448-x>

Wilson, G., Bryan, J., Cranston, K., Kitzes, J., **Nederbragt, L.**, & Teal, T. K. (2017). Good enough practices in scientific computing. *PLOS Computational Biology*, 13(6), e1005510. <https://doi.org/10.1371/journal.pcbi.1005510>

Frank, J. A., Pan, Y., Tooming-Klunderud, A., Eijssink, V. G. H., McHardy, A. C., **Nederbragt, A. J.**, & Pope, P. B. (2016). Improved metagenome assemblies and taxonomic binning using long-read circular consensus sequence data. *Scientific Reports*, 6, 25373. <https://doi.org/10.1038/srep25373>

Haverkamp, T. H., Tourasse, N. J., **Nederbragt, A. J.**, Jakobsen, K. S., Kolstø, A.-B., & Økstad, O. A. (2016). Draft genomes of clinical *Bacillus cereus* isolates AH725 and B06.009 closely related to reference strains ATCC 14579 and ATCC 10987. *bioRxiv*, 073924. <https://doi.org/10.1101/073924>

Lien, S., Koop, B. F., Sandve, S. R., Miller, J. R., Kent, M. P., Nome, T., Hvidsten, T. R., Leong, J. S., Minkley, D. R., Zimin, A., Grammes, F., Grove, H., Gjuvsland, A., Walenz, B., Hermansen, R. A., Schalburg, K. von, Rondeau, E. B., Di Genova, A., Samy, J. K. A., Olav Vik, J., Vigeland, M. D., Caler, L., Grimholt, U., Jentoft, S., Inge Våge, D., Jong, P. de, Moen, T., Baranski, M., Palti, Y., Smith, D. R., Yorke, J. A., **Nederbragt, A. J.**, Tooming-Klunderud, A., Jakobsen, K. S., Jiang, X., Fan, D., Hu, Y., Liberles, D. A., Vidal, R., Iturra, P., Jones, S. J. M., Jonassen, I., Maass, A., Omholt, S. W., & Davidson, W. S. (2016). The Atlantic salmon genome provides insights into rediploidization. *Nature*, 533(7602), 200–205. <https://doi.org/10.1038/nature17164>

Malmstrøm, M., Matschiner, M., Tørresen, O. K., Star, B., Snipen, L. G., Hansen, T. F., Baalsrud, H. T., **Nederbragt, A. J.**, Hanel, R., Salzburger, W., Stenseth, N. C., Jakobsen, K. S., & Jentoft, S. (2016). Evolution of the immune system influences speciation rates in teleost fishes. *Nature Genetics*, 48(10), 1204–1210. <https://doi.org/10.1038/ng.3645>

Solbakken, M. H., Tørresen, O. K., **Nederbragt, A. J.**, Seppola, M., Gregers, T. F., Jakobsen, K. S., & Jentoft, S. (2016). Evolutionary redesign of the Atlantic cod (*Gadus morhua* L.) Toll-like receptor repertoire by gene losses and expansions. *Scientific Reports*, 6, 25211. <https://doi.org/10.1038/srep25211>

Star, B., Tørresen, O. K., **Nederbragt, A. J.**, Jakobsen, K. S., Pampoulie, C., & Jentoft, S. (2016). Genomic characterization of the Atlantic cod sex-locus. *Scientific Reports*, 6, 31235. <https://doi.org/10.1038/srep31235>

- Brembu, T., Winge, P., Tooming-Klunderud, A., **Nederbragt, A. J.**, Jakobsen, K. S., & Bones, A. M. (2014). The chloroplast genome of the diatom *Seminavis robusta*: New features introduced through multiple mechanisms of horizontal gene transfer. *Marine Genomics*, 16, 17–27. <https://doi.org/10.1016/j.margen.2013.12.002>
- Hermansen, J. S., Haas, F., Trier, C. N., Bailey, R. I., **Nederbragt, A. J.**, Marzal, A., & Sætre, G.-P. (2014). Hybrid speciation through sorting of parental incompatibilities in Italian sparrows. *Molecular Ecology*, 23(23), 5831–5842. <https://doi.org/10.1111/mec.12910>
- Nederbragt, A. J.** (2014). On the middle ground between open source and commercial software - the case of the Newbler program. *Genome Biology*, 15(4), 113. <https://doi.org/10.1186/gb4173>
- Röblitz, T., Saastad, O. W., Eide, H. A., Michalickova, K., **Nederbragt, A. J.**, & Star, B. (2014). Scaling of Biological Data Work ows to Large HPC Systems - A Case Study in Marine Genomics -. Zenodo. <https://doi.org/10.5281/zenodo.823031>
- Siddiqui, H., Lagesen, K., **Nederbragt, A. J.**, Eri, L. M., Jeansson, S. L., & Jakobsen, K. S. (2014). Pathogens in Urine from a Female Patient with Overactive Bladder Syndrome Detected by Culture-independent High Throughput Sequencing: A Case Report. *The Open Microbiology Journal*, 8(1). <https://doi.org/10.2174/1874285801408010148>
- Star, B., **Nederbragt, A. J.**, Hansen, M. H. S., Skage, M., Gilfillan, G. D., Bradbury, I. R., Pampoulie, C., Stenseth, N. C., Jakobsen, K. S., & Jentoft, S. (2014). Palindromic Sequence Artifacts Generated during Next Generation Sequencing Library Preparation from Historic and Ancient DNA. *PLOS ONE*, 9(3), e89676. <https://doi.org/10.1371/journal.pone.0089676>
- Tooming-Klunderud, A., Sogge, H., Rounge, T. B., **Nederbragt, A. J.**, Lagesen, K., Glöckner, G., Hayes, P. K., Rohrlack, T., & Jakobsen, K. S. (2013). From Green to Red: Horizontal Gene Transfer of the Phycoerythrin Gene Cluster between Planktothrix Strains. *Appl. Environ. Microbiol.*, 79(21), 6803–6812. <https://doi.org/10.1128/AEM.01455-13>
- Espelund, M., Minge, M. A., Gabrielsen, T. M., **Nederbragt, A. J.**, Shalchian-Tabrizi, K., Otis, C., Turmel, M., Lemieux, C., & Jakobsen, K. S. (2012). Genome Fragmentation Is Not Confined to the Peridinin Plastid in Dinoflagellates. *PLOS ONE*, 7(6), e38809. <https://doi.org/10.1371/journal.pone.0038809>
- Logares, R., Haverkamp, T. H. A., Kumar, S., Lanzén, A., **Nederbragt, A. J.**, Quince, C., & Kauserud, H. (2012). Environmental microbiology through the lens of high-throughput DNA sequencing: Synopsis of current platforms and bioinformatics approaches. *Journal of Microbiological Methods*, 91(1), 106–113. <https://doi.org/10.1016/j.mimet.2012.07.017>
- Siddiqui, H., Lagesen, K., **Nederbragt, A. J.**, Jeansson, S. L., & Jakobsen, K. S. (2012). Alterations of microbiota in urine from women with interstitial cystitis. *BMC Microbiology*, 12(1), 205. <https://doi.org/10.1186/1471-2180-12-205>
- Brede, D. A., Snipen, L. G., Ussery, D. W., **Nederbragt, A. J.**, & Nes, I. F. (2011). Complete Genome Sequence of the Commensal *Enterococcus faecalis* 62, Isolated from a Healthy Norwegian Infant. *Journal of Bacteriology*, 193(9), 2377–2378. <https://doi.org/10.1128/JB.00183-11>
- Gabrielsen, T. M., Minge, M. A., Espelund, M., Tooming-Klunderud, A., Patil, V., **Neder-**

**bragt, A. J.**, Otis, C., Turmel, M., Shalchian-Tabrizi, K., Lemieux, C., & Jakobsen, K. S. (2011). Genome Evolution of a Tertiary Dinoflagellate Plastid. *PLOS ONE*, 6(4), e19132. <https://doi.org/10.1371/journal.pone.0019132>

Siddiqui, H., **Nederbragt, A. J.**, Lagesen, K., Jeansson, S. L., & Jakobsen, K. S. (2011). Assessing diversity of the female urine microbiota by high throughput sequencing of 16S rDNA amplicons. *BMC Microbiology*, 11(1), 244. <https://doi.org/10.1186/1471-2180-11-244>

Star, B., **Nederbragt, A. J.**, Jentoft, S., Grimholt, U., Malmstrøm, M., Gregers, T. F., Rounge, T. B., Paulsen, J., Solbakken, M. H., Sharma, A., Wetten, O. F., Lanzén, A., Winer, R., Knight, J., Vogel, J.-H., Aken, B., Andersen, Ø., Lagesen, K., Tooming-Klunderud, A., Edvardsen, R. B., Tina, K. G., Espelund, M., Nepal, C., Previti, C., Karlsen, B. O., Moum, T., Skage, M., Berg, P. R., Gjøn, T., Kuhl, H., Thorsen, J., Malde, K., Reinhardt, R., Du, L., Johansen, S. D., Searle, S., Lien, S., Nilsen, F., Jonassen, I., Omholt, S. W., Stenseth, N. C., & Jakobsen, K. S. (2011). The genome sequence of Atlantic cod reveals a unique immune system. *Nature*, 477(7363), 207–210. <https://doi.org/10.1038/nature10342>

Løvoll, M., Wiik-Nielsen, J., Grove, S., Wiik-Nielsen, C. R., Kristoffersen, A. B., Faller, R., Poppe, T., Jung, J., Pedamallu, C. S., **Nederbragt, A. J.**, Meyerson, M., Rimstad, E., & Tengs, T. (2010a). A novel totivirus and piscine reovirus (PRV) in Atlantic salmon (*Salmo salar*) with cardiomyopathy syndrome (CMS). *Virology Journal*, 7(1), 309. <https://doi.org/10.1186/1743-422X-7-309>

Løvoll, M., Wiik-Nielsen, J., Grove, S., Wiik-Nielsen, C. R., Kristoffersen, A. B., Faller, R., Poppe, T., Jung, J., Pedamallu, C. S., **Nederbragt, A. J.**, Meyerson, M., Rimstad, E., & Tengs, T. (2010b). A novel totivirus and piscine reovirus (PRV) in Atlantic salmon (*Salmo salar*) with cardiomyopathy syndrome (CMS). *Virology Journal*, 7(1), 309. <https://doi.org/10.1186/1743-422X-7-309>

**Nederbragt, A. J.**, Rounge, T. B., Kausrud, K. L., & Jakobsen, K. S. (2010). Identification and Quantification of Genomic Repeats and Sample Contamination in Assemblies of 454 Pyrosequencing Reads. *Sequencing. Research article*. <https://doi.org/10.1155/2010/782465>

Wetten, O. F., **Nederbragt, A. J.**, Wilson, R. C., Jakobsen, K. S., Edvardsen, R. B., & Andersen, Ø. (2010). Genomic organization and gene expression of the multiple globins in Atlantic cod: Conservation of globin-flanking genes in chordates infers the origin of the vertebrate globin clusters. *BMC Evolutionary Biology*, 10(1), 315. <https://doi.org/10.1186/1471-2148-10-315>

Johansen, S. D., Coucheron, D. H., Andreassen, M., Karlsen, B. O., Furmanek, T., Jørgensen, T. E., Emblem, Å., Breines, R., Nordeide, J. T., Moum, T., **Nederbragt, A. J.**, Stenseth, N. C., & Jakobsen, K. S. (2009). Large-scale sequence analyses of Atlantic cod. *New Biotechnology*, 25(5), 263–271. <https://doi.org/10.1016/j.nbt.2009.03.014>

Rounge, T. B., Rohrlack, T., **Nederbragt, A. J.**, Kristensen, T., & Jakobsen, K. S. (2009). A genome-wide analysis of nonribosomal peptide synthetase gene clusters and their peptides in a *Planktothrix rubescens* strain. *BMC Genomics*, 10(1), 396. <https://doi.org/10.1186/1471-2164-10-396>

Siddiqui, H., **Nederbragt, A. J.**, & Jakobsen, K. S. (2009). A solid-phase method for preparing human DNA from urine for diagnostic purposes. *Clinical Biochemistry*, 42(10), 1128–1135. <https://doi.org/10.1016/j.clinbiochem.2009.03.010>

**Nederbragt, A. J.**, Balasingham, A., Sirevåg, R., Utkilen, H., Jakobsen, K. S., & Anderson-Glenna, M. J. (2008). Multiple-locus variable-number tandem repeat analysis of *Legionella pneumophila* using multi-colored capillary electrophoresis. *Journal of Microbiological Methods*, 73(2), 111–117. <https://doi.org/10.1016/j.mimet.2008.02.007>

Lespinet, O., **Nederbragt, A. J.**, Cassan, M., Dictus, W. J., Loon, A. E. van, & Adoutte, A. (2002). Characterisation of two snail genes in the gastropod mollusc *Patella vulgata*. Implications for understanding the ancestral function of the snail-related genes in Bilateria. *Development Genes and Evolution*, 212(4), 186–195. <https://doi.org/10.1007/s00427-002-0228-1>

**Nederbragt, A. J.**, Lespinet, O., Wageningen, S. V., Loon, A. E. V., Adoutte, A., & Dictus, W. J. A. G. (2002). A lophotrochozoan twist gene is expressed in the ectomesoderm of the gastropod mollusk *Patella vulgata*. *Evolution & Development*, 4(5), 334–343. <https://doi.org/10.1046/j.1525-142X.2002.02020.x>

**Nederbragt, A. J.**, Loon, A. E. van, & Dictus, W. J. A. G. (2002a). Evolutionary biology: Hedgehog crosses the snail's midline. *Nature*, 417(6891), 811–812. <https://doi.org/10.1038/417811b>

**Nederbragt, A. J.**, Loon, A. E. van, & Dictus, W. J. A. G. (2002b). Expression of *Patella vulgata* Orthologs of engrailed and dpp-BMP2/4 in Adjacent Domains during Molluscan Shell Development Suggests a Conserved Compartment Boundary Mechanism. *Developmental Biology*, 246(2), 341–355. <https://doi.org/10.1006/dbio.2002.0653>

**Nederbragt, A. J.**, Welscher, P. te, Driesche, S. van den, Loon, A. E. van, & Dictus, W. J. (2002). Novel and conserved roles for orthodenticle/otx and orthopedia/otp orthologs in the gastropod mollusc *Patella vulgata*. *Development Genes and Evolution*, 212(7), 330–337. <https://doi.org/10.1007/s00427-002-0246-z>

Kooij, A. van der, **Nederbragt, A. J.**, Goedemans, H. J., & Loon, A. van. (1996). The string-like genes of the limpet *Patella vulgata*. *Gene*, 172(2), 261–265. [https://doi.org/10.1016/0378-1119\(96\)00164-3](https://doi.org/10.1016/0378-1119(96)00164-3)

Genomic architecture of haddock (*Melanogrammus aeglefinus*) shows expansions of innate immune genes and short tandem repeats. (n.d.). Retrieved from <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5894186/>

## Thesis

**Nederbragt, A. J.** (2002, February). The evolution of developmental programs : A case study in the gastropod mollusc *Patella vulgata* (Dissertation). Retrieved from <http://dspace.library.uu.nl/handle/1874/213>

## Book chapters

Tørresen, O. K., Rise, M. L., Jin, X., Star, B., MacKenzie, S., Jakobsen, K. S., **Nederbragt, A. J.**, & Jentoft, S. (2016). 3 - An improved version of the Atlantic cod genome and advancements

in functional genomics: Implications for the future of cod farming. In *Genomics in Aquaculture* (pp. 45–72). San Diego: Academic Press. <https://doi.org/10.1016/B978-0-12-801418-9.00003-2>

Tørresen, O. K., Star, B., Jentoft, S., Jakobsen, K. S., & **Nederbragt, A. J.** (2016). 1 - The new era of genome sequencing using high-throughput sequencing technology: Generation of the first version of the Atlantic cod genome. In *Genomics in Aquaculture* (pp. 1–20). San Diego: Academic Press. <https://doi.org/10.1016/B978-0-12-801418-9.00001-9>

## Software publications

Crusoe, M. R., Alameldin, H. F., Awad, S., Boucher, E., Caldwell, A., Cartwright, R., Charbonneau, A., Constantinides, B., Edverson, G., Fay, S., Fenton, J., Fenzl, T., Fish, J., Garcia-Gutierrez, L., Garland, P., Gluck, J., González, I., Guermond, S., Guo, J., Gupta, A., Herr, J. R., Howe, A., Hyer, A., Härpfer, A., Irber, L., Kidd, R., Lin, D., Lippi, J., Mansour, T., McA’Nulty, P., McDonald, E., Mizzi, J., Murray, K. D., Nahum, J. R., Nanlohy, K., **Nederbragt, A. J.**, Ortiz-Zuazaga, H., Ory, J., Pell, J., Pepe-Ranney, C., Russ, Z. N., Schwarz, E., Scott, C., Seaman, J., Sievert, S., Simpson, J., Skennerton, C. T., Spencer, J., Srinivasan, R., Standage, D., Stapleton, J. A., Steinman, S. R., Stein, J., Taylor, B., Trimble, W., Wiencko, H. L., Wright, M., Wyss, B., Zhang, Q., zyme, en, & Brown, C. T. (2015). The khmer software package: Enabling efficient nucleotide sequence analysis. *F1000Research*. <https://doi.org/10.12688/f1000research.6924.1>

## Published lesson materials

Wilson, G., Becker, E., McKay, S., Michonneau, F., Williams, J. J., Mayes, A. C., Silva, R., (hoytpr), P., Crosby, K., **Nederbragt, L.**, NiellInfante, Psomopoulos, F. E., Gourelé, H., (gajusjaugustus), G., dbmarchant, Emonet, R., Cock, P., Banaszkiwicz, P., Teal, T., HLindsay, Thomas, A., Hamm, C., Allen, J., Jordan, K. L., EvanWill, Belkin, M., Pipitone, J., Young, N., Tang, M., Paudel, D., synesthesiam, Mills, B., Devenyi, G. A., Carroll, I., King, T. W., & gtehennepe. (2017, November). Data carpentry wrangling genomics lesson. <https://doi.org/10.5281/zenodo.1064254>

Achterberg, H., Adams, J., Adelman, J., Allen, J., Aranda, J., Bae, S., Banaszkiwicz, P., Barmby, P., Barr, E., Beitey, D., Bekolay, T., Berghold, J., Bjørnstad, M., Blischak, J., Boissonneault, M., Bosley, C., Bostroem, A., Boughton, A., Brase, R., Brown, A., Brown, K., Cabunoc Mayes, A., Carroll, I., Chase, J., Childs, S., Choi, J., Clare, R., Clayton, S., Cock, P., Connell, M., Corvellec, M., Coudrat, T., Dale, R., Davis, M., Davis, N., Davison, A., Demichelis, R., Devenyi, G. A., Dolson, E., Dotson, D., Duchesne, L., Duckles, J., Emonet, R., Endsley, K. A., Fauchereau, N., Ford, T., Förstner, K., Gonzalez, I., Gosmann, J., Gosset, J., Gray, J., Greshake, B., Guillou, S., Haley, M., Hames, S., Hamrick, J. B., Hannon, E., Hansen, M., Hertweck, K., Hinsen, K., Hjelm, J., Hodges, T., Howard, D., Irving, D., Jackson, M., Jolly, B., Jones, N., Joyce, B., Ketcheson, D., King, W. T., Klerke, S., Ko, L., Kwong, A., Laken, B., Lapp, H., Latornell, D., Leeman, J. R., Leyder, J.-C., Ligtenberg, W., Lin, J., Lonsdale, A., Manhaes Savio, A., May, R., Mazur, D., Michonneau, F., Mills, B., Mughal, Z., **Nederbragt, L.**, Neufeld, R., O’Leary, A., Obeng, A., Ory,

J., Osiecka, N., Pipitone, J., Pińska, A., Poisot, T., Pomorski, P., Raghupathy, N., Rathgeber, F., Rawls, M., Richie-Halford, A., Riley, J., Robitaille, T., Rokem, A., Roswell, M., Sadjadi, M., Sales de Andrade, E., Schmeier, S., Sheneman, L., Shiffer, A., Shkurti, A., Silva, R., Soranzo, N., Spence, E., Srinath, A., Staneva, V., Stapleton, J., Stucky, B., Taylor, C., Teal, T., Telenczuk, B., Thomas, I., Thorne, B., Torres, G., Tröndle, T., Upani, J., Vahtras, O., Helm, E. van der, Walsh, A., Walter, N., Weitzel, D., Wheeler, D., White, E., Williamson, E. P., Willmore, F., Wilson, A., Wilson, G., Xiao, X., & Zonca, A. (2017, February). Software Carpentry: Programming with Python. Retrieved from <https://zenodo.org/record/278222#.WUvbc3XytE4>

Ahmadia, A., Allen, J., Appling, A., Aubin, S., Bachant, P., Baird, D., Banaszkiewicz, P., Barmby, P., Batut, B., Bekolay, T., Belkin, M., Blischak, J., Bonsma, M., Borrelli, J., Boughton, A., Bouquin, D., Brauning, R., Brett, M., Brown, A., Cabunoc Mayes, A., Charlesworth, J., Charlton, B., Chen, D., Christensen, G., Collings, R., Corvellec, M., Davis, M., Devenyi, G. A., Dolson, E., Duchesne, L., Duckles, J., Emonet, R., Estève, L., Farsarakis, E., Fauber, B., Fouilloux, A., Förstner, K., Geiger, S., Gonzalez, I., Guarinello, M., Guillou, S., Hadwin, J., Haeni, M., Haessig, P., Hannah, N., Hansen, M., Harihareswara, S., Heilmaier, A., Heroux, M., Hertweck, K., Hilboll, A., Hinsén, K., Huang, D., Ismiraldi, Y., Jackson, M., Jacobs, C., Jarecka, D., Johnston, L. W., Jones, D., Jędrzejewski-Szmek, Z., Kelly, T., King, W. T., Kluyver, T., Konrad, B., Kuzak, M., Küderle, A., Labrie, K., Lapp, H., Latornell, D., Laufersweiler, M., LeBauer, D., Lee, K., Liffers, M., Llebot, C., Loucks, C., Ma, K., Marwaha, K., May, R., Michonneau, F., Mills, B., Mueller, A., Munk, M., Nagraj, V., **Nederbragt, L.**, Nunez-Iglesias, J., O'Brien, B., O'Leary, A., Olsson, C., Panitz, M., Pawsey, C., Pfenninger, S., Pipitone, J., Poisot, T., Preney, P., Rice, T., Riemer, K., Rio Deiros, D., Robinson, N., Rockenberger, A., Rohl, A., Rokem, A., Sacks, B., Sarahan, M., Schmeier, S., Schmider, H., Shellito, P., Shriwise, P. C., Silva, R., Smithyman, B., Soranzo, N., Steinbach, P., Stevens, S., Stueker, O., Stuermer, B., Timbers, T., Traphagen, D., Tröndle, T., Walt, A. van der, Vandervalk, S., Watson, G., Weaver, B., Wheelhouse, M., White, E., Williamson, E. P., Wilson, G., Wu, S., & Zhang, Q. (2017a, February). Software Carpentry: Version Control with Git. Retrieved from <https://zenodo.org/record/278219#.WUvbgHXytE4>

Ahmadia, A., Allen, J., Banaszkiewicz, P., Becker, E., Bekolay, T., Belkin, M., Blischak, J., Boughton, A., Bray, E., Cabunoc Mayes, A., Carroll, I., Crouch, S., Davis, M., Davis, N., Devenyi, G. A., Duckles, J., Emonet, R., Fortin, F.-A., Gonzalez, I., Hamm, C., Hansen, M., Harris, R. M., Henninger, F., Hertweck, K., Hinsén, K., Hodge, A., Jackson, M., King, W. T., Kitzes, J., Koch, C., Lang, D., Liversidge, T., Michonneau, F., Mills, B., **Nederbragt, L.**, Nelson, E., O'Leary, A., Ortiz-Zuazaga, H., Patitsas, E., Pawlik, A., Perez, F., Pipitone, J., Poisot, T., Rokem, A., Silva, R., Steyn, J., Teal, T., Tröndle, T., Tweedie, F., Walt, A. van der, Vie, J.-J., Walker, J., Walsh, A., Weaver, B., White, E., Wilkerson, C., Williams, J., Williamson, E. P., Wilson, G., & Woo, K. (2017b, February). Software Carpentry: Instructor Training. Retrieved from <https://zenodo.org/record/278229#.WUvbfHXytE4>

Aldazabal Mensa, I., Alexander, H., Allen, J., Alsheikh-Hussain, A., Attali, D., Baird, D., Baltzell, A., Banaszkiewicz, P., Barmby, P., Beagrie, R., Beane, G., Bedini, A., Bekolay, T., Belikov, E., Bell, J., Bill, B., Blin, K., Blischak, J., Boardman, S., Boissonneault, M., Bonnie, J., Boughton, A., Brase, R., Brown, A., Brunson, D., Bryk, J., Buske, O., Cabunoc Mayes, A., Carlise, M., Chen, D., Chung, K., Chung, K., Deveau, D., Devenyi, G. A., Doehle, P., Dolson, E., Doyle, M., Duckles, J., Emonet, R., Eyers, D., Fernandes, F., Fontenelle, H., Gacenga, F., Gardner, P., Gidden, M.,

Gonzalez, I., Gray, N., Guillou, S., Hagh, V. F., Hansen, M., Harstad, E., Hohenstein, T., Howe, A., Imamoglu, F., Irving, D., Jackson, M., Jane McTavish, E., Jennings, M., Jones, D., Jones, M. A., Keener, A., Keipert, K., Kelly, T., Kim, J. T., King, W. T., Koch, C., Konrad, B., Lake, S., Lang, D., Latornell, D., Lijnzaad, P., Ma, E., Mac, A., Madin, J., Magle, T., Mandel, M., Marini, C., Marwaha, K., Mashchenko, S., McCloy, D., Michonneau, F., Middleton, R., Milhans, J., Mills, B., Miotto, A., Mount, S., **Nederbragt, L.**, Nielsen, D., Nielsen, D., Noga, K., O’Leary, A., Olson, R., Orr, A., Overgard Therkildsen, N., Palamartchouk, K., Perry, A., Peterson, M., Pipitone, J., Poisot, T., Pourreza, H., Povall, T., Richie-Halford, A., Ritchie, S., Rocha, C. B., Ross, N., Rydbeck, H., Sadjadi, M., Sanders, S., Schloss, P., Seyffert, B., Shattow, G., Silva, R., Simpkin, S., Simpson, J., Smith, B., Sobhani, A., Soranzo, N., Srinath, A., Standage, D., Staton, M., Steinbach, P., Stimberg, M., Telenczuk, B., Thoele, F., Timbers, T., Turner, S., Walt, A. van der, Schyndel, J. van, Vollmer, D., Linden, J. von der, Walker, A., Waterfall, J., Watson, G., White, E., Williamson, E. P., Willing, C., Wilson, G., Winston, D., Wolff, H., Young, L., & Zamparo, L. (2017, February). Software Carpentry: The Unix Shell. Retrieved from <https://zenodo.org/record/278226#.WUvbd3XytE4>

Allen, J., Bachant, P., Banaszkiewicz, P., Bekolay, T., Blischak, J., Boissonneault, M., Boughton, A., Cabunoc Mayes, A., Capes, G., Devenyi, G. A., Digges, D., Duckles, J., Emonet, R., Fraser, A., Hansen, M., Hertweck, K., Irber, L., Jackson, M., King, W. T., Liu, G., Michonneau, F., Mills, B., **Nederbragt, L.**, O’Leary, A., Pipitone, J., Poisot, T., Richie-Halford, A., Sherman, J., Silva, R., Smith, B., St-Onge, P.-L., Teucher, A., Williamson, E. P., & Wilson, G. (2017, February). Software Carpentry: Automation and Make. Retrieved from <https://zenodo.org/record/278220#.WUvbbXXytE4>