



Prof. Dr. Gianni Panagiotou

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Curriculum vitae

Main Research Areas

- Medical & Environmental Metagenomics: human, mice, marine, plants;
- Systems Biology: -omics integration, chemical-protein & protein-protein interaction networks;
- Synthetic Biology: genome-scale metabolic modelling, design of probiotics, discovery of postbiotics

Publications

Bruch A^{*}, Lazarova V^{*}, Krueger T, Schaeuble S, Kelani AA, Lehenberger P, Kniemeyer O, Panagiotou G, Blango MG (2024) Mod5 mediates a molecular trade-off between optimal gene expression and antifungal resistance. *bioRxiv* [Preprint]

[Details](#)



Chen J, Lu RS, Diaz-Canestro C, Song E, Jia X, Liu Y, Wang C, Cheung CKY, Panagiotou G[#], Xu A[#] (2024) Distinct changes in serum metabolites and lipid species in the onset and progression of NAFLD in obese Chinese. *Comput Struct Biotechnol J* 23(2024), 791-800.

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Garcia-Morena D, Fernandez-Cantos MV, Lopez Escalera S, Lok J, Iannone V, Cancellieri P, Maathuis W, Panagiotou G, Aranzamendi C, El Aidy S, Kolehmainen M, El-Nezami H, Wellejus A, Kuipers OP (2024) *In-vitro* influence of specific Bacteroidales strains on gut and liver health related to Metabolic dysfunction-associated fatty liver disease. *Probiotics Antimicrob Proteins* [Epub ahead of print]

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Li H^{*}, Zhang L^{*}, Li J^{*}, Wu Q^{*}, Qian L, He J, Ni Y, Kovatcheva-Datchary P, Yuan R, Liu S, Shen L, Zhang M, Sheng B, Li P, Kang K, Wu L, Fang Q, Long X, Liu X, Wang X, Li Y, Ye Y, Ye J, Bao Y, Zhao Y, Xu G, Panagiotou G[#], Xu A[#], and Jia W[#] (2024) Resistant starch intake facilitates weight loss in humans by reshaping the gut microbiota. *Nat Metab* 6(3), 578-597.

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Loos D^{*}, Pereira da Costa Filho A^{*}, Dutilh B E, Barber AE[#], Panagiotou G[#] (2024) A global survey of host, aquatic, and soil microbiomes reveals shared abundance and genomic features between bacterial and fungal generalists. *Cell Rep* 43(4), 114046.

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McIlroy SE[#], Guibert I, Archana A, Chung WYH, Duffy JE, Gotama R, Hui J, Knowlton N, Leray M, Meyer C, Panagiotou G, Paulay G, Russell B, Thompson PD, Baker DM [#] (2024) Life goes on: Spatial heterogeneity promotes biodiversity in an urbanized coastal marine ecosystem. *Glob Chang Biol* 30(4), e17248.

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Peng H, Schmiederer J, Chen X, Panagiotou G, Kries H[#] (2024) Controlling substrate- and stereospecificity of condensation domains in nonribosomal peptide synthetases. *ACS Chem Bio* 19(3), 599-606.

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Sprague JL, Schille TB, Allert S, Trümper V, Lier A, Großmann P, Priest EL, Tsavou A, Panagiotou G, Naglik JR, Wilson D, Schäuble S, Kasper L^{*}, Hube B^{*#} (2024) *Candida albicans* translocation through the intestinal epithelial barrier is promoted by fungal zinc acquisition and limited by NFκBmediated barrier protection. *Plos Pathogens* 20(3), e1012031.

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Brandt P^{*}, Mirhakkak MH^{*}, Wagner L, Driesch D, Möslinger A, Fänder P, Schäuble S, Panagiotou G, Vylkova S[#] (2023) High-throughput profiling of *Candida auris* isolates reveals clade-specific metabolic differences. *Microbiol Spectr* 11(3), e0049823.

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Chao YY, Puhach A, Frieser D, Arunkumar M, Lehner L, Seeholzer T, Garcia-Lopez A, van der Wal M, Fibi-Smetana S, Dietschmann A, Sommermann T, Ćiković T, Taher L, Gresnigt MS, Vastert SJ, van Wijk F, Panagiotou G, Krappmann D, Groß O, Zielinski CE (2023) Human TH17 cells engage gasdermin E pores to release IL-1 α on NLRP3 inflammasome activation. *Nat Immunol* 24(2), 295-308.

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Page 1 of 11

- [1](#)
- [2](#)
- [3](#)
- [4](#)
- [5](#)
- [6](#)

- [7](#)
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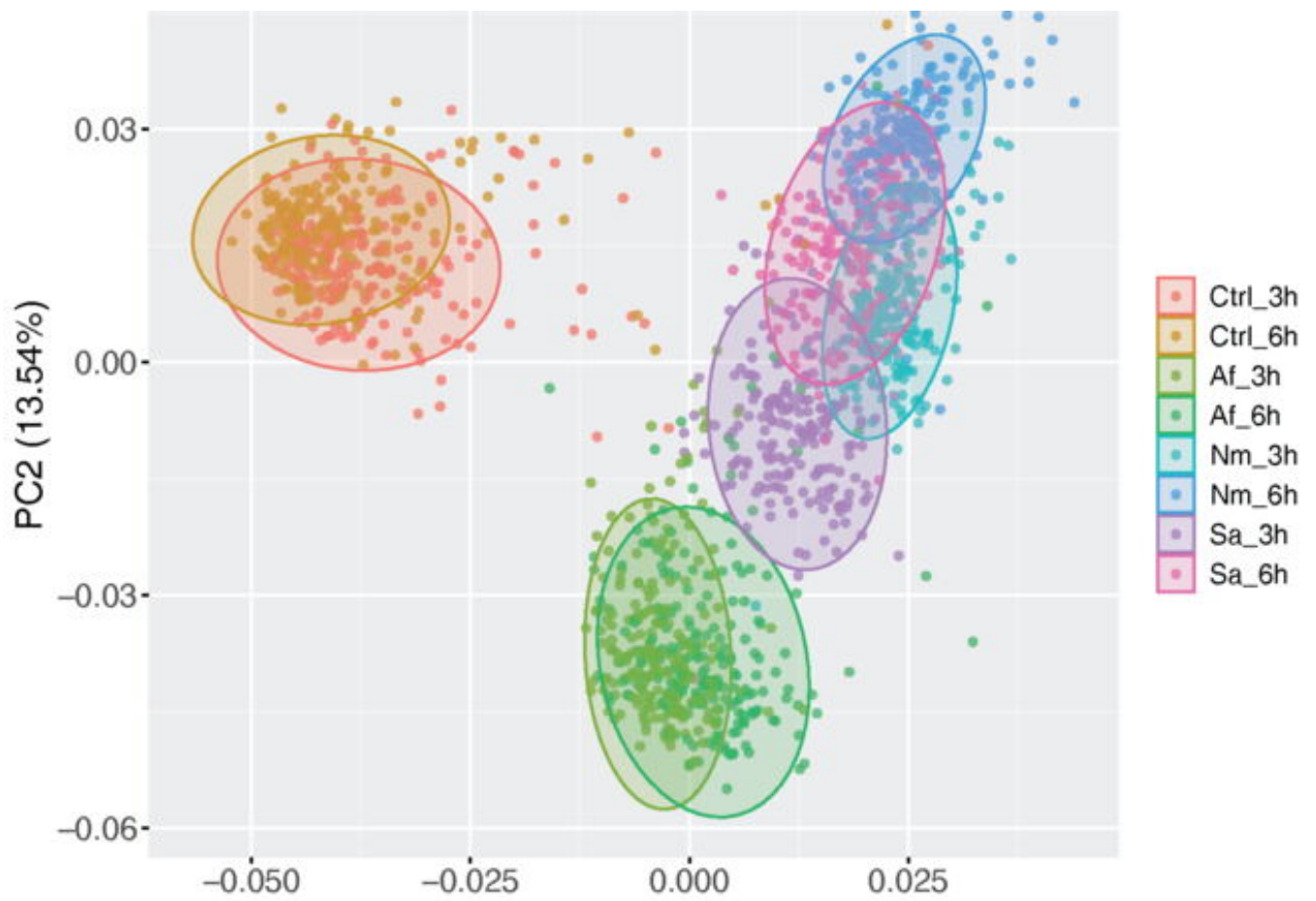
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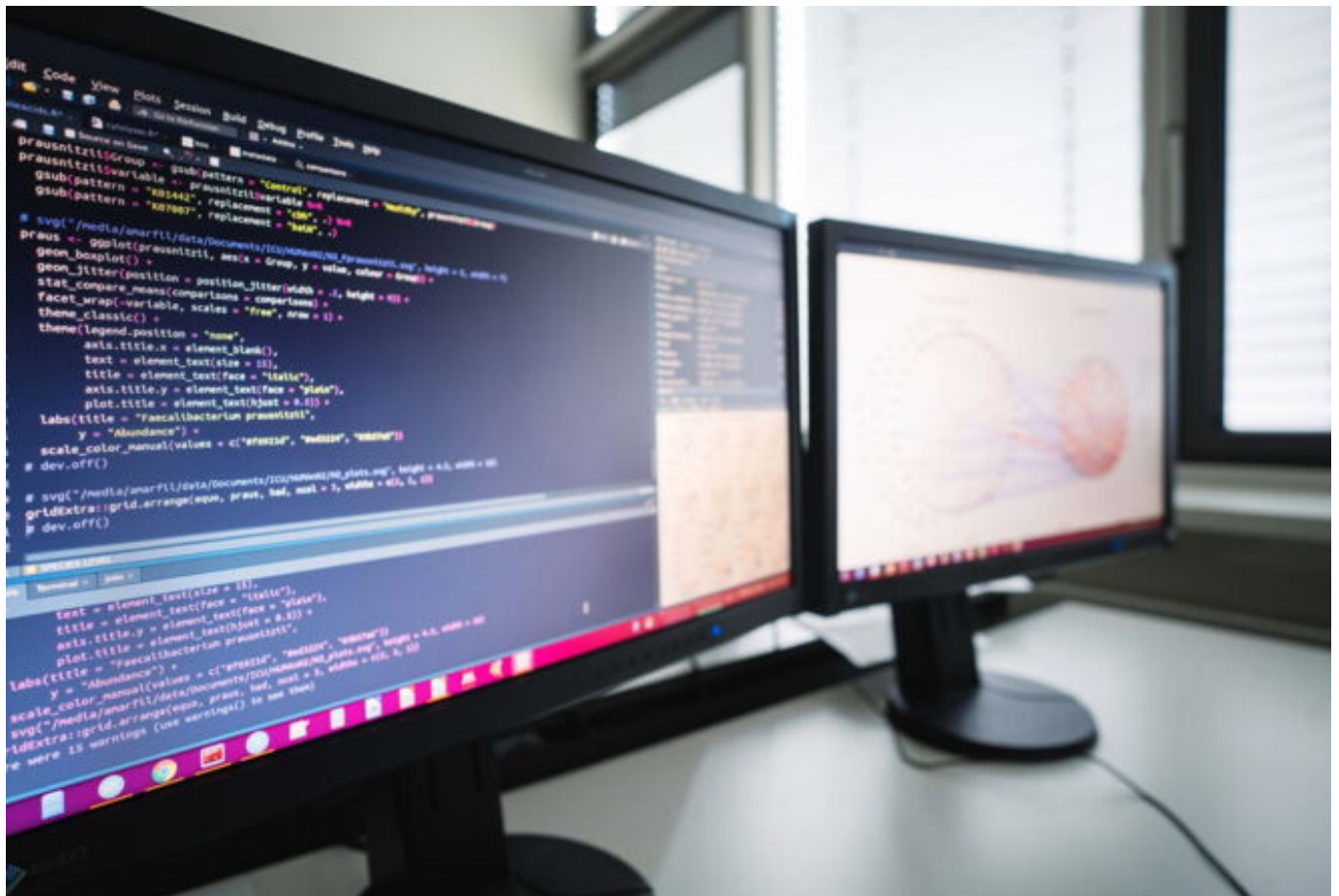
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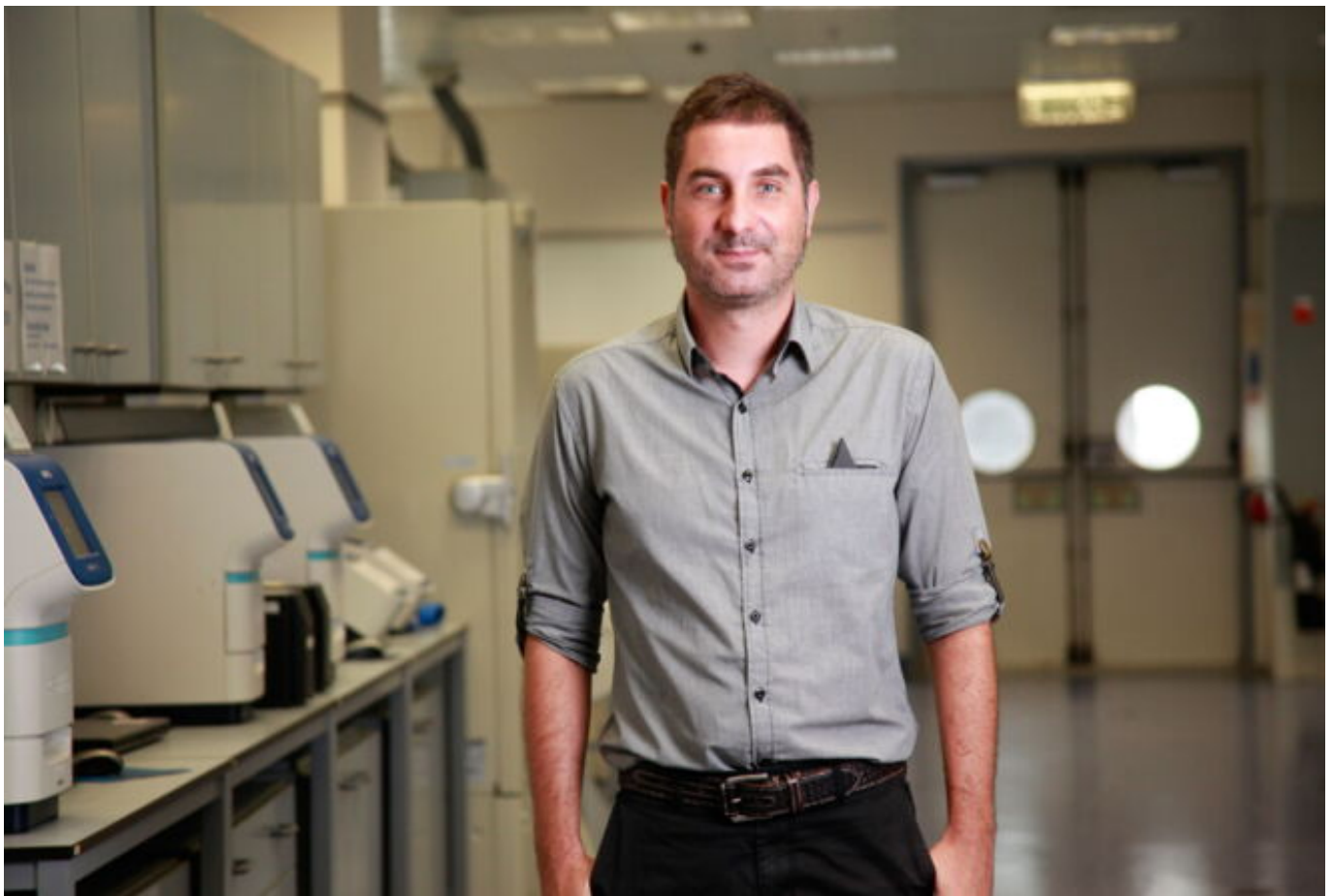
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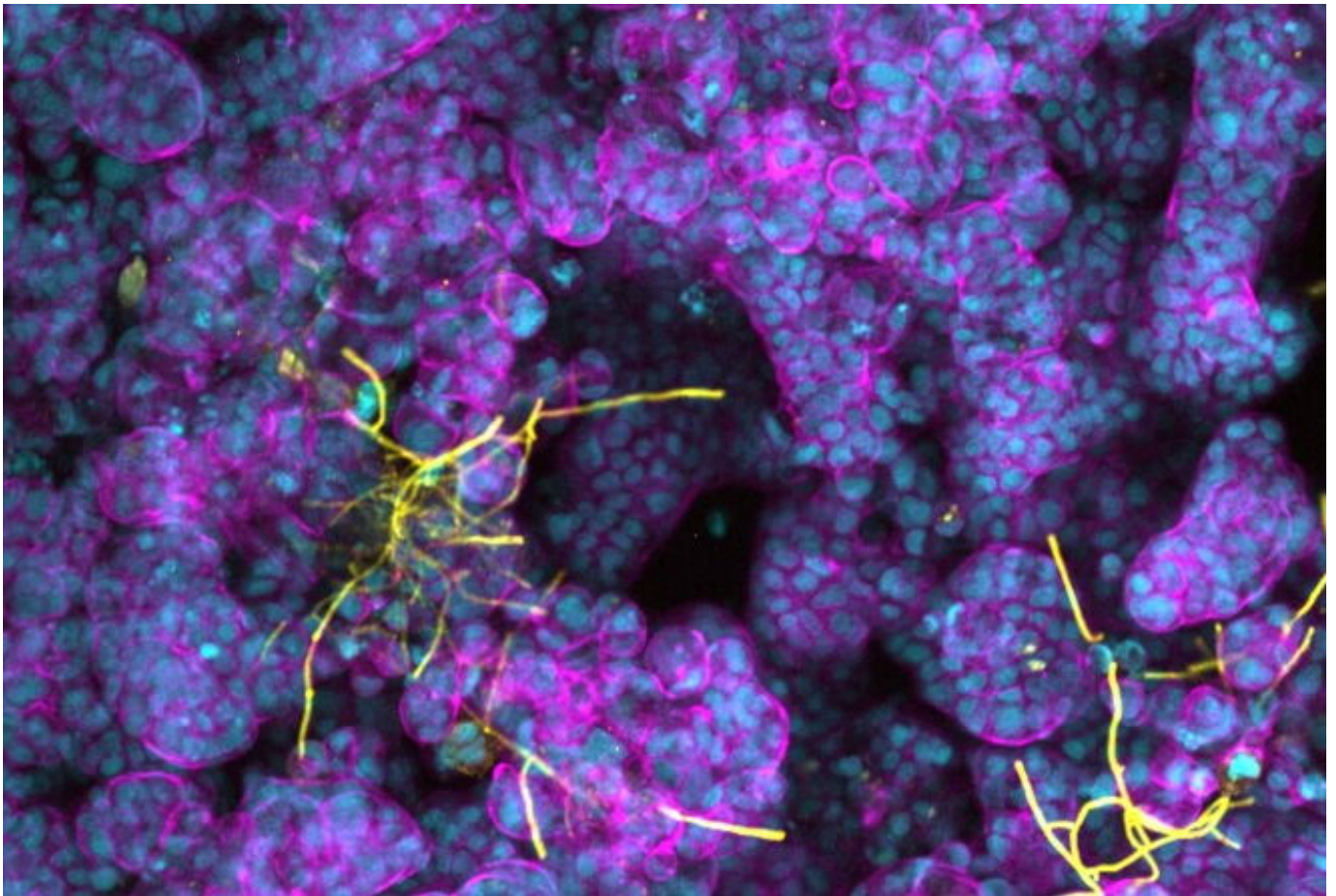
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```

lims <- if (max(abs(E(ig)$Cor)) > 0.80) {
  c(-1, 1)
} else {
  c(-0.75, 0.75)
}

ig_tbl <- ig %>%
  tidygraph::as_tbl_graph() %>%
  tidygraph::activate(nodes) %>%
  left_join(label_group, by = c("name" = "name")) %>%
  #filter(!is.na(ClusterID)) %>%
  #mutate(ClusterID = as.factor(ClusterID)) %>%
  tidygraph::activate(edges) %>%
  mutate(
    strength = cut(abs(weight), breaks = c(0, 0.25, 0.5, 1.0)),
    sign = sign(weight) %>% factor(levels = c(1, -1), labels = c("Positive", "Negative"))
    #sign = sign(weight) %>% factor(levels = c(1, -1), labels = c("solid", "dashed"))
  )

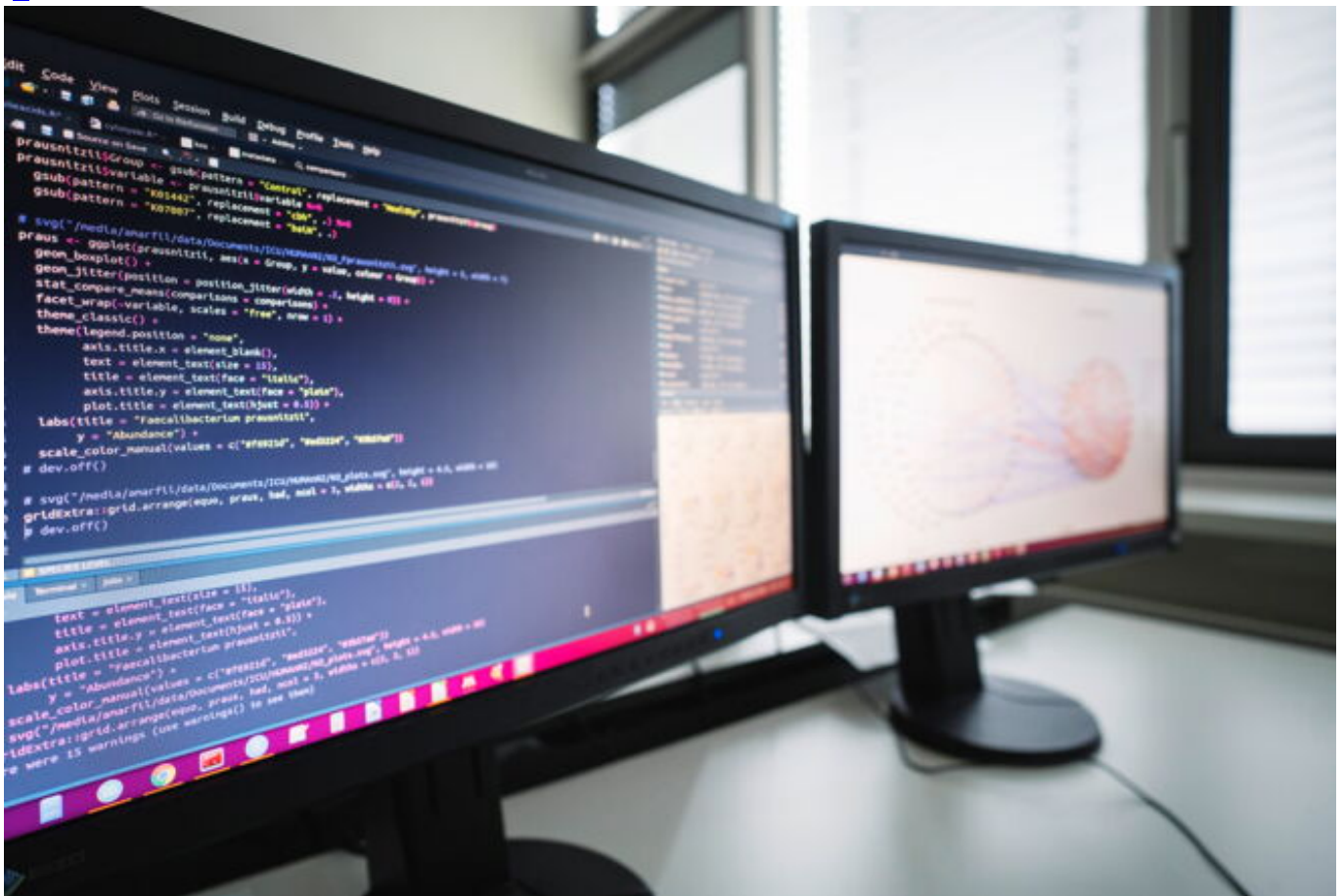
ig_tbl %>%
  ggraph::ggraph(layout = coords) +
  ggraph::geom_edge_diagonal(aes(color = sign, width = strength), alpha = 0.75, strength = 4) +
  ggraph::scale_edge_color_manual(values = c("Positive" = "#457b9d", "Negative" = "#d62728")) +
  #scale_edge_color_percept()
  #scale_edge_color_percept(palette = "roma", discrete = FALSE, limits = lims, breaks = c(0.25, 0.5, 1.0)) +
  #ggraph::scale_edge_color_gradient(guide = ggraph::guide_edge_colorbar()) +
  #scale_edge_color_continuous() +
  #scale_edge_color_continuous(type = "div", palette = "rdylbu", limits = lims, breaks =

```

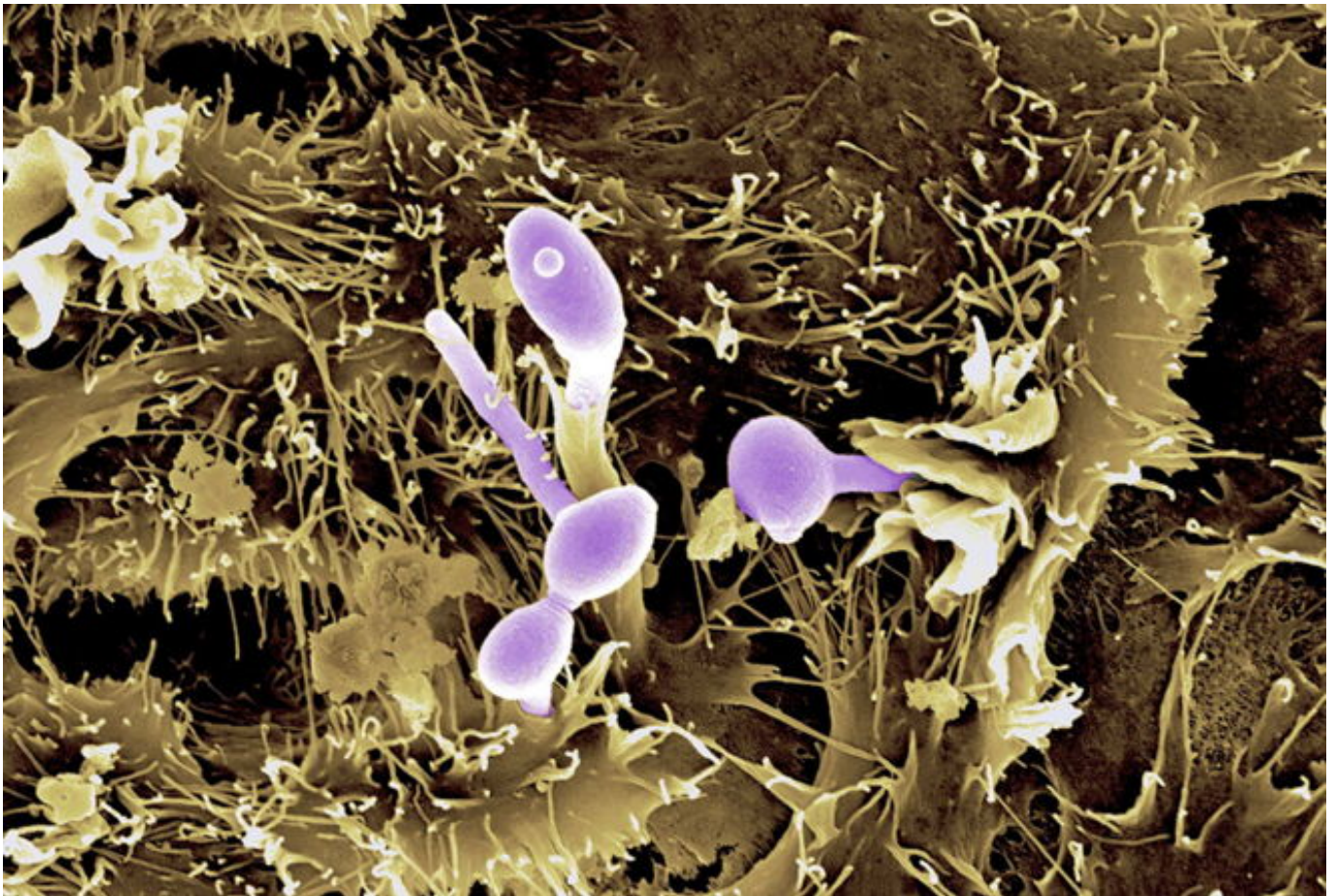
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