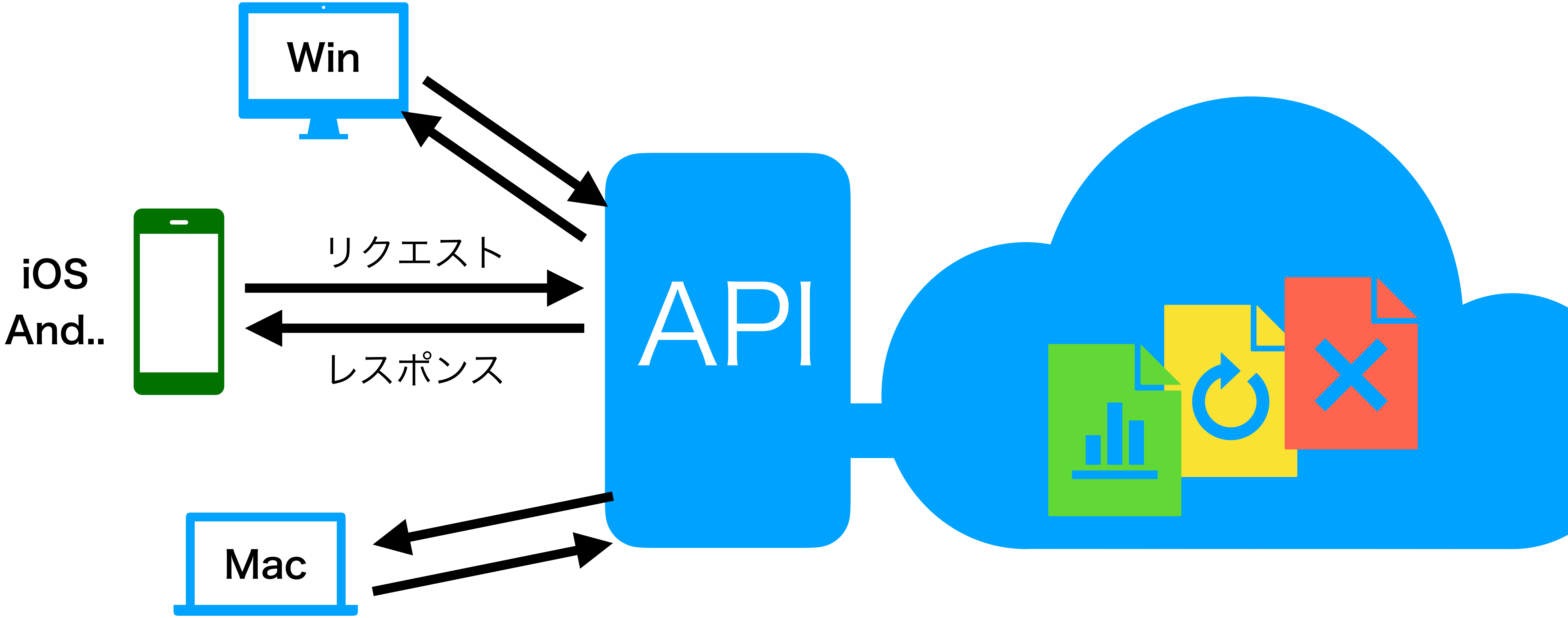
# 基盤モデル
# 使い方

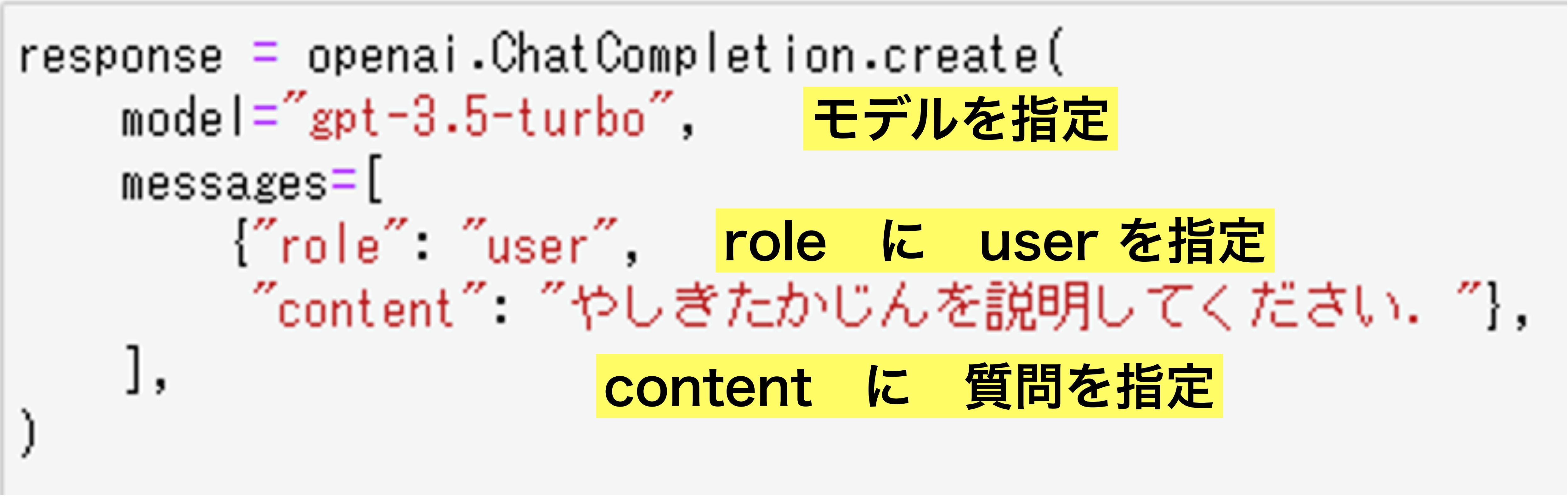
# API

Application Programming Interface

他のアプリやネットワークなどと接続する仕組み



# 問い合わせ方



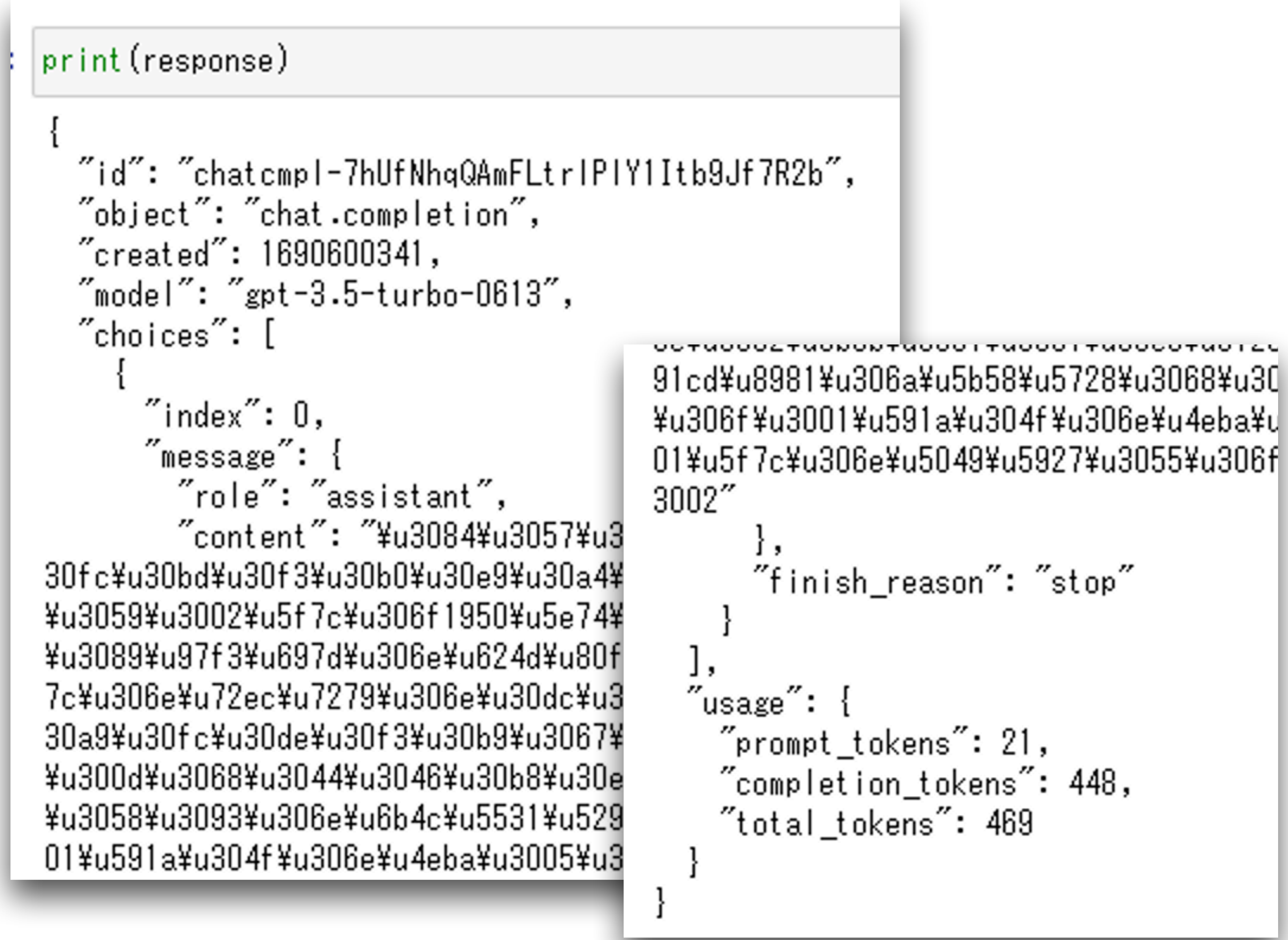
```
response = openai.ChatCompletion.create(
    model="gpt-3.5-turbo",
    messages=[
        {"role": "user",
         "content": "やしきたかじんを説明してください．"},
    ],
)
```

モデルを指定

role　に　user を指定

content　に　質問を指定

# 返答



```
print(response)
```

```
{
  "id": "chatcmpl-7hUfNhqQAmFLtrlPlY1Itb9Jf7R2b",
  "object": "chat.completion",
  "created": 1690600341,
  "model": "gpt-3.5-turbo-0613",
  "choices": [
    {
      "index": 0,
      "message": {
        "role": "assistant",
        "content": "¥u3084¥u3057¥u3
30fc¥u30bd¥u30f3¥u30b0¥u30e9¥u30a4¥
¥u3059¥u3002¥u5f7c¥u306f1950¥u5e74¥
¥u3089¥u97f3¥u697d¥u306e¥u624d¥u80f
7c¥u306e¥u72ec¥u7279¥u306e¥u30dc¥u3
30a9¥u30fc¥u30de¥u30f3¥u30b9¥u3067¥
¥u300d¥u3068¥u3044¥u3046¥u30b8¥u30e
¥u3058¥u3093¥u306e¥u6b4c¥u5531¥u529
01¥u591a¥u304f¥u306e¥u4eba¥u3005¥u3
```

```
91cd¥u8981¥u306a¥u5b58¥u5728¥u3068¥u30
¥u306f¥u3001¥u591a¥u304f¥u306e¥u4eba¥u
01¥u5f7c¥u306e¥u5049¥u5927¥u3055¥u306f
3002"
      },
      "finish_reason": "stop"
    }
  ],
  "usage": {
    "prompt_tokens": 21,
    "completion_tokens": 448,
    "total_tokens": 469
  }
}
```

# ChatGPT API

| Role | 内容 |
|---|---|
| system | ChatGPTに役を与える |
| user | ChatGPTにテキストを提供する |
| assistant | 以前の回答を加えて回答を求める |

```
text = "やしきたかじんを説明してください．"

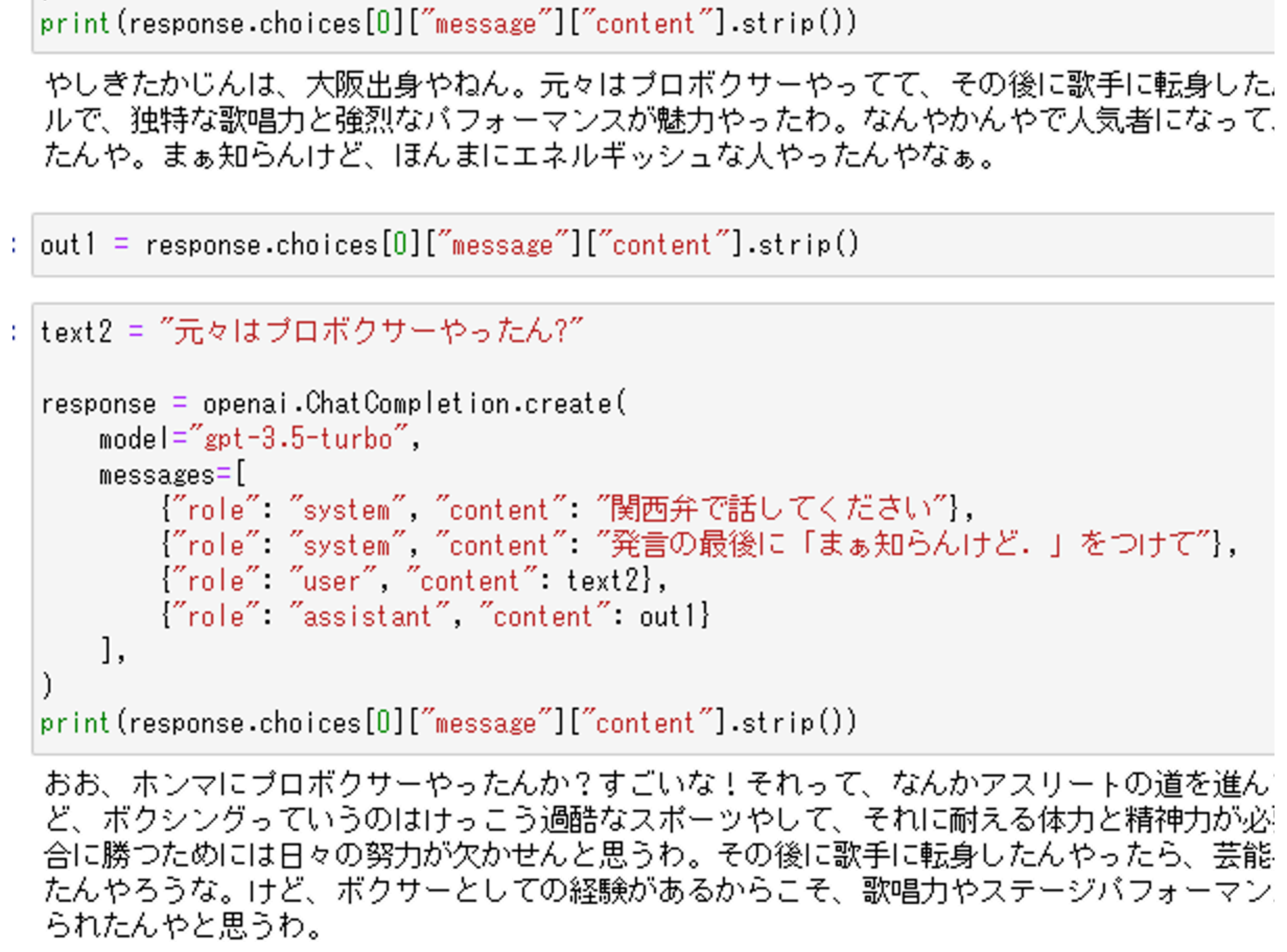
response = openai.ChatCompletion.create(
    model="gpt-3.5-turbo",
    messages=[
        {"role": "system", "content": "関西弁で話してください"},
        {"role": "system", "content": "発言の最後に「まぁ知らんけど．」をつけて"},
#        {"role": "user", "content": text},
        {"role": "assistant", "content": text}
    ],
)
print(response.choices[0]["message"]["content"].strip())
```

```
やしきたかじんは、大阪出身やねん。元々はプロボクサーやってて、その後に歌手に転身した
ルで、独特な歌唱力と強烈なパフォーマンスが魅力やったわ。なんやかんやで人気者になって
たんや。まぁ知らんけど、ほんまにエネルギッシュな人やったんやなぁ。
```

```
out1 = response.choices[0]["message"]["content"].strip()
```

```
text2 = "元々はプロボクサーやったん?"

response = openai.ChatCompletion.create(
    model="gpt-3.5-turbo",
    messages=[
        {"role": "system", "content": "関西弁で話してください"},
```



```
print(response.choices[0]["message"]["content"].strip())
```

```
やしきたかじんは、大阪出身やねん。元々はプロボクサーやってて、その後に歌手に転身した
ルで、独特な歌唱力と強烈なパフォーマンスが魅力やったわ。なんやかんやで人気者になって
たんや。まぁ知らんけど、ほんまにエネルギッシュな人やったんやなぁ。
```

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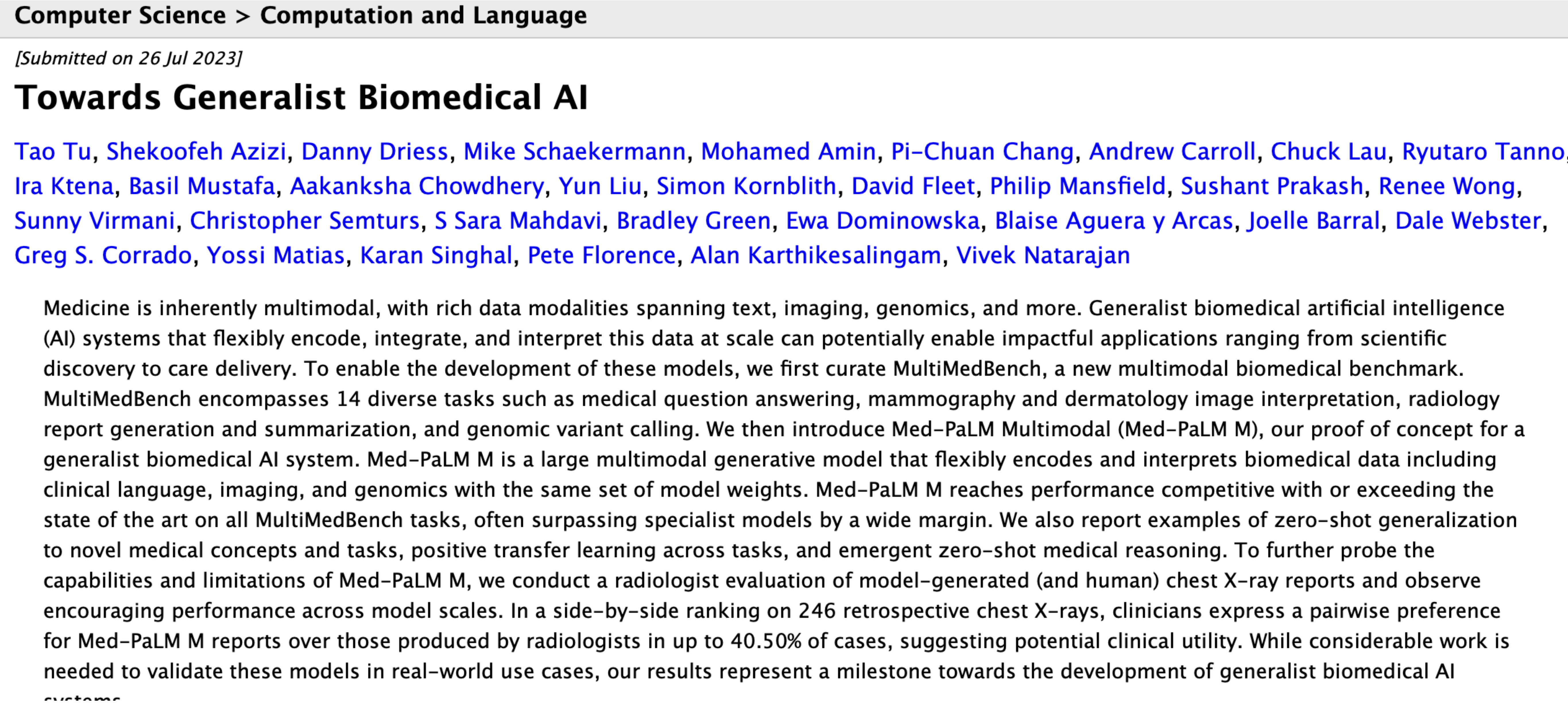
```

```
text2 = "元々はプロボクサーやったん?"


response = openai.ChatCompletion.create(
    model="gpt-3.5-turbo",
    messages=[
        {"role": "system", "content": "関西弁で話してください"},
        {"role": "system", "content": "発言の最後に「まぁ知らんけど．」をつけて"},
        {"role": "user", "content": text2},
        {"role": "assistant", "content": out1}
    ],
)
print(response.choices[0]["message"]["content"].strip())
```

```
おお、ホンマにプロボクサーやったんか？すごいな！それって、なんかアスリートの道を進ん
ど、ボクシングっていうのはけっこう過酷なスポーツやして、それに耐える体力と精神力が
合に勝つためには日々の努力が欠かせんと思うわ。その後に歌手に転身したんやったら、芸能
たんやろうな。けど、ボクサーとしての経験があるからこそ、歌唱力やステージパフォーマン
られたんやと思うわ。
```

# 医療用モデル



**Computer Science > Computation and Language**

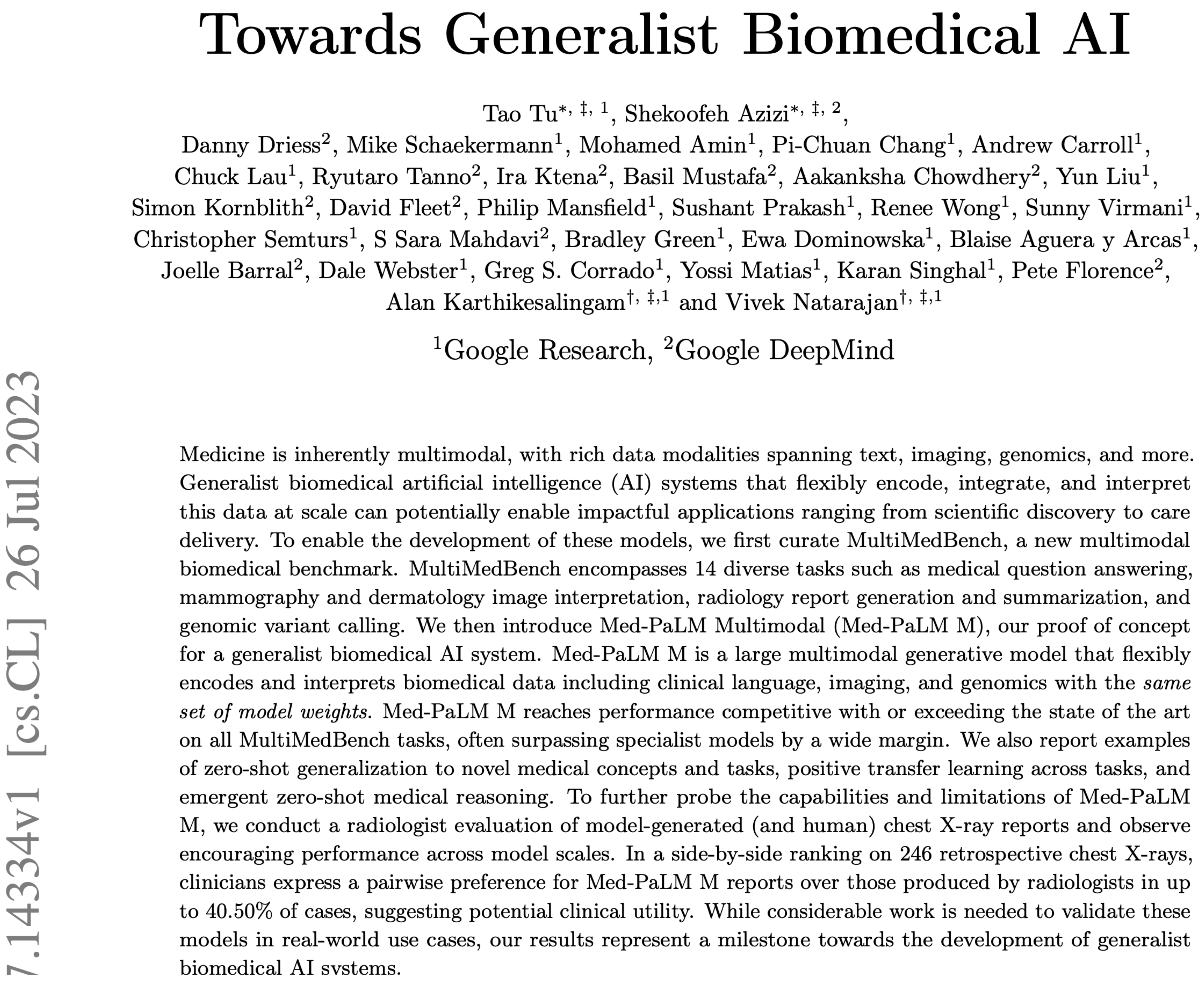
*[Submitted on 26 Jul 2023]*

# Towards Generalist Biomedical AI

Tao Tu, Shekoofeh Azizi, Danny Driess, Mike Schaekermann, Mohamed Amin, Pi-Chuan Chang, Andrew Carroll, Chuck Lau, Ryutaro Tanno, Ira Ktena, Basil Mustafa, Aakanksha Chowdhery, Yun Liu, Simon Kornblith, David Fleet, Philip Mansfield, Sushant Prakash, Renee Wong, Sunny Virmani, Christopher Semturs, S Sara Mahdavi, Bradley Green, Ewa Dominowska, Blaise Aguera y Arcas, Joelle Barral, Dale Webster, Greg S. Corrado, Yossi Matias, Karan Singhal, Pete Florence, Alan Karthikesalingam, Vivek Natarajan

Medicine is inherently multimodal, with rich data modalities spanning text, imaging, genomics, and more. Generalist biomedical artificial intelligence (AI) systems that flexibly encode, integrate, and interpret this data at scale can potentially enable impactful applications ranging from scientific discovery to care delivery. To enable the development of these models, we first curate MultiMedBench, a new multimodal biomedical benchmark. MultiMedBench encompasses 14 diverse tasks such as medical question answering, mammography and dermatology image interpretation, radiology report generation and summarization, and genomic variant calling. We then introduce Med-PaLM Multimodal (Med-PaLM M), our proof of concept for a generalist biomedical AI system. Med-PaLM M is a large multimodal generative model that flexibly encodes and interprets biomedical data including clinical language, imaging, and genomics with the same set of model weights. Med-PaLM M reaches performance competitive with or exceeding the state of the art on all MultiMedBench tasks, often surpassing specialist models by a wide margin. We also report examples of zero-shot generalization to novel medical concepts and tasks, positive transfer learning across tasks, and emergent zero-shot medical reasoning. To further probe the capabilities and limitations of Med-PaLM M, we conduct a radiologist evaluation of model-generated (and human) chest X-ray reports and observe encouraging performance across model scales. In a side-by-side ranking on 246 retrospective chest X-rays, clinicians express a pairwise preference for Med-PaLM M reports over those produced by radiologists in up to 40.50% of cases, suggesting potential clinical utility. While considerable work is needed to validate these models in real-world use cases, our results represent a milestone towards the development of generalist biomedical AI systems

https://arxiv.org/abs/2307.14334



# Towards Generalist Biomedical AI

Tao Tu[*, ‡, 1], Shekoofeh Azizi[*, ‡, 2],
Danny Driess[2], Mike Schaekermann[1], Mohamed Amin[1], Pi-Chuan Chang[1], Andrew Carroll[1],
Chuck Lau[1], Ryutaro Tanno[2], Ira Ktena[2], Basil Mustafa[2], Aakanksha Chowdhery[2], Yun Liu[1],
Simon Kornblith[2], David Fleet[2], Philip Mansfield[1], Sushant Prakash[1], Renee Wong[1], Sunny Virmani[1],
Christopher Semturs[1], S Sara Mahdavi[2], Bradley Green[1], Ewa Dominowska[1], Blaise Aguera y Arcas[1],
Joelle Barral[2], Dale Webster[1], Greg S. Corrado[1], Yossi Matias[1], Karan Singhal[1], Pete Florence[2],
Alan Karthikesalingam[†, ‡,1] and Vivek Natarajan[†, ‡,1]

[1]Google Research, [2]Google DeepMind

Medicine is inherently multimodal, with rich data modalities spanning text, imaging, genomics, and more. Generalist biomedical artificial intelligence (AI) systems that flexibly encode, integrate, and interpret this data at scale can potentially enable impactful applications ranging from scientific discovery to care delivery. To enable the development of these models, we first curate MultiMedBench, a new multimodal biomedical benchmark. MultiMedBench encompasses 14 diverse tasks such as medical question answering, mammography and dermatology image interpretation, radiology report generation and summarization, and genomic variant calling. We then introduce Med-PaLM Multimodal (Med-PaLM M), our proof of concept for a generalist biomedical AI system. Med-PaLM M is a large multimodal generative model that flexibly encodes and interprets biomedical data including clinical language, imaging, and genomics with the *same set of model weights*. Med-PaLM M reaches performance competitive with or exceeding the state of the art on all MultiMedBench tasks, often surpassing specialist models by a wide margin. We also report examples of zero-shot generalization to novel medical concepts and tasks, positive transfer learning across tasks, and emergent zero-shot medical reasoning. To further probe the capabilities and limitations of Med-PaLM M, we conduct a radiologist evaluation of model-generated (and human) chest X-ray reports and observe encouraging performance across model scales. In a side-by-side ranking on 246 retrospective chest X-rays, clinicians express a pairwise preference for Med-PaLM M reports over those produced by radiologists in up to 40.50% of cases, suggesting potential clinical utility. While considerable work is needed to validate these models in real-world use cases, our results represent a milestone towards the development of generalist biomedical AI systems.

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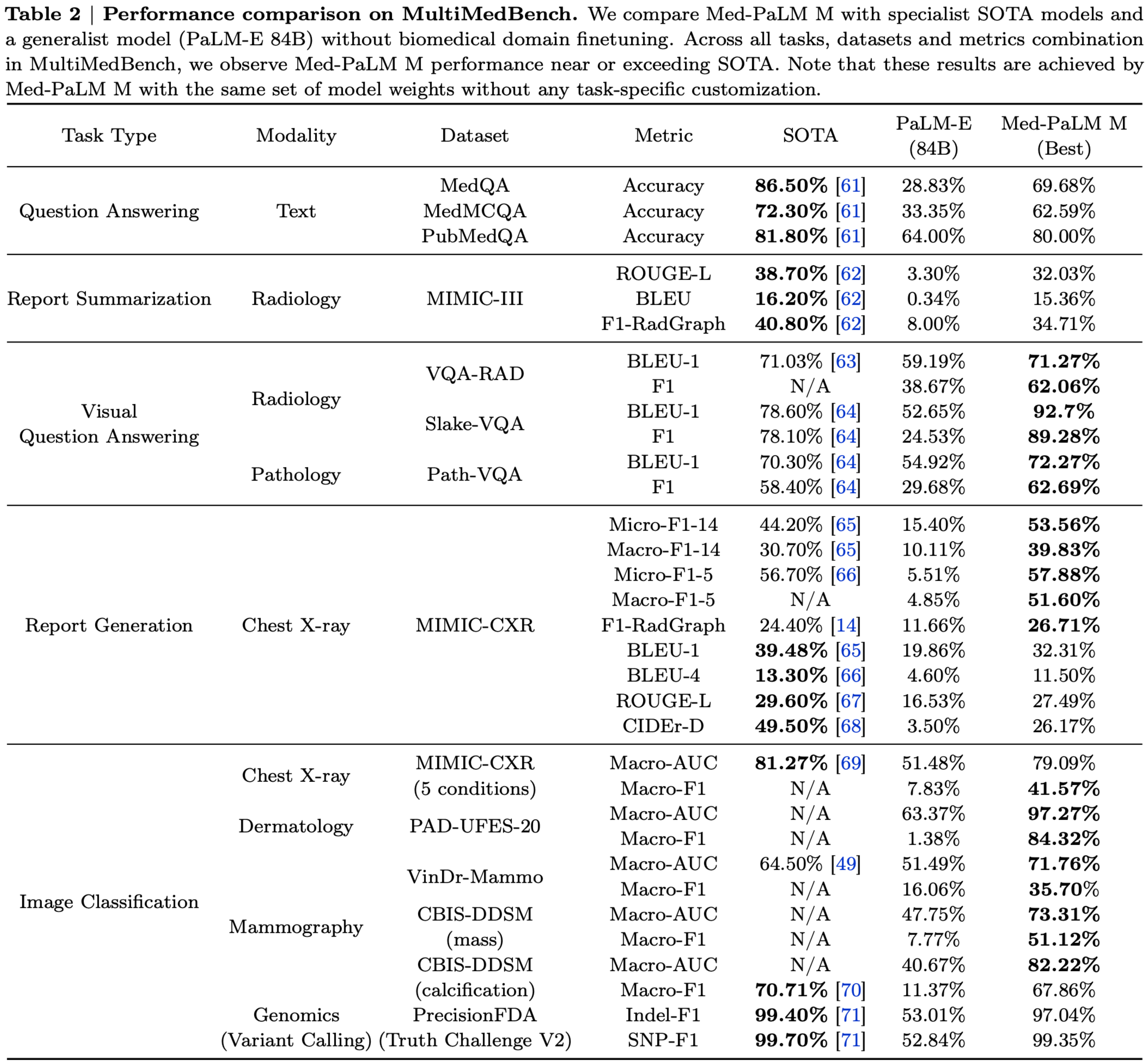


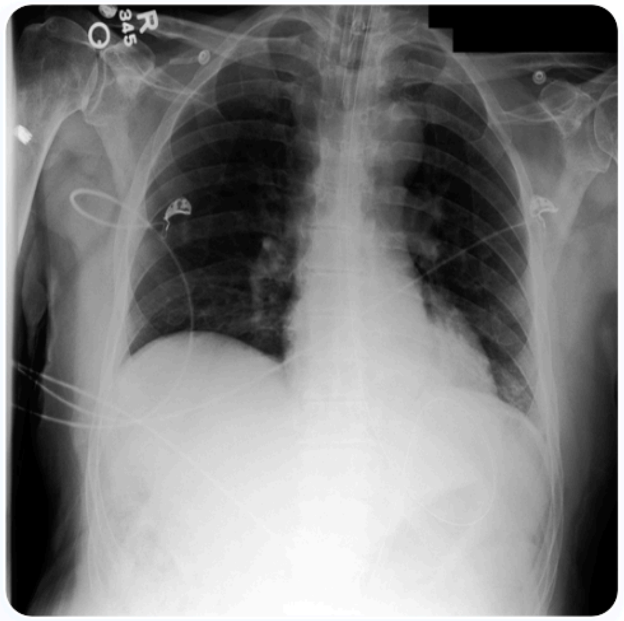
**Table 2 | Performance comparison on MultiMedBench.** We compare Med-PaLM M with specialist SOTA models and a generalist model (PaLM-E 84B) without biomedical domain finetuning. Across all tasks, datasets and metrics combination in MultiMedBench, we observe Med-PaLM M performance near or exceeding SOTA. Note that these results are achieved by Med-PaLM M with the same set of model weights without any task-specific customization.

| Task Type | Modality | Dataset | Metric | SOTA | PaLM-E (84B) | Med-PaLM M (Best) |
|---|---|---|---|---|---|---|
| Question Answering | Text | MedQA | Accuracy | **86.50%** [61] | 28.83% | 69.68% |
| | | MedMCQA | Accuracy | **72.30%** [61] | 33.35% | 62.59% |
| | | PubMedQA | Accuracy | **81.80%** [61] | 64.00% | 80.00% |
| Report Summarization | Radiology | MIMIC-III | ROUGE-L | **38.70%** [62] | 3.30% | 32.03% |
| | | | BLEU | **16.20%** [62] | 0.34% | 15.36% |
| | | | F1-RadGraph | **40.80%** [62] | 8.00% | 34.71% |
| Visual Question Answering | Radiology | VQA-RAD | BLEU-1 | 71.03% [63] | 59.19% | **71.27%** |
| | | | F1 | N/A | 38.67% | **62.06%** |
| | | Slake-VQA | BLEU-1 | 78.60% [64] | 52.65% | **92.7%** |
| | | | F1 | 78.10% [64] | 24.53% | **89.28%** |
| | Pathology | Path-VQA | BLEU-1 | 70.30% [64] | 54.92% | **72.27%** |
| | | | F1 | 58.40% [64] | 29.68% | **62.69%** |
| Report Generation | Chest X-ray | MIMIC-CXR | Micro-F1-14 | 44.20% [65] | 15.40% | **53.56%** |
| | | | Macro-F1-14 | 30.70% [65] | 10.11% | **39.83%** |
| | | | Micro-F1-5 | 56.70% [66] | 5.51% | **57.88%** |
| | | | Macro-F1-5 | N/A | 4.85% | **51.60%** |
| | | | F1-RadGraph | 24.40% [14] | 11.66% | **26.71%** |
| | | | BLEU-1 | **39.48%** [65] | 19.86% | 32.31% |
| | | | BLEU-4 | **13.30%** [66] | 4.60% | 11.50% |
| | | | ROUGE-L | **29.60%** [67] | 16.53% | 27.49% |
| | | | CIDEr-D | **49.50%** [68] | 3.50% | 26.17% |
| Image Classification | Chest X-ray | MIMIC-CXR (5 conditions) | Macro-AUC | **81.27%** [69] | 51.48% | 79.09% |
| | | | Macro-F1 | N/A | 7.83% | **41.57%** |
| | Dermatology | PAD-UFES-20 | Macro-AUC | N/A | 63.37% | **97.27%** |
| | | | Macro-F1 | N/A | 1.38% | **84.32%** |
| | Mammography | VinDr-Mammo | Macro-AUC | 64.50% [49] | 51.49% | **71.76%** |
| | | | Macro-F1 | N/A | 16.06% | **35.70%** |
| | | CBIS-DDSM (mass) | Macro-AUC | N/A | 47.75% | **73.31%** |
| | | | Macro-F1 | N/A | 7.77% | **51.12%** |
| | | CBIS-DDSM (calcification) | Macro-AUC | N/A | 40.67% | **82.22%** |
| | | | Macro-F1 | **70.71%** [70] | 11.37% | 67.86% |
| | Genomics (Variant Calling) | PrecisionFDA (Truth Challenge V2) | Indel-F1 | **99.40%** [71] | 53.01% | 97.04% |
| | | | SNP-F1 | **99.70%** [71] | 52.84% | 99.35% |

https://arxiv.org/abs/2307.14334

**Indication**

-year-old male with intubation. No prior examinations for comparison.



**Reference Report**

Endotracheal tube terminates 6 cm from the carina. Nasogastric tube loops within the stomach with side port within the gastric body. There are no significant pleural effusions or pneumothorax. Mild retrocardiac atelectasis is present. Heart size is normal. The aorta is tortuous.

**Med-PaLM M 12B**

An endotracheal tube terminates 5 cm above the carina. There is no pneumothorax or large pleural effusion. Opacities in the medial right lower lobe and retrocardiac region may represent atelectasis aspiration or pneumonia. A calcified lymph node is noted in the aortopulmonary window. Cardiac size is normal. *[No comment about NG/OG tube]*

**Med-PaLM M 84B**

Endotracheal tube terminates 5 cm above the carina. Nasogastric tube courses below the diaphragm and inferiorly beyond the film. There is retrocardiac opacity which may represent atelectasis or aspiration. The heart size is normal. The aorta is tortuous and unfolded. No pleural effusions or pneumothorax.

**Med-PaLM M 562B**

Endotracheal tube terminates 5 cm above the carina. Nasogastric tube courses below the diaphragm and inferiorly beyond the film. Lung volumes are low with crowding of bronchovascular markings. There is a left retrocardiac opacity. There is no pneumothorax or pleural effusions.

Significant error

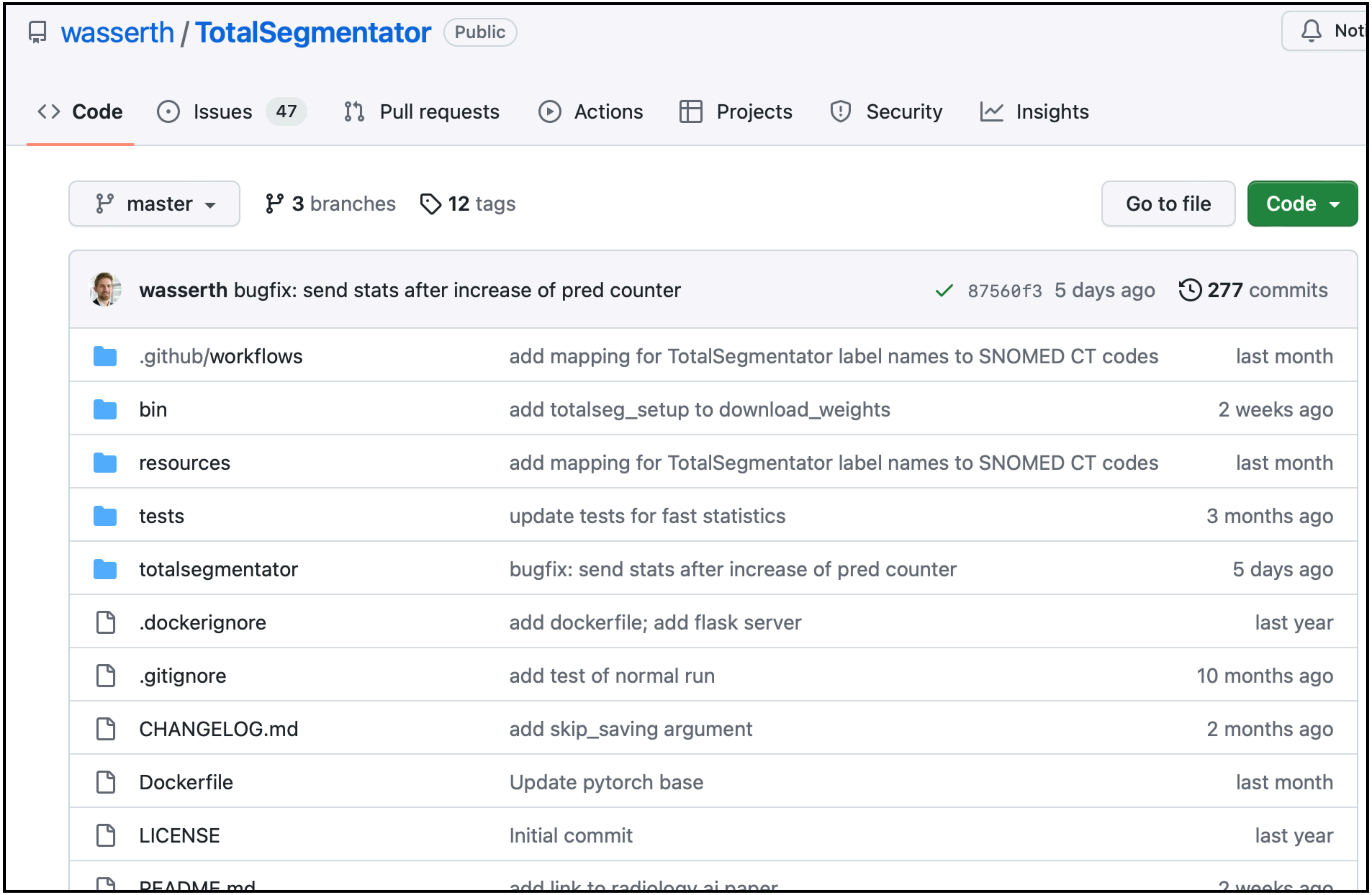
Insignificant error

*[Omission]*

**Figure 6 | Qualitative example of reference and Med-PaLM M generated chest X-ray reports.** We present a qualitative example of chest X-ray reports generated by Med-PaLM M across model scales along with the target reference report. In this example, a panel of radiologists adjudicated the Med-PaLM M 12B report to have two clinically significant errors and one omission, the Med-PaLM M 84B report to have zero errors and zero omissions, and the Med-PaLM M 562B report to have one clinically insignificant error and no omissions.

https://arxiv.org/abs/2307.14334

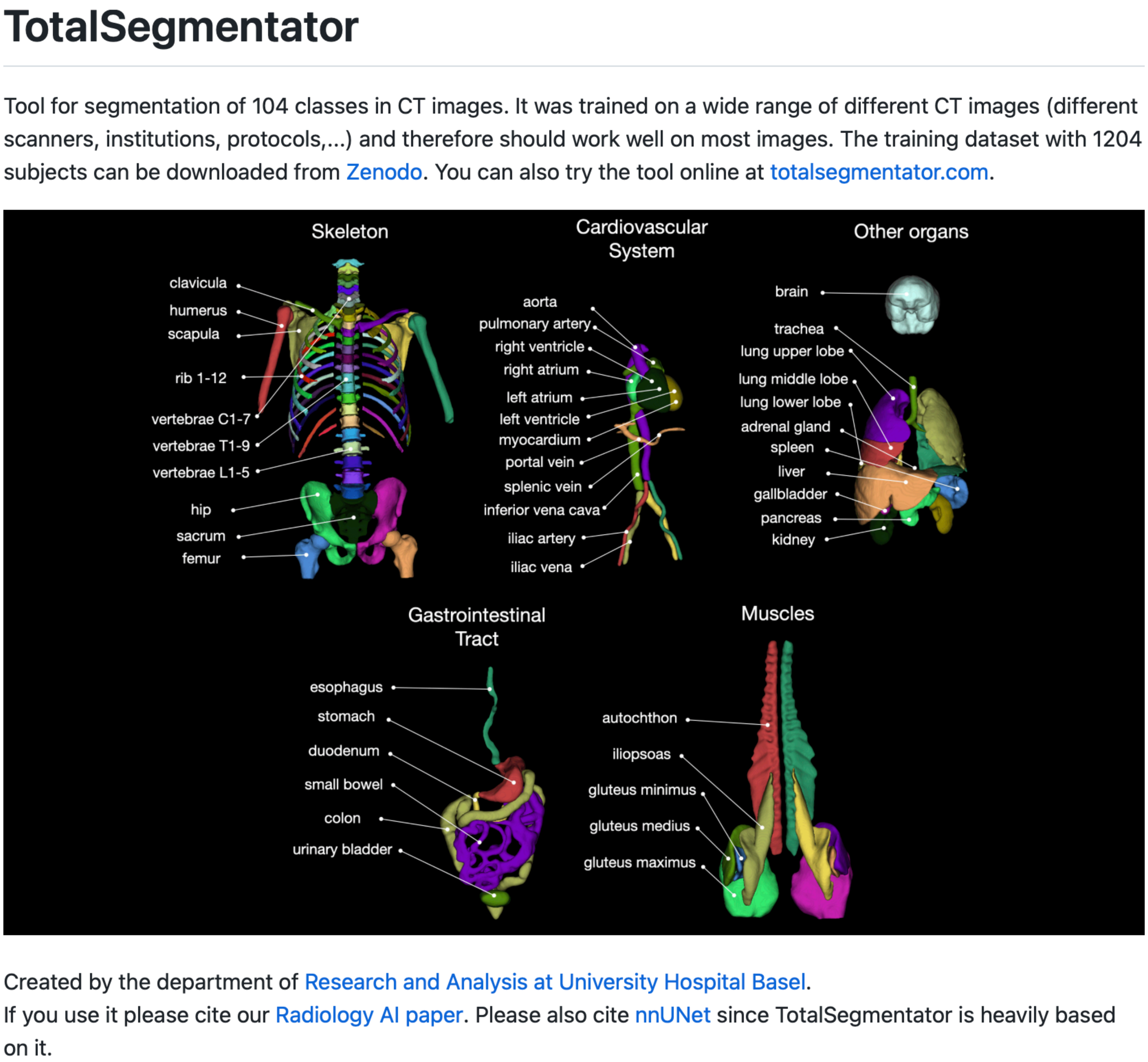
# 臓器分割
# 基盤モデル



**wasserth** bugfix: send stats after increase of pred counter ✓ 87560f3 5 days ago **277** commits

| | | |
|---|---|---|
| .github/workflows | add mapping for TotalSegmentator label names to SNOMED CT codes | last month |
| bin | add totalseg_setup to download_weights | 2 weeks ago |
| resources | add mapping for TotalSegmentator label names to SNOMED CT codes | last month |
| tests | update tests for fast statistics | 3 months ago |
| totalsegmentator | bugfix: send stats after increase of pred counter | 5 days ago |
| .dockerignore | add dockerfile; add flask server | last year |
| .gitignore | add test of normal run | 10 months ago |
| CHANGELOG.md | add skip_saving argument | 2 months ago |
| Dockerfile | Update pytorch base | last month |
| LICENSE | Initial commit | last year |
| README.md | add link to radiology ai paper | 2 weeks ago |

https://github.com/wasserth/TotalSegmentator

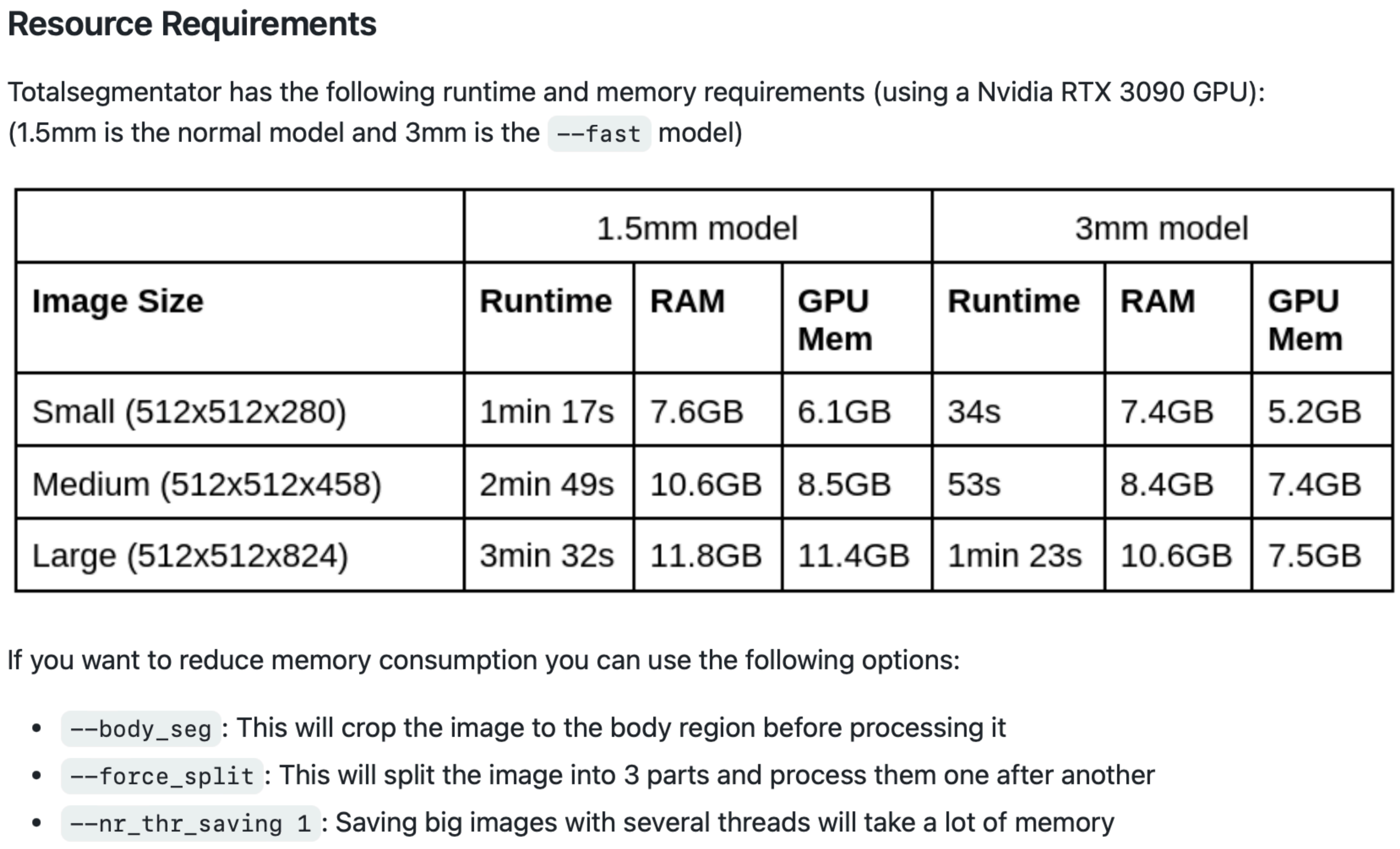


# TotalSegmentator

Tool for segmentation of 104 classes in CT images. It was trained on a wide range of different CT images (different scanners, institutions, protocols,...) and therefore should work well on most images. The training dataset with 1204 subjects can be downloaded from Zenodo. You can also try the tool online at totalsegmentator.com.

Created by the department of Research and Analysis at University Hospital Basel.
If you use it please cite our Radiology AI paper. Please also cite nnUNet since TotalSegmentator is heavily based on it.

https://github.com/wasserth/TotalSegmentator



## Resource Requirements

Totalsegmentator has the following runtime and memory requirements (using a Nvidia RTX 3090 GPU):
(1.5mm is the normal model and 3mm is the `--fast` model)

| | 1.5mm model | | | 3mm model | | |
|---|---|---|---|---|---|---|
| **Image Size** | **Runtime** | **RAM** | **GPU Mem** | **Runtime** | **RAM** | **GPU Mem** |
| Small (512x512x280) | 1min 17s | 7.6GB | 6.1GB | 34s | 7.4GB | 5.2GB |
| Medium (512x512x458) | 2min 49s | 10.6GB | 8.5GB | 53s | 8.4GB | 7.4GB |
| Large (512x512x824) | 3min 32s | 11.8GB | 11.4GB | 1min 23s | 10.6GB | 7.5GB |

If you want to reduce memory consumption you can use the following options:

- `--body_seg`: This will crop the image to the body region before processing it
- `--force_split`: This will split the image into 3 parts and process them one after another
- `--nr_thr_saving 1`: Saving big images with several threads will take a lot of memory

https://github.com/wasserth/TotalSegmentator